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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, polypeptide sequences encoded by these nucleic acids and uses thereof.

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NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such
5 polynucleotides, along with uses for these polynucleotides and proteins, for example in
therapeutic, diagnostic and research methods.

2. BACKGROUND

Technology aimed at the discovery of protein factors (including e.g., cytokines, such
10 as lymphokines, interferons, circulating soluble factors, chemokines, and interleukins) has
matured rapidly over the past decade. The now routine hybridization cloning and expression
cloning techniques clone novel polynucleotides "directly" in the sense that they rely on
information directly related to the discovered protein (i.e., partial DNA/amino acid sequence
of the protein in the case of hybridization cloning; activity of the protein in the case of
15 expression cloning). More recent "indirect" cloning techniques such as signal sequence
cloning, which isolates DNA sequences based on the presence of a now well-recognized
secretory leader sequence motif, as well as various PCR-based or low stringency
hybridization-based cloning techniques, have advanced the state of the art by making
available large numbers of DNA/amino acid sequences for proteins that are known to have
20 biological activity, for example, by virtue of their secreted nature in the case of leader
sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques,
or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in,
for example, diagnostics, forensics, gene mapping; identification of mutations responsible for
25 genetic disorders or other traits, to assess biodiversity, and to produce many other types of
data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel
30 isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules,
cloned genes or degenerate variants thereof, especially naturally occurring variants such as
allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize

one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-93. The polypeptides sequences are designated SEQ ID NO: 94-186. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is unknown or any of the four bases.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1-93 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1-93. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1-93 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-93. The sequence information can be a segment of any one of SEQ ID NO: 1-93 that uniquely identifies or represents the sequence information of SEQ ID NO: 1-93.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information are provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-93 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-93 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1-93; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1-93; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-93. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-93; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in SEQ ID NO: 94-186; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a

nucleotide sequence set forth in SEQ ID NO: 1-93; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%,
5 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention.
10 Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention
15 comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of
20 techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides
25 of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for
30 physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the

polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

5 Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

10 In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions.

15 The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a

20 method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention.

25 Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein.

30 Such methods can include, but are not limited to, assays for identifying compounds and other

substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provide methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2); for which they have a signature region (as set forth in Table 3); or for which they have homology to a gene family (as set forth in Table 4). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the

natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or

synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T
5 (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or
10 viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11
15 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from
20 about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures, or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a
25 sequence substantially similar to any one of SEQ ID NO: 1-93.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well
30 known in the art. Probes of the present invention, their preparation, and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular

Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-93. The sequence information
5 can be a segment of any one of SEQ ID NO: 1-93 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO: 1-93. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more
10 twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise
15 less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1+4^{25}$) times the increased probability for mismatch at each nucleotide position (3×25). The
20 probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

25 The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding
30 sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 500 amino acids, more preferably less than 200 amino acids more preferably less than 150 amino acids, and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include an initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant"(or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, e.g., recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by

comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions, or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells

chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include

an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers.

5
10 Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2): 134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

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Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell.. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

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The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

30

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

5 As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more
10 than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the
15 invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially
20 equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower
25 percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least
30 about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence

(e.g., via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J. (1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

5 The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

 The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the
10 introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

 As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based
15 systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

20 Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

25 The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO: 1-93; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO: 94-186; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO: 94-186. The polynucleotides of the present invention also include, but are not limited to, a
30 polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO: 1-93; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing as SEQ ID NO: 94-186; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a

polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 94-186. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1-93 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-93 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1-93 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpr, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least

about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-93, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e. specifically hybridize to) any one of the polynucleotides of the invention are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1-93, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO: 1-93 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO: 1-93, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

5 The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids
10 encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative
15 choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions
20 ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine
25 sequences useful for purifying the expressed protein.

 In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent
30 nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith,

Nucleic Acids Res. 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-93, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et

al. (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a

5 polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic

10 cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-93 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a

15 nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-93 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available

20 for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

25 The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods*

30 *in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced

or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

5 Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid
10 sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE NUCLEIC ACIDS

Another aspect of the invention pertains to isolated antisense nucleic acid molecules
15 that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1-93, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific
20 aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID NO: 94-186 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO: 1-93 are additionally provided.

25 In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence
30 of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO: 1-93), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of an mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of an mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (*v*), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (*v*), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)*w*, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or

genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific

5 interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed

10 on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III

15 promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641).

20 The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

25 In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a

30 mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO: 1-93). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is

complementary to the nucleotide sequence to be cleaved in an mRNA of SEQ ID NO: 1-93 (see, e.g., Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742). Alternatively, polynucleotides of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel *et al.*, (1993)

5 *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (e.g., promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med*
15 *Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed
20 using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting
25 replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

30 In another embodiment, PNAs of the invention can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-1124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

25

4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

30

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells
5 express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the
10 multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

15 The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one
20 of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1
25 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to
30 produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition,

Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the

control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (*gpt*) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No.

PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

5 4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 94-186 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO: 1-93 or the corresponding full length or mature protein. Polypeptides of the invention also
10 include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-93 or (b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 94-186 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention
15 also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 94-186 or the corresponding full length or mature protein; and "substantial equivalents" thereof (*e.g.*, with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least
20 about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 94-186.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein
25 may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding
30 sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide

sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic

sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying
5 the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate
10 prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated
15 polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, *e.g.*, Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*.
20 Polypeptide fragments that retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules
25 include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

30 In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 94-186.

The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

5 The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement,
10 insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or
15 deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in
20 biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the
25 disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego,
30 Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography.

5 The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

10 Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and
15 Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl
20 or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

25 The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic
30 agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes,

dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be
5 fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the
10 sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic
15 Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference), the GeneAtlas software (Molecular Simulations
20 Inc. (MSI), San Diego, CA) (Sanchez and Sali (1998) Proc. Natl. Acad. Sci., 95, 13597-13602; Kitson DH et al, (2000) "Remote homology detection using structural modeling – an evaluation" Submitted; Fischer and Eisenberg (1996) Protein Sci. 5, 947-955), Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark), and the Kyte-Doolittle hydrophobicity prediction
25 algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

30 The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a

fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention
5 and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein. In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide
10 sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprise one or more domains fused to sequences derived from a member of the immunoglobulin protein family. The
15 immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for
20 both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

25 A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together *in-frame* in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as
30 appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs

between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENE THERAPY

Mutations in the polynucleotides of the invention may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element.

5 Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA,
10 allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous
15 recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (*gpt*) gene.

The gene targeting or gene activation techniques which can be used in accordance with
20 this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

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4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science
30 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals,

can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals,
5 preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using
10 homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development,
15 through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the
20 invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination
25 are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals,
30 preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the

polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant

protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map
5 related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other
10 support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that
15 described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the
20 labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to
25 screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A
30 Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate.

- 5 In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

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4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

- A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or
15 inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of therapeutic compositions of the
20 present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

- 25 Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986;
30 Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of
 5 mouse and human interleukin- γ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current
 10 Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in
 15 Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and
 20 Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current
 25 Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

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4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent

stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder layer for the stem cell populations in culture or *in vivo*. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for

generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies
5 would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells
10 that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to
15 neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated
20 cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., *Differentiation*, 48: 173-182, (1991); Klug et al., *J. Clin.*
25 *Invest.*, 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow
30 differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell sources (including hematopoietic stem cells and embryonic stem cells) and

cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation,

those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of

bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as

stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with
5 vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such
10 tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and
15 conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

20 Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in:
25 Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

30 A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and

disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from
5 autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may
10 be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis,
15 graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic
20 contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present
25 invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animal models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health
30 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of

an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing
5 non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without
10 limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in
15 tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the
20 necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in
25 humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed.,
30 Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In

addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation,

those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, *Immunologic studies in Humans*); Takai et al., *J. Immunol.* 137:3494-3500, 1986; 5 Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al., *J. Immunol.* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., *J. Immunol.* 134:536-544, 1995; Inaba et al., *Journal of* 10 *Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology* 154:5071-5079, 1995; Porgador et al., *Journal of Experimental Medicine* 182:255-260, 1995; Nair et al., *Journal of Virology* 67:4062-4069, 1993; Huang et al., *Science* 264:961-965, 1994; Macatonia et al., *Journal of Experimental Medicine* 169:1255-1264, 1989; Bhardwaj et al., *Journal of Clinical Investigation* 94:797-807, 1994; and Inaba et al., *Journal of* 15 *Experimental Medicine* 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., *Cytometry* 13:795-808, 1992; Gorczyca et al., *Leukemia* 7:659-670, 1993; Gorczyca et al., *Cancer* 20 *Research* 53:1945-1951, 1993; Itoh et al., *Cell* 66:233-243, 1991; Zacharchuk, *Journal of Immunology* 145:4037-4045, 1990; Zamai et al., *Cytometry* 14:891-897, 1993; Gorczyca et al., *International Journal of Oncology* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., *Blood* 84:111-117, 1994; Fine et 25 al., *Cellular Immunology* 155:111-122, 1994; Galy et al., *Blood* 85:2770-2778, 1995; Toki et al., *Proc. Nat. Acad Sci. USA* 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related 30 activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present

invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of

cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

- 5 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, 10 A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

15

4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

- A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders 20 (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

- 25 Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

30

4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the

invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be
5 associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor
10 growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck
15 cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and
20 prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor
25 progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be
30 administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without

necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a

5 pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl
10 (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX),
15 Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic
20 treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

25 *In vitro* models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst.,
30 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-

97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

5 A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved
10 in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present
15 invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described
20 in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.
25

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

30 Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide

to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules.

- 5 Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis

methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, 5 *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.* 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein 10 permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

15 The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

20 4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For 25 example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular 30 small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population

expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this

invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other
5 autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

10 Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic
15 myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of
20 intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient
25 (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or
30 compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- 5 (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of
10 the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not
15 limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
- (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
- (viii) demyelinated lesions in which a portion of the nervous system is destroyed or
20 injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or
25 differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*,
30 e.g., choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set

forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of

the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity
5 which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for
10 diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to
15 inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of
20 the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that
25 hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The
30 array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

5 4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

15 The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would
20 reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies
25 or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

30 One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An

exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of

5 polypeptide administered per dose will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1 µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution,

10 dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

15 4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be

20 administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic

25 material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2,

30 G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming

growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use
5 in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-
10 inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hyl, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical
15 compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that
20 therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or
25 amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in
30 combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the

present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated

from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

5 Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of
10 conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or
15 elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water,
20 petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90%
25 by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a
30 pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or

other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene

glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable

polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with

inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

5 The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins
10 including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T
15 cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution.
20 Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

25 The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient.
30 Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not

increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μg to about 100 mg (preferably about 0.1 μg to about 10 mg, more preferably about 0.1 μg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For

5 compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a

10 viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the

15 methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted

20 medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate,

25 tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised

30 of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole

weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

5 A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate,
10 poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby
15 providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors
20 (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue
25 regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used
30 in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by

periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD_{50} and ED_{50} . Compounds which exhibit high therapeutic

indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form
5 employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective
10 concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be
15 administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention
20 will be in the range of about 0.01 $\mu\text{g/kg}$ to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 $\mu\text{g/kg}$ to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject
25 being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which
30 may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be

prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

5 Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab},
10 F_{ab}' and F_{(ab)2} fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a
15 reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively,
20 the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as the amino acid sequences shown in SEQ ID NO: 94-186, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that
25 contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the
30 antigenic peptide is a region of -related protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for

targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; 5 Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

10 A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: 15 A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

4.13.1 POLYCLONAL ANTIBODIES

20 For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a 25 recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response 30 include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory agents.

Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

4.13.2 MONOCLONAL ANTIBODIES

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly

myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine
5 phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a
10 medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984);
15 Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by
20 immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target
25 antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.
30 The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

4.13.3 HUMANIZED ANTIBODIES

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the

imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

4.13.4 HUMAN ANTIBODIES

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al., (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature

Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in

culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically
5 relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

4.13.5 F_{ab} FRAGMENTS AND SINGLE CHAIN ANTIBODIES

10 According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective
15 identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F_{(ab)₂} fragment produced by pepsin digestion of an antibody molecule;
20 (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_{(ab)₂} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

4.13.6 BISPECIFIC ANTIBODIES

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the
25 binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two
30 immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, *Nature*, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the

correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen
5 combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the
10 immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers
15 which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody
20 molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from
25 antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab'
30 fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB

derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992)

5 describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

10 Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced
15 at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a
20 light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et
25 al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an
30 immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific

antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further
5 binds tissue factor (TF).

4.13.7 HETEROCONJUGATE ANTIBODIES

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such
10 antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by
15 forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

4.13.8 EFFECTOR FUNCTION ENGINEERING

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-
25 dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis
30 and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

4.13.9 IMMUNOCONJUGATES

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

5 Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, 10 PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of 15 bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates 20 (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

25 In another embodiment, the antibody can be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

30

4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media"

refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as

5 magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for

10 recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means

15 chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application,

20 such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO: 1-93 or a representative

25 fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO: 1-93 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which

30 implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important

proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif.

There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with

nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise
5 contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for
10 binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization,
15 amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3
20 (1985); Tijssen, P., *Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay
25 format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the
30 necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the

following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO: 1-93, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

(a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and

(b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a
5 polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to
10 a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can
15 also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

20 Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in
25 the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be
30 selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein

encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed anti-peptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the

ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

5 Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO: 1-93. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide
10 sequences SEQ ID NO: 1-93 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used
15 in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the
20 cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective
25 genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The
30 technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal
5 map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

10 Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is
15 to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

20 Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any
25 surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed CovaLink NH. CovaLink NH is a polystyrene surface grafted with
30 secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound

to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) *Anal. Biochem.* 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.*, (1991). In this technology, a phosphoramidate bond is employed (Chu *et al.*, (1983) *Nucleic Acids Res.* 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ μ l) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. The single-stranded DNA solution is then dispensed into CovaLink NH strips (75 μ l/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 μ l added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) *Science* 251(4995) 767-73, incorporated herein by reference. Probes may

also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991),
5 requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to
10 generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

15 4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from
20 mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

25 The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are
30 passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The

results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*JI, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI**), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*JI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *Cvi*JI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 µg instead of 2-5 µg); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type

of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one
5 example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm
10 space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to
15 flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following
20 examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently,
25 the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5. EXAMPLES

5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences

5.2 EXAMPLE 2

Assemblage of Novel Nucleic Acids

The nucleic acids of the present invention, designated as SEQ ID NO: 1-93 were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST, gb pri, UniGene, and exons from public domain genomic sequences predicated by GenScan) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Further, inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), full-length gene sequences and their corresponding protein sequences were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTXY algorithm against Genbank (i.e., dbEST, gb pri, UniGene, and Genpept). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq,

Inc.). The full-length nucleotide sequences are shown in the Sequence Listing as SEQ ID NO: 1-93. The corresponding polypeptide sequences are SEQ ID NO: 94-186.

Table 1 shows the various tissue sources of SEQ ID NO: 1-93.

The nearest neighbor results for polypeptides encoded by SEQ ID NO: 1-93 (i.e. SEQ ID NO: 94-186) were obtained by a BLASTP (version 2.0a1 19MP-WashU) search against Genpept, Geneseq and SwissProt databases using BLAST algorithm. The nearest neighbor result showed the closest homologue with functional annotation for SEQ ID NO: 1-93. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1-93 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), polypeptides encoded by SEQ ID NO: 1-93 (i.e. SEQ ID NO: 94-186) were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the Pfam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) polypeptides encoded by SEQ ID NO: 1-93 (i.e. SEQ ID NO: 94-186) were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the product of all the e-value of similar domains found, the pFam score for the identified domain within the sequence, number of similar domains found, and the position of the domain in the SEQ ID NO: being interrogated..

The GeneAtlas™ software package (Molecular Simulations Inc. (MSI), San Diego, CA) was used to predict the three-dimensional structure models for the polypeptides encoded by SEQ ID NO: 1-93 (i.e. SEQ ID NO: 94-186). Models were generated by (1) PSI-BLAST which is a multiple alignment sequence profile-based searching developed by Altschul et al, (Nucl. Acids. Res. 25, 3389-3408 (1997)), (2) High Throughput Modeling (HTM) (Molecular Simulations Inc. (MSI) San Diego, CA,) which is an automated sequence and structure searching procedure (<http://www.msi.com/>), and (3) SeqFold™ which is a fold recognition method described by Fischer and Eisenberg (J. Mol. Biol. 209, 779-791 (1998)). This analysis was carried out, in part, by comparing the polypeptides of the invention with the known NMR (nuclear magnetic resonance) and x-ray crystal three-dimensional structures as

templates. Table 5 shows, "PDB ID", the Protein DataBase (PDB) identifier given to template structure; "Chain ID", identifier of the subcomponent of the PDB template structure; "Compound Information", information of the PDB template structure and/or its subcomponents; "PDB Function Annotation" gives function of the PDB template as annotated by the PDB files (<http://www.rcsb.org/PDB/>); start and end amino acid position of the protein sequence aligned; PSI-BLAST score, the verify score, the SeqFold score, and the Potential(s) of Mean Force (PMF). The verify score is produced by GeneAtlas™ software (MSI), is based on Dr. Eisenberg's Profile-3D threading program developed in Dr. David Eisenberg's laboratory (US patent no. 5,436,850 and Luthy, Bowie, and Eisenberg, Nature, 356:83-85 (1992)) and a publication by R. Sanchez and A. Sali, Proc. Natl. Acad. Sci. USA, 95:13597-12502. The verify score produced by GeneAtlas normalizes the verify score for proteins with different lengths so that a unified cutoff can be used to select good models as follows:

Verify score (normalized) = (raw score – 1/2 high score)/(1/2 high score)

The PFM score, produced by GeneAtlas™ software (MSI), is a composite scoring function that depends in part on the compactness of the model, sequence identity in the alignment used to build the model, pairwise and surface mean force potentials (MFP). As given in Table 5, a verify score between 0 to 1.0, with 1 being the best, represents a good model. Similarly, a PMF score between 0 to 1.0, with 1 being the best, represents a good model. A SeqFold™ score of more than 50 is considered significant. A good model may also be determined by one of skill in the art based all the information in Table 5 taken in totality.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determined from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et al, as reference, were obtained for the polypeptide sequences. Table 6 shows the position of the last

amino acid of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

Table 7 correlates each of SEQ ID NO: 1-93 to a specific chromosomal location.

Table 8 is a correlation table of the novel polynucleotide sequences SEQ ID NO: 1-93, novel polypeptide sequences SEQ ID NO: 94-186, and their corresponding priority nucleotide sequences in the priority application USSN 09/728,952, herein incorporated by reference in its entirety.

TABLE 1

Tissue Origin	RNA/Tissue Source	Library Name	SEQ ID NO:
adult brain	GIBCO	AB3001	26 40 43
adult brain	GIBCO	ABD003	2-5 40 47 54-55 57
adult brain	Clontech	ABR001	2 39 85
adult brain	Clontech	ABR006	3-4 40 47 69 80
adult brain	Clontech	ABR008	1 3-6 10 12 15-16 30-31 40 42 47 50 54-55 57 67-68 72-74 86
adult brain	Invitrogen	ABR013	1
adult brain	Invitrogen	ABR015	47
brain	Invitrogen	ABR016	57
adult brain	Invitrogen	ABT004	10 15 42 47
cultured preadipocytes	Stratagene	ADP001	43
adrenal gland	Clontech	ADR002	2 24 39-40 43 46 50 56 68 73
adult heart	GIBCO	AHR001	2-5 14 40 43 49 60 64-65 71
adult kidney	GIBCO	AKD001	2 7 15 19 40 43-44 49-51 53 71 77
adult kidney	Invitrogen	AKT002	2-5 39-40 43 49-50 53 57 83 85
adult lung	GIBCO	ALG001	39-40 43-44 85
lymph node	Clontech	ALN001	38 44
young liver	GIBCO	ALV001	7
adult liver	Invitrogen	ALV002	7 9 38 43 47 52 82
adult liver	Clontech	ALV003	56
adult ovary	Invitrogen	AOV001	2-5 7 15-18 38-40 43-44 49 52 56-57 77 85
placenta	Invitrogen	APL002	44
adult spleen	GIBCO	ASP001	10 38 43 50 61-62
testis	GIBCO	ATS001	24 44 53 56
adult bladder	Invitrogen	BLD001	15 56
bone marrow	Clontech	BMD001	40-41 48 50 57-58
bone marrow	Clontech	BMD002	2-5 17-18 24 30-31 38 41 43 48 53-55 58-60 68 73 86
Mixture of 16 tissues- mRNAs	Various Vendors*	CTL016	24
adult cervix	BioChain	CVX001	11 15 39-40 54-55 63 66 71 77 82 85
endothelial cells	Stratagene	EDT001	2-4 15-16 40 43-44 47 50 57
fetal brain	Clontech	FBR006	2-6 10 13 16 31 42 46 49 66-68 73 78 86
fetal brain	Invitrogen	FBT002	24 44 47 61-62
fetal heart	Invitrogen	FHR001	43 68 73 77 86
fetal kidney	Clontech	FKD001	44 72
fetal kidney	Clontech	FKD002	49 66 77 88

Tissue Origin	RNA/Tissue Source	Library Name	SEQ ID NO:
fetal lung	Clontech	FLG001	64-65
fetal lung	Invitrogen	FLG003	15 39 63-65 71-72 85
fetal liver-spleen	Columbia University	FLS001	2-5 7 9 22-24 26 35 38-41 44-46 49 51-52 54-55 59-62 68 73 77 85 87
fetal liver-spleen	Columbia University	FLS002	7 22-24 35 39-41 43-46 54-55 59-62 67 73 76 83-85
fetal liver-spleen	Columbia University	FLS003	26
fetal liver	Invitrogen	FLV001	22-24 44 49-50 52 61-62
fetal liver	Clontech	FLV004	41 68 73
fetal muscle	Invitrogen	FMS001	3-5 15 24 50 52
fetal muscle	Invitrogen	FMS002	56
fetal skin	Invitrogen	FSK001	3-5 15 22-24 39-40 44 51-53 57 61-62 79-82 85
fetal skin	Invitrogen	FSK002	3-5 31 49 72
fetal spleen	BioChain	FSP001	43
umbilical cord	BioChain	FUC001	3-5 10 15 39-40 44 72
fetal brain	GIBCO	HFB001	2 10 40 47 50 63 77 86
macrophage	Invitrogen	HMP001	43
infant brain	Columbia University	IB2002	1 6 12 31 40 42 44 47 52 56 61-62 66 72 82 86
infant brain	Columbia University	IB2003	50 56 86
infant brain	Columbia University	IBS001	72
fibroblast	Stratagene	LFB001	39-40 49 57
lung tumor	Invitrogen	LGT002	3-5 38-40 43 49 54-57 85
lymphocytes	ATCC	LPC001	58
leukocyte	GIBCO	LUC001	3-5 15 17-19 26 31 38 43-44 50 54-55 58
leukocyte	Clontech	LUC003	41 43
melanoma from cell line ATCC #CRL 1424	Clontech	MEL004	2 57
mammary gland	Invitrogen	MMG001	3-5 15 30 38 43-44 47 50 54-57 71
induced neuron cells	Stratagene	NTD001	42
neuronal cells	Stratagene	NTU001	1 24 42 72
pituitary gland	Clontech	PIT004	47
placenta	Clontech	PLA003	14 19 43 63-65
rectum	Invitrogen	REC001	10 22-24 61-62 68 73
salivary gland	Clontech	SAL001	40
small intestine	Clontech	SIN001	2 22-24 30 66 68-69 73 84
skeletal muscle	Clontech	SKM001	3-5 40 51
spinal cord	Clontech	SPC001	40 45 50 70
adult spleen	Clontech	SPLc01	8 15-16 40 43 68 73 86
stomach	Clontech	STO001	57-58 75
thalamus	Clontech	THA002	30 51 57 82
thymus	Clontech	THM001	2-5 24 43 86
thymus	Clontech	THMc02	2 15 33 38 44 46 48-49 66 73 86
thyroid gland	Clontech	THR001	2 7 15 39-40 54-55 58 69 71 86-87
trachea	Clontech	TRC001	44 54-55
uterus	Clontech	UTR001	8

The 16 tissue/mRNAs and their vendor sources are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) Normal adult kidney mRNA (Invitrogen), 3) Normal fetal brain mRNA (Invitrogen), 4) Normal adult liver mRNA (Invitrogen), 5) Normal fetal kidney mRNA (Invitrogen), 6) Normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) Human bone marrow mRNA (Clontech), 10) Human leukemia lymphoblastic mRNA (Clontech), 11) Human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human so\spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

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TABLE 2

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
94	gi15080005	Homo sapiens	nogo receptor, clone MGC:19831 IMAGE:4040540, mRNA, complete cds.	1305	100
94	gi12407653	Homo sapiens	Nogo receptor mRNA, complete cds.	1305	100
94	gi15385806	Homo sapiens	Predicted human Nogo receptor gene	1305	100
95	AAB53348	Homo sapiens	Human colon cancer antigen protein sequence SEQ ID NO:888.	1864	99
95	AAG73782	Homo sapiens	Human colon cancer antigen protein SEQ ID NO:4546.	1864	99
95	gi15928738	Mus musculus	RIKEN cDNA 1110064N10 gene	1407	94
96	gi5531827	Homo sapiens	p47	1694	98
96	gi12803909	Homo sapiens	p47, clone MGC:3347 IMAGE:3635947, mRNA, complete cds.	1689	98
96	gi8979825	Homo sapiens	Human DNA sequence from clone RP4-776F14 on chromosome 20p12.2-13. Contains the 5' end of the FKBP1A gene for FK506-binding protein 1A (12kD), the gene for P47 protein, part of a novel member of the PTPNS (protein tyrosine phosphatase, non-receptor type substrate 1) gene family, ESTs, STSs, GSSs and two CpG islands, complete sequence.	1689	98
97	gi7022811	Homo sapiens	cDNA FLJ10649 fis, clone NT2RP2005835, weakly similar to SHP1 PROTEIN.	1541	99
97	AAB93031	Homo sapiens	Human protein sequence SEQ ID NO:11803.	1541	99

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
97	gi6563210	Homo sapiens	p47 protein mRNA, complete cds.	813	90
98	AAB42552	Homo sapiens	Human ORFX ORF2316 polypeptide sequence SEQ ID NO:4632.	826	90
98	AAB12868	Homo sapiens	Human P47 amino acid sequence.	815	89
98	gi12803909	Homo sapiens	p47, clone MGC:3347 IMAGE:3635947, mRNA, complete cds.	806	89
99	gi12836289	Mus musculus	putative	347	68
99	gi1006665	Homo sapiens	H.sapiens mRNA for transcript associated with monocyte to macrophage differentiation.	346	68
99	gi7290797	Drosophila melanogaster	CG4615 gene product	159	37
100	gi7020785	Homo sapiens	cDNA FLJ20581 fis, clone REC00491.	2996	99
100	gi2988399	Homo sapiens	Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.	1874	60
100	gi666014	Homo sapiens	Human SA mRNA for SA gene product, complete cds.	1873	60
101	gi5915662	Homo sapiens	integrin alpha 11 subunit precursor (ITGA11) mRNA, complete cds.	497	98
101	AAB30929	Homo sapiens	Amino acid sequence of a human alpha11 integrin chain.	497	98
101	AAB50085	Homo sapiens	Human A259.	497	98
102	gi431608	Oncorhynchus mykiss	complement component C3	223	30
102	gi213373	Naja naja	complement component C3	209	29
102	gi755815	Gallus gallus	complement C3 precursor	206	31
103	gi7020791	Homo sapiens	cDNA FLJ20584 fis, clone KAT09532.	1052	100
103	gi14250646	Homo sapiens	Similar to hypothetical protein FLJ20584, clone MGC:3446 IMAGE:3627081, mRNA, complete cds.	810	89
103	gi13278391	Mus musculus	Similar to hypothetical protein FLJ20584	729	70
104	gi10799397	Homo sapiens	chromosome 19, BAC BC349142 (CTC-518B2), complete sequence.	1404	99
104	gi6249632	Homo sapiens	kallikrein-like protein 5 gene, alternative splice products, complete cds.	1404	99
104	gi11244770	Homo sapiens	serine protease gene cluster, complete sequence.	1301	100
105	gi12310959	Homo sapiens	unnamed protein product	2095	100
105	AAY33741	Homo sapiens	Beta-secretase.	1694	99
105	AAB61142	Homo sapiens	Human NOV12 protein.	2088	99
106	gi14017771	Homo sapiens	mRNA for KIAA1776 protein (fibrillin3), complete cds.	2940	55
106	gi762831	Mus musculus	fibrillin 2	2153	50
106	gi3688648	Mus musculus	mutant fibrillin-1	2102	46

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
107	AAB24199	Homo sapiens	Human GTP-binding protein-coupled receptor BG3 protein sequence.	925	100
107	gi7328047	Homo sapiens	mRNA; cDNA DKFZp434B1272 (from clone DKFZp434B1272); partial cds.	760	100
107	AAB01249	Homo sapiens	Human EMR1 hormone receptor.	254	41
108	AAAY93948	Homo sapiens	Amino acid sequence of a lectin ss3939 polypeptide.	1979	98
108	AAE03651	Homo sapiens	Human extracellular matrix and cell adhesion molecule-15 (XMAD-15).	1979	98
108	AAAY91490	Homo sapiens	Human secreted protein sequence encoded by gene 40 SEQ ID NO:163.	1969	98
109	gi6979311	Homo sapiens	cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds.	2875	99
109	AAAY82776	Homo sapiens	Human chordin related protein (Clone dj167_19).	2875	99
109	AAAY53034	Homo sapiens	Human secreted protein clone dj167_19 protein sequence SEQ ID NO:74.	2875	99
110	AAW99070	Homo sapiens	Human PIGR-1.	678	100
110	gi12405479	Homo sapiens	unnamed protein product	672	99
110	AAB31568	Homo sapiens	Amino acid sequence of human leukocyte surface receptor (LSR).	672	99
111	AAW99070	Homo sapiens	Human PIGR-1.	612	100
111	gi12405479	Homo sapiens	unnamed protein product	606	99
111	AAB31568	Homo sapiens	Amino acid sequence of human leukocyte surface receptor (LSR).	606	99
112	gi9663958	Homo sapiens	mRNA for cysteinyl leukotriene CysLT2 receptor, complete cds; cDNA: PSEC0146 from clone PLACE1006979.	1788	100
112	gi10442008	Homo sapiens	cysteinyl leukotriene receptor CYSLT2 gene, complete cds.	1788	100
112	gi14582394	Homo sapiens	cysteinyl leukotriene receptor type 2 (CYSLT2) gene, complete cds.	1788	100
113	gi4580013	Homo sapiens	TRAF4-associated factor 2 mRNA, partial cds.	1432	70
113	gi4689252	Homo sapiens	sorting nexin 6 (SNX6) mRNA, complete cds.	1432	70
113	AAB58368	Homo sapiens	Lung cancer associated polypeptide sequence SEQ ID 706.	1432	70
114	gi14042571	Homo sapiens	cDNA FLJ14791 fis, clone NT2RP4001064, weakly similar to SYNAPTONEMAL COMPLEX PROTEIN SC65.	3090	92
114	gi14272600	Homo sapiens	unnamed protein product	3090	92
114	AAB93215	Homo sapiens	Human protein sequence SEQ	3090	92

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			ID NO:12194.		
115	gi12053261	Homo sapiens	mRNA; cDNA DKFZp434A196 (from clone DKFZp434A196); complete cds.	1502	76
115	gi9754902	Mus musculus	espin	1462	78
115	gi5327035	Homo sapiens	Human DNA sequence from clone 202O8 on chromosome 1p36.11-36.31. Contains the 5' part of a gene for a novel rat Espin LIKE protein containing Ank repeats, the gene for the ortholog of rodent HES2 (Hairy and Enhancer of Split 2) and the 5' end of the gene for HBACH (Brain Acyl-CoA Hydrolase (Acyl Coenzyme A Thioester Hydrolase, EC 3.1.2.2). Contains ESTs, GSSs and putative CpG islands, complete sequence.	2451	69
116	gi5327035	Homo sapiens	Human DNA sequence from clone 202O8 on chromosome 1p36.11-36.31. Contains the 5' part of a gene for a novel rat Espin LIKE protein containing Ank repeats, the gene for the ortholog of rodent HES2 (Hairy and Enhancer of Split 2) and the 5' end of the gene for HBACH (Brain Acyl-CoA Hydrolase (Acyl Coenzyme A Thioester Hydrolase, EC 3.1.2.2). Contains ESTs, GSSs and putative CpG islands, complete sequence.	3530	91
116	gi4375916	Homo sapiens	H.sapiens gene from PAC 163M9, similar to rat Espin gene, partial cds.	3333	93
116	gi3320122	Rattus norvegicus	espin	3269	75
117	AAE01020	Homo sapiens	Human pif-1 type helicase protein.	1875	78
117	gi5523990	Homo sapiens	DNA helicase homolog (PIF1) mRNA, partial cds.	1842	97
117	gi7295800	Drosophila melanogaster	CG3238 gene product	1196	46
118	AAE01020	Homo sapiens	Human pif-1 type helicase protein.	911	99
118	gi5523990	Homo sapiens	DNA helicase homolog (PIF1) mRNA, partial cds.	834	85
118	gi7295800	Drosophila melanogaster	CG3238 gene product	620	46
119	gi10434929	Homo sapiens	cDNA FLJ13080 fis, clone NT2RP3002007, weakly similar to SAP1 PROTEIN.	3490	99
119	AAB94461	Homo sapiens	Human protein sequence SEQ ID NO:15114.	3490	99
119	AAB95164	Homo sapiens	Human protein sequence SEQ	3483	99

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			ID NO:17211.		
120	gi29715	Homo sapiens	Human mRNA for pro-cathepsin L (major excreted protein MEP).	1597	87
120	gi190418	Homo sapiens	Human cathepsin L gene, complete cds.	1597	87
120	AAW47031	Homo sapiens	Human procathepsin L.	1597	87
121	AAG63220	Homo sapiens	Amino acid sequence of a human lipid metabolism enzyme.	4116	99
121	gi15862521	Homo sapiens	unnamed protein product	3834	99
121	gi14715017	Homo sapiens	Similar to phospholipase C, delta, clone MGC:9744 IMAGE:3854215, mRNA, complete cds.	3195	99
122	gi13676465	Macaca fascicularis	hypothetical protein	495	41
122	gi2253280	Bos taurus	butyrophilin	490	44
122	gi162773	Bos taurus	butyrophilin precursor	487	44
123	AAB25682	Homo sapiens	Human secreted protein sequence encoded by gene 18 SEQ ID NO:71.	1616	96
123	gi2982501	Homo sapiens	mRNA for neuropathy target esterase.	952	65
123	AAY70474	Homo sapiens	Human cyclic nucleotide-associated protein-2 (CNAP-2).	952	65
124	AAB24084	Homo sapiens	Human PRO1317 protein sequence SEQ ID NO:71.	1739	100
124	AAB37984	Homo sapiens	Human secreted protein encoded by gene 1 clone HTDAA93.	1739	100
124	AAY99418	Homo sapiens	Human PRO1317 (UNQ783) amino acid sequence SEQ ID NO:277.	1739	100
126	gi292057	Homo sapiens	Human EBV induced G-protein coupled receptor (EBI2) mRNA, complete cds.	196	40
126	AAR54080	Homo sapiens	Epstein Barr virus induced (EBI-2) polypeptide.	196	40
126	AAW53623	Homo sapiens	Epstein Barr virus induced gene 2 (EBI-2).	196	40
127	gi63426	Gallus gallus	lysozyme	428	43
127	gi12843551	Mus musculus	putative	367	41
127	gi12578467	Homo sapiens	unnamed protein product	366	40
128	gi13195239	Homo sapiens	complement factor H-related protein 5 mRNA, complete cds.	1492	100
128	gi180498	Homo sapiens	Human complement H factor mRNA, complete cds.	585	51
128	gi309166	Mus musculus	complement factor H-related protein	583	44
129	gi11275568	Homo sapiens	mucin 5B (MUC5B) gene, partial cds.	7389	99
129	gi3789927	Homo sapiens	mucin (MUC5B) mRNA, partial cds.	7176	97
129	gi4038587	Homo sapiens	partial MUC5B gene, exon 1-29.	7151	98
130	gi2853301	Homo sapiens	mucin (MUC3) mRNA, partial cds.	3473	77
130	gi6466801	Homo sapiens	intestinal mucin 3 (MUC3) gene,	3218	76

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			partial cds.		
130	gi9929920	Homo sapiens	MUC3A mRNA for intestinal mucin, partial cds.	2904	100
131	gi1235725	Homo sapiens	mRNA for macrophage lectin 2, complete cds.	1014	79
131	gi204303	Rattus norvegicus	Gal/GalNAc-specific lectin precursor	879	55
131	gi15928688	Mus musculus	Similar to macrophage galactose N-acetyl-galactosamine specific lectin	806	51
132	AAB43122	Homo sapiens	Human ORFX ORF2886 polypeptide sequence SEQ ID NO:5772.	3123	94
132	gi11177164	Mus musculus	polydom protein	2668	77
132	gi14198157	Mus musculus	polydomain protein	2668	77
133	gi7110160	Homo sapiens	guanine nucleotide exchange factor (LARG) mRNA, complete cds.	7932	99
133	AAW64468	Homo sapiens	Human secreted protein from clone CW420 2.	6937	99
133	AAB90743	Homo sapiens	Human CW420 2 protein sequence SEQ ID 186.	6937	99
134	AAM00758	Homo sapiens	Human bone marrow protein, SEQ ID NO: 121.	1804	100
134	gi13937956	Homo sapiens	clone MGC:14710 IMAGE:4250452, mRNA, complete cds.	1677	67
134	gi32645	Homo sapiens	Human mRNA for 56-KDa protein induced by interferon.	1671	67
135	gi4580013	Homo sapiens	TRAF4-associated factor 2 mRNA, partial cds.	1432	70
135	gi4689252	Homo sapiens	sorting nexin 6 (SNX6) mRNA, complete cds.	1432	70
135	AAB58368	Homo sapiens	Lung cancer associated polypeptide sequence SEQ ID 706.	1432	70
136	gi6165618	Homo sapiens	gamma-interferon inducible lysosomal thiol reductase (GILT) mRNA, complete cds.	1149	100
136	AAB58455	Homo sapiens	Lung cancer associated polypeptide sequence SEQ ID 793.	1149	100
136	AAY71214	Homo sapiens	Human irritable bowel disease related polypeptide IMX44.	1142	99
137	gi14042571	Homo sapiens	cDNA FLJ14791 fis, clone NT2RP4001064, weakly similar to SYNAPTONEMAL COMPLEX PROTEIN SC65.	3090	92
137	gi14272600	Homo sapiens	unnamed protein product	3090	92
137	AAB93215	Homo sapiens	Human protein sequence SEQ ID NO:12194.	3090	92
138	gi35330	Homo sapiens	H.sapiens mRNA for procarboxypeptidase A1.	1198	97
138	gi2299431	unidentified	unnamed protein product	1198	97
138	AAW01504	Homo sapiens	Wild-type human pancreatic carboxypeptidase 1.	1198	97

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
139	gi12053081	Homo sapiens	mRNA; cDNA DKFZp434L0718 (from clone DKFZp434L0718); complete cds.	2766	100
139	AAY10853	Homo sapiens	Amino acid sequence of a human secreted protein.	417	87
139	AAB42173	Homo sapiens	Human ORFX ORF1937 polypeptide sequence SEQ ID NO:3874.	202	39
141	AAB93455	Homo sapiens	Human protein sequence SEQ ID NO:12712.	546	100
141	gi599683	Bos taurus	Cleavage and Polyadenylation specificity factor (CPSF) 100kD subunit	546	100
141	gi2331036	Mus musculus	cleavage and polyadenylation specificity factor	538	98
142	gi29715	Homo sapiens	Human mRNA for pro-cathepsin L (major excreted protein MEP).	1597	87
142	gi190418	Homo sapiens	Human cathepsin L gene, complete cds.	1597	87
142	AAW47031	Homo sapiens	Human procathepsin L.	1597	87
143	gi1103582	Homo sapiens	H.sapiens mRNA for ARP1 protein.	1055	100
143	gi9843764	Homo sapiens	Human DNA sequence from clone RP4-583P15 on chromosome 20 Contains ESTs, STSs, GSSs and ten CpG islands. Contains the TNFRSF6B gene for tumor necrosis factor receptor 6b (decoy), the 3' part of the KIAA1088 gene, the ARFRP1 gene for ADP-ribosylation factor related protein 1, two genes for novel proteins, the gene for a GLUT4 enhancer factor and the gene for a novel zinc finger protein similar to rat RIN ZF and the gene for a novel BTB/POZ domain containing zinc finger protein, complete sequence.	1055	100
143	gi7012932	Homo sapiens	SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds.	1055	100
144	gi13623501	Homo sapiens	clone MGC:12837 IMAGE:4124286, mRNA, complete cds.	1008	100
144	gi571466	Rattus norvegicus	phospholipase C delta-4	741	73
144	gi1304189	Rattus norvegicus	phospholipase C delta4	734	72
145	gi12053129	Homo sapiens	mRNA; cDNA DKFZp434C2322 (from clone DKFZp434C2322); complete	1185	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			cds.		
145	gi16117338	Homo sapiens	vWF-CP(ADAMTS13) mRNA for von Willebrand factor-cleaving protease, complete cds.	1185	100
145	gi15963593	Homo sapiens	ADAMTS13 (ADAMTS13) mRNA, complete cds, alternatively spliced.	1185	100
146	gi6624133	Homo sapiens	PAC clone RP4-539M6 from 22, complete sequence.	322	98
146	gi4164418	Rattus norvegicus	45 kDa secretory protein	247	75
146	gi13543184	Mus musculus	Unknown (protein for MGC:6302)	245	75
147	AAB98640	Homo sapiens	Human autoimmune disease associated protein 16.	766	99
147	gi7768747	Homo sapiens	genomic DNA, chromosome 21q, section 92/105.	292	68
147	gi12654677	Homo sapiens	U2(RNU2) small nuclear RNA auxillary factor 1 (non-standard symbol), clone MGC:2223 IMAGE:3534272, mRNA, complete cds.	292	68
148	AAB98640	Homo sapiens	Human autoimmune disease associated protein 16.	757	98
148	gi7768747	Homo sapiens	genomic DNA, chromosome 21q, section 92/105.	691	79
148	gi12654677	Homo sapiens	U2(RNU2) small nuclear RNA auxillary factor 1 (non-standard symbol), clone MGC:2223 IMAGE:3534272, mRNA, complete cds.	691	79
149	AAG63220	Homo sapiens	Amino acid sequence of a human lipid metabolism enzyme.	4116	99
149	gi15862521	Homo sapiens	unnamed protein product	3834	99
149	gi14715017	Homo sapiens	Similar to phospholipase C, delta, clone MGC:9744 IMAGE:3854215, mRNA, complete cds.	3195	99
150	gi11493982	Homo sapiens	TLH29 protein precursor (TLH29) mRNA, complete cds.	538	95
150	AAY12410	Homo sapiens	Human 5' EST secreted protein SEQ ID NO:441.	527	94
150	AAG89188	Homo sapiens	Human secreted protein, SEQ ID NO: 308.	505	98
151	gi11863671	Homo sapiens	mRNA for putative tumor stroma and activated macrophage protein DLM-1 (DLM-1 gene).	1362	99
151	gi13160377	Homo sapiens	Human DNA sequence from clone RP4-718J7 on chromosome 20q13.31-13.33 Contains the PCK1 gene for soluble phosphoenolpyruvate carboxykinase 1, part of a novel gene similar to mouse DLM-1	1246	94

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			(tumour stroma and activated macrophage protein), the 3' end of the TMEPAI gene encoding an androgen induced 1b transmembrane protein (PMEPA1), two putative novel genes, a CpG island, ESTs, STSs and GSSs, complete sequence.		
151	gi6563280	Mus musculus	tumor stroma and activated macrophage protein DLM-1	565	51
152	gi13592175	Leishmania major	ppg3	220	26
152	gi601930	Oryctolagus cuniculus	neurofilament-H	184	25
152	gi5420387	Leishmania major	proteophosphoglycan	186	26
153	AAB42658	Homo sapiens	Human ORFX ORF2422 polypeptide sequence SEQ ID NO:4844.	8542	99
153	gi15077826	Homo sapiens	rap guanine nucleotide exchange factor mRNA, complete cds.	7521	98
153	gi6650766	Homo sapiens	PDZ domain-containing guanine nucleotide exchange factor I mRNA, complete cds.	6208	100
154	gi1657312	Homo sapiens	H.sapiens mRNA for FAA protein.	7165	98
154	AAW48663	Homo sapiens	Fanconi anaemia of complementation group A protein.	7165	98
154	gi2230888	Homo sapiens	H.sapiens Fanconi anaemia group A gene, exon 1 and joined CDS.	7162	98
155	gi1657312	Homo sapiens	H.sapiens mRNA for FAA protein.	4876	100
155	AAW48663	Homo sapiens	Fanconi anaemia of complementation group A protein.	4876	100
155	gi2230888	Homo sapiens	H.sapiens Fanconi anaemia group A gene, exon 1 and joined CDS.	4873	99
156	AAB60469	Homo sapiens	Human cell cycle and proliferation protein CCYPR-17, SEQ ID NO:17.	846	100
156	AAY76403	Homo sapiens	Fragment of human secreted protein encoded by gene 85.	600	100
156	gi12861086	Mus musculus	putative	512	66
157	gi16041826	Homo sapiens	interferon regulatory factor 2, clone MGC:9260 IMAGE:3920890, mRNA, complete cds.	1626	100
157	gi33967	Homo sapiens	Human mRNA for interferon regulatory factor-2 (IRF-2).	1612	99
157	AAB70698	Homo sapiens	Human IRF-2 protein sequence SEQ ID NO:7.	1612	99
158	gi16041826	Homo sapiens	interferon regulatory factor 2, clone MGC:9260	892	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			IMAGE:3920890, mRNA, complete cds.		
158	gi33967	Homo sapiens	Human mRNA for interferon regulatory factor-2 (IRF-2).	892	100
158	AAB70698	Homo sapiens	Human IRF-2 protein sequence SEQ ID NO:7.	892	100
159	gi7637906	Homo sapiens	Ral guanine nucleotide exchange factor RalGPS1A mRNA, complete cds.	2768	100
159	gi2224643	Homo sapiens	Human mRNA for KIAA0351 gene, complete cds.	1758	100
159	gi11321424	Mus musculus	Ral-A exchange factor RalGPS2	1228	70
160	gi7716046	Mus musculus	regulator factor X 5	606	38
160	gi840789	Homo sapiens	H.sapiens mRNA for DNA binding regulatory factor.	580	35
160	AAB40374	Homo sapiens	Human ORFX ORF138 polypeptide sequence SEQ ID NO:276.	565	98
161	gi13436464	Homo sapiens	Similar to cleavage and polyadenylation specific factor 6, 68kD subunit, clone MGC:4425 IMAGE:2958189, mRNA, complete cds.	364	48
161	gi12653847	Homo sapiens	Similar to cleavage and polyadenylation specific factor 6, 68kD subunit, clone MGC:1242 IMAGE:3506481, mRNA, complete cds.	364	48
161	gi871299	Homo sapiens	H.sapiens HPBRII-4 mRNA.	359	47
162	gi4699969	Homo sapiens	PAC clone RP4-568B10 from 7q31.1-q31.2, complete sequence.	1379	99
162	gi13876344	Mus musculus	protocadherin gamma A9	265	28
162	gi14625441	Homo sapiens	mRNA for KIAA1773 protein (dachous homologue), complete cds.	246	29
163	gi7959299	Homo sapiens	mRNA for KIAA1516 protein, partial cds.	8192	99
163	gi11065786	Homo sapiens	phospholipase C epsilon mRNA, partial cds.	8186	99
163	gi10518469	Homo sapiens	phosphoinositide-specific phospholipase C PLC-epsilon mRNA, complete cds.	8127	99
164	gi386827	Homo sapiens	Human inhibin beta-B-subunit gene, exon 2, and complete cds.	2197	99
164	AAY92017	Homo sapiens	Human inhibin B beta subunit.	2197	99
164	AAY92019	Homo sapiens	Human activin B subunit.	2197	99
165	gi16040975	Homo sapiens	HIF-3A mRNA for hypoxia-inducible factor-3 alpha, complete cds.	1480	99
165	gi4558637	Homo sapiens	chromosome 19, BAC 82621 (CIT-B-139a18), complete sequence.	1480	99
165	gi14042618	Homo sapiens	cDNA FLJ14819 fis, clone OVARC1000241, moderately similar to HYPOXIA-	1476	98

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			INDUCIBLE FACTOR 1 ALPHA.		
166	gi10434070	Homo sapiens	cDNA FLJ12529 fis, clone NT2RM4000156, weakly similar to H.sapiens HPBR11-7 gene.	975	98
166	AAB94099	Homo sapiens	Human protein sequence SEQ ID NO:14318.	975	98
166	gi13436464	Homo sapiens	Similar to cleavage and polyadenylation specific factor 6, 68kD subunit, clone MGC:4425 IMAGE:2958189, mRNA, complete cds.	883	48
167	gi7533125	Homo sapiens	fibroblast growth factor receptor 3 (FGFR3) mRNA, complete cds, alternatively spliced.	3664	100
167	gi211443	Gallus gallus	cek2 protein	1842	92
167	gi186782	Homo sapiens	Human secreted fibroblast growth factor receptor (K-sam-III) mRNA, complete cds.	2482	73
169	gi13543469	Homo sapiens	Similar to Natriuretic peptide precursor A, (pronatriodilatin, also Anf, Pnd), clone MGC:14467 IMAGE:4273949, mRNA, complete cds.	181	97
169	gi3171893	Homo sapiens	DNA sequence from PAC 934G17 on chromosome 1p36.21. Contains the alternatively spliced CLCN6 gene for chloride channel proteins CLC-6A (KIAA0046) -B, -C and -D, the alternatively spliced NPPA gene coding for Atrial Natriuretic Factor ANF precursor (Atrial Natriuretic peptide ANP, Prepronatriodilatin), the NPPB gene for Brain Natriuretic Protein BNP, and a pseudogene similar to SBF1 (and other Myotubularin-related protein genes). Contains ESTs, STSs and the genomic marker D1S2740, complete sequence.	181	97
169	gi825625	Homo sapiens	Human gene fragment for pronatriodilatin precursor (exons 1 and 2).	181	97
170	gi13274524	Homo sapiens	complement-clq tumor necrosis factor-related protein (CTRP7) mRNA, complete cds.	1576	100
170	gi12228258	Homo sapiens	unnamed protein product	1576	100
170	AAB50371	Homo sapiens	Human ZACRP7.	1576	100
171	AAB08783	Homo sapiens	Amino acid sequence of a human serpin polypeptide.	742	87
171	gi2077914	Bos taurus	thrombin inhibitor	516	67
171	gi12655087	Homo sapiens	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin),	511	66

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			member 6, clone MGC:2180 IMAGE:3051381, mRNA, complete cds.		
172	gi63426	Gallus gallus	lysozyme	428	43
172	gi12843551	Mus musculus	putative	367	41
172	gi12578467	Homo sapiens	unnamed protein product	366	40
173	gi2443367	Homo sapiens	mRNA for Nck, Ash and phospholipase C gamma-binding protein NAP4, partial cds.	2432	100
173	AAW93275	Homo sapiens	Human SOCS19 protein.	2432	100
173	AAW62623	Homo sapiens	Homo sapiens SOCS11 protein.	953	100
174	gi12834584	Mus musculus	putative	414	97
174	gi7582391	Mus musculus	p53 apoptosis-associated target	414	97
174	AAB70474	Homo sapiens	PERP (p53 apoptosis effector related to PMP-22) protein sequence.	414	97
175	gi12834584	Mus musculus	putative	1054	99
175	gi7582391	Mus musculus	p53 apoptosis-associated target	1054	99
175	AAAY33261	Homo sapiens	Human p99 protein.	1054	99
176	AAB95035	Homo sapiens	Human protein sequence SEQ ID NO:16788.	221	62
177	gi6650766	Homo sapiens	PDZ domain-containing guanine nucleotide exchange factor I mRNA, complete cds.	243	87
177	gi15077826	Homo sapiens	rap guanine nucleotide exchange factor mRNA, complete cds.	243	87
177	AAB42658	Homo sapiens	Human ORFX ORF2422 polypeptide sequence SEQ ID NO:4844.	243	87
178	AAB43122	Homo sapiens	Human ORFX ORF2886 polypeptide sequence SEQ ID NO:5772.	3099	94
178	gi11177164	Mus musculus	polydom protein	3095	79
178	gi14198157	Mus musculus	polydomain protein	3095	79
179	gi6572379	Homo sapiens	Human DNA sequence from clone 579N16 on chromosome 22. Contains the 3' part of the gene for KIAA0685, the SBF1 gene for SET binding factor 1, a novel gene, ESTs, an STS, GSSs and three putative CpG islands, complete sequence.	8482	99
179	gi3015538	Homo sapiens	nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds.	8315	98
179	gi12698077	Homo sapiens	mRNA for KIAA1766 protein, partial cds.	3621	62
180	gi1234787	Xenopus laevis	up-regulated by thyroid hormone in tadpoles; expressed specifically in the tail and only at metamorphosis; membrane bound or extracellular protein; C-terminal basic region	1563	69
180	gi10435980	Homo sapiens	cDNA FLJ13840 fis, clone THYRO1000783, moderately similar to Xenopus laevis tail-	1562	94

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			specific thyroid hormone up-regulated (gene 5) mRNA.		
180	AAB94773	Homo sapiens	Human protein sequence SEQ ID NO:15860.	1562	94
181	gi12848947	Mus musculus	putative	582	60
181	gi5453324	Mus musculus	syntaxin4-interacting protein synip	576	59
181	AAB57636	Homo sapiens	Af-6 protein PDZ domain.	143	35
182	gi14041850	Homo sapiens	cDNA FLJ14369 fis, clone HEMBA1001174, highly similar to ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.	940	100
182	gi12855057	Mus musculus	putative	940	100
182	AAB92480	Homo sapiens	Human protein sequence SEQ ID NO:10563.	940	100
183	gi11275568	Homo sapiens	mucin 5B (MUC5B) gene, partial cds.	7389	99
183	gi3789927	Homo sapiens	mucin (MUC5B) mRNA, partial cds.	7176	97
183	gi4038587	Homo sapiens	partial MUC5B gene, exon 1-29.	7151	98
184	gi2853301	Homo sapiens	mucin (MUC3) mRNA, partial cds.	3473	77
184	gi6466801	Homo sapiens	intestinal mucin 3 (MUC3) gene, partial cds.	3218	76
184	gi9929920	Homo sapiens	MUC3A mRNA for intestinal mucin, partial cds.	2904	100
185	gi6492116	Homo sapiens	carboxylesterase-related protein mRNA, complete cds.	210	61
185	gi550147	Rattus norvegicus	carboxylesterase ES-3 (egasyn)	215	62
185	gi15929734	Mus musculus	Similar to carboxylesterase 2 (intestine, liver)	207	59
186	gi854065	Human herpesvirus 6	U88	540	54
186	gi10434098	Homo sapiens	cDNA FLJ12547 fis, clone NT2RM4000634.	417	44
186	AAB95124	Homo sapiens	Human protein sequence SEQ ID NO:17122.	417	44

TABLE 3

SEQ ID NO:	Accession No.	Description	Results*
102	BL00477	Alpha-2-macroglobulin family thiolester region proteins.	BL00477J 19.04 6.604e-19 15-46
104	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134B 15.99 5.154e-25 194-218 BL00134A 11.96 7.158e-19 47-64
104	BL00021	Kringle domain proteins.	BL00021B 13.33 1.000e-16 47-65
104		CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE	PR00722A 12.27 3.348e-16 48-64 PR00722C 10.87 4.000e-16 193-206
104	PR00722	Type I fibronectin domain proteins.	BL01253G 11.34 9.234e-18 193-207 BL01253D 4.84 4.877e-11 47-61
104	BL00495	Apple domain proteins.	BL00495K 12.58 5.631e-09 49-82 BL00495N 11.04 6.919e-09 186-221
105	PD02327	GLYCOPROTEIN ANTIGEN PRECURSOR IMMUNOGLO.	PD02327B 19.84 4.098e-10 154-176
105	PR00442	G-PROTEIN ALPHA SUBUNIT GROUP Q SIGNATURE	PR00442E 7.23 1.740e-09 292-301
105	PR00440	G-PROTEIN ALPHA SUBUNIT GROUP 12 SIGNATURE	PR00440E 11.16 3.192e-09 292-301
105	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 6.478e-09 106-116 DM00179 13.97 9.609e-09 298-308
106	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243H 17.53 4.391e-11 162-188
106	DM00864	EGF-LIKE DOMAIN.	DM00864B 11.34 5.836e-10 878-897
106	PR00907	THROMBOMODULIN SIGNATURE	PR00907G 11.63 5.366e-11 955-982 PR00907G 11.63 5.366e-11 1092-1119 PR00907G 11.63 9.066e-10 1356-1383 PR00907G 11.63 3.351e-09 1314-1341
106	PR00010	TYPE II EGF-LIKE SIGNATURE	PR00010C 11.16 3.250e-12 920-931 PR00010A 11.79 7.923e-11 490-502 PR00010C 11.16 5.071e-09 1404-1415 PR00010C 11.16 6.571e-09 1361-1372
106	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 7.520e-09 1388-1434
106	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 1.000e-15 915-931 BL01187B 12.04 8.412e-15 1482-1498 BL01187B 12.04 7.750e-14 546-562 BL01187B 12.04 7.750e-14 1356-1372 BL01187A 9.98 4.214e-13 939-951 BL01187B 12.04 4.913e-13 873-889 BL01187B 12.04 4.913e-13 1399-1415 BL01187A 9.98 1.000e- 12 488-500 BL01187B 12.04 8.000e-12 465- 481 BL01187B 12.04 1.900e-11 1314-1330 BL01187B 12.04 3.100e-11 1441-1457 BL01187B 12.04 4.600e-11 504-520

SEQ ID NO:	Accession No.	Description	Results*
			BL01187B 12.04 8.500e-11 955-971 BL01187B 12.04 8.500e-11 1092-1108 BL01187B 12.04 9.400e-11 1197-1213 BL01187B 12.04 2.286e-10 302-318 BL01187B 12.04 8.200e-10 1524-1540 BL01187A 9.98 9.143e-10 1338-1350 BL01187A 9.98 9.571e-10 1423-1435 BL01187A 9.98 9.571e-10 1506-1518 BL01187B 12.04 2.125e-09 762-778 BL01187A 9.98 7.000e-09 284-296 BL01187A 9.98 7.000e-09 897-909 BL01187A 9.98 7.000e-09 1179-1191 BL01187A 9.98 8.125e-09 1381-1393
106	BL00022	EGF-like domain proteins.	BL00022B 7.54 1.000e-09 924-931 BL00022A 7.48 9.000e-09 194-201
107	BL00649	G-protein coupled receptors family 2 proteins.	BL00649G 13.52 4.194e-13 102-128
107	PR00249	SECRETIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00249E 14.90 6.958e-09 20-46
107	BL00890	ABC-2 type transport system integral membrane proteins signal.	BL00890A 12.19 1.000e-08 17-28
108	BL00615	C-type lectin domain proteins.	BL00615B 12.25 9.400e-12 163-177
108	PD02205	POLYPROTEIN GLYCOPROTEIN M PRECURSOR CONTAINS:.	PD02205O 15.72 7.140e-09 163-195
109	BL01208	VWFC domain proteins.	BL01208B 15.83 1.000e-13 443-458 BL01208B 15.83 1.000e-12 377-392
109	BL00222	Insulin-like growth factor binding proteins.	BL00222B 11.09 1.333e-09 58-74
110	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 8.372e-10 84-116
111	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 8.372e-10 81-113
112	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 6.211e-23 104-144 BL00237C 13.19 4.115e-13 240-267 BL00237D 11.23 5.286e-13 297-314
112	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237G 19.63 5.680e-15 287-314 PR00237A 11.48 4.706e-14 40-65 PR00237B 13.50 9.550e-14 73-95 PR00237F 13.57 9.609e-14 245-270 PR00237C 15.69 7.300e-11 118-141 PR00237E 13.03 1.000e-10 202-226
112	PR00425	BRADYKININ RECEPTOR SIGNATURE	PR00425C 13.23 5.759e-09 104-124
115	PF01140	Matrix protein (MA), p15.	PF01140D 15.54 1.209e-09 845-880
115	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 4.717e-13 510-543 DM00215 19.43 5.941e-11 494-527 DM00215 19.43 1.000e-10 501-534 DM00215 19.43 4.857e-10

SEQ ID NO:	Accession No.	Description	Results*
			511-544 DM00215 19.43 9.357e-10 627-660 DM00215 19.43 9.518e-10 506-539 DM00215 19.43 1.610e-09 508-541 DM00215 19.43 1.610e-09 515-548 DM00215 19.43 2.831e-09 499-532 DM00215 19.43 4.356e-09 640-673
115	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 6.417e-09 513-534
115	PR00546	THYROID HORMONE RECEPTOR SIGNATURE	PR00546D 9.44 6.444e-09 848-867
115	PD02059	CORE POLYPROTEIN PROTEIN GAG CONTAINS: P.	PD02059B 24.48 6.958e-09 636-671
115	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.639e-11 511-526 PR00049D 0.00 8.714e-11 508-523 PR00049D 0.00 1.643e-10 512-527 PR00049D 0.00 8.857e-10 643-658 PR00049D 0.00 2.678e-09 644-659 PR00049D 0.00 5.271e-09 510-525 PR00049D 0.00 6.949e-09 645-660 PR00049D 0.00 7.254e-09 646-661
115	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 8.435e-09 293-306
115	PF00023	Ank repeat proteins.	PF00023A 16.03 3.625e-10 132-148 PF00023A 16.03 6.786e-09 300-316 PF00023A 16.03 8.393e-09 200-216 PF00023A 16.03 9.357e-09 40-56 PF00023A 16.03 1.000e-08 166-182
116	PF01140	Matrix protein (MA), p15.	PF01140D 15.54 1.209e-09 787-822
116	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 4.717e-13 452-485 DM00215 19.43 5.941e-11 436-469 DM00215 19.43 1.000e-10 443-476 DM00215 19.43 4.857e-10 453-486 DM00215 19.43 9.357e-10 569-602 DM00215 19.43 9.518e-10 448-481 DM00215 19.43 1.610e-09 450-483 DM00215 19.43 1.610e-09 457-490 DM00215 19.43 2.831e-09 441-474 DM00215 19.43 4.356e-09 582-615
116	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 6.417e-09 455-476
116	PR00546	THYROID HORMONE RECEPTOR SIGNATURE	PR00546D 9.44 6.444e-09 790-809
116	PD02059	CORE POLYPROTEIN PROTEIN GAG CONTAINS: P.	PD02059B 24.48 6.958e-09 578-613
116	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.639e-11 453-468 PR00049D 0.00 8.714e-11 450-465 PR00049D 0.00 1.643e-10 454-469 PR00049D 0.00 8.857e-10 585-600 PR00049D 0.00 2.678e-09 586-601 PR00049D 0.00 5.271e-09 452-467 PR00049D 0.00 6.949e-09 587-602 PR00049D 0.00 7.254e-09 588-603

SEQ ID NO:	Accession No.	Description	Results*
116	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 8.435e-09 293-306
116	PF00023	Ank repeat proteins.	PF00023A 16.03 3.625e-10 132-148 PF00023A 16.03 6.786e-09 300-316 PF00023A 16.03 8.393e-09 200-216 PF00023A 16.03 9.357e-09 40-56 PF00023A 16.03 1.000e-08 166-182
119	PR00830	ENDOPEPTIDASE LA (LON) SERINE PROTEASE (S16) SIGNATURE	PR00830A 8.41 6.286e-11 441-461
119	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE	PR00300A 9.56 8.859e-10 437-456
119	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 8.875e-10 436-452
119	BL00113	Adenylate kinase proteins.	BL00113A 12.74 6.262e-09 438-455
119	PR00918	CALICIVIRUS NON-STRUCTURAL POLYPROTEIN FAMILY SIGNATURE	PR00918A 13.76 7.341e-09 431-452
119	BL00674	AAA-protein family proteins.	BL00674C 22.60 5.696e-24 467-510 BL00674D 23.41 8.740e-18 525-572 BL00674B 4.46 1.000e-17 434-456 BL00674E 15.24 3.571e-10 602-622 BL00674A 16.91 8.826e-09 400-421
119	BL01128	Shikimate kinase proteins.	BL01128A 18.84 8.953e-09 437-471
120	PR00705	PAPAIN CYSTEINE PROTEASE (C1) FAMILY SIGNATURE	PR00705A 10.55 4.000e-21 132-148 PR00705B 10.22 2.385e-10 276-287
120	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.	BL00139D 9.24 1.818e-18 295-312 BL00139A 10.29 1.000e-14 132-142 BL00139C 9.23 2.800e-10 275-285
120	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE	PR00704C 11.88 6.162e-09 132-149
121	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 8.636e-11 715-729
121	PR00390	PHOSPHOLIPASE C SIGNATURE	PR00390A 15.09 5.390e-20 342-361 PR00390E 14.63 9.357e-20 608-627 PR00390D 15.76 3.250e-17 587-609 PR00390C 12.52 5.714e-14 471-489 PR00390B 12.57 1.269e-11 373-394 PR00390F 12.03 5.333e-10 758-769
121	PF01140	Matrix protein (MA), p15.	PF01140D 15.54 8.535e-09 498-533
121	BL50007	Phosphatidylinositol-specific phospholipase X-box domain proteins	BL50007D 19.54 7.698e-35 582-624 BL50007B 20.90 6.571e-30 407-445 BL50007A 19.61 4.671e-21 343-389

SEQ ID NO:	Accession No.	Description	Results*
		prof.	BL50007E 25.63 7.585e-20 744-781 BL50007C 8.97 4.522e-14 472-489 BL50007A 19.61 8.946e-09 348-394
123	PR00336	LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN SIGNATURE	PR00336D 9.96 2.393e-09 29-52
126	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237E 13.03 6.400e-12 76-100 PR00237D 8.94 1.450e-11 26-48
126	BL00237	G-protein coupled receptors proteins.	BL00237B 5.28 9.182e-09 84-96
127	PR00749	LYSOZYME G SIGNATURE	PR00749C 7.26 4.600e-16 84-103 PR00749F 13.63 2.364e-13 157-174 PR00749D 13.61 1.222e-12 103-124 PR00749E 18.92 5.061e-10 124-143 PR00749B 16.54 6.589e-09 60-82 PR00749H 8.22 7.368e-09 191-212
129	PF00094	von Willebrand factor type D domain proteins.	PF00094B 10.43 3.935e-18 596-614 PF00094B 10.43 8.286e-14 1060-1078
129	PD02576	PRECURSOR GLYCOPROTEIN SIGNAL CELL.	PD02576A 27.60 6.118e-34 894-943 PD02576A 27.60 9.182e-25 424-473 PD02576A 27.60 8.147e-10 791-840
129	BL01253	Type I fibronectin domain proteins.	BL01253G 11.34 8.989e-09 1151-1165
130	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243H 17.53 4.375e-10 1190-1216
130	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.508e-11 1195-1214 PR00011B 13.08 4.522e-10 1195-1214 PR00011A 14.06 2.479e-09 1195-1214
130	DM00191	w SPAC8A4.04C RESISTANCE SPAC8A4.05C DAUNORUBICIN.	DM00191D 13.94 6.009e-09 438-477
130	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 7.485e-09 232-281
130	PF00624	Flocculin repeat proteins.	PF00624J 6.21 9.782e-10 256-311 PF00624F 11.04 1.218e-09 726-762 PF00624G 10.91 3.032e-09 69-124 PF00624J 6.21 4.488e-09 257-312 PF00624J 6.21 6.512e-09 633-688 PF00624J 6.21 7.279e-09 270-325 PF00624G 10.91 8.476e-09 643-698 PF00624J 6.21 8.744e-09 161-216 PF00624J 6.21 9.233e-09 74-129
130	PF00997	Kappa casein.	PF00997D 9.95 9.894e-09 136-171
131	BL00615	C-type lectin domain proteins.	BL00615A 16.68 7.231e-16 195-213 BL00615B 12.25 7.750e-13 294-308
131	PR00356	TYPE II ANTIFREEZE PROTEIN SIGNATURE	PR00356B 14.85 2.648e-09 195-213
132	PR00343	SELECTIN	PR00343C 16.85 4.906e-12 10-29 PR00343C

SEQ ID NO:	Accession No.	Description	Results*
		SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE	16.85 4.098e-10 125-144 PR00343C 16.85 5.636e-09 68-87 PR00343C 16.85 7.818e-09 418-437
132	PF00084	Sushi domain proteins (SCR repeat proteins.	PF00084B 9.45 7.188e-10 351-363 PF00084B 9.45 5.950e-09 59-71 PF00084C 11.25 7.353e-09 199-209 PF00084B 9.45 7.750e-09 174-186 PF00084C 11.25 9.471e-09 434-444
134	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 8.615e-10 456-477
138	BL00132	Zinc carboxypeptidases, zinc-binding region 1 proteins.	BL00132C 21.35 2.552e-35 25-66 BL00132E 17.72 8.333e-27 95-122 BL00132F 13.26 2.500e-24 123-145 BL00132D 12.70 7.000e-18 69-84 BL00132G 10.94 8.594e-17 180-198
138	PR00765	CARBOXYPEPTIDASE A METALLOPROTEASE (M14) FAMILY SIGNATURE	PR00765D 14.16 1.857e-14 128-142 PR00765C 12.55 1.667e-11 75-84
139	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 2.800e-12 493-506 PD00078B 13.14 6.400e-10 460-473
139	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 6.417e-10 467-522
139	PF00023	Ank repeat proteins.	PF00023B 14.20 1.818e-09 496-506 PF00023B 14.20 9.182e-09 463-473 PF00023A 16.03 9.679e-09 467-483
142	PR00705	PAPAIN CYSTEINE PROTEASE (C1) FAMILY SIGNATURE	PR00705A 10.55 4.000e-21 132-148 PR00705B 10.22 2.385e-10 276-287
142	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.	BL00139D 9.24 1.818e-18 295-312 BL00139A 10.29 1.000e-14 132-142 BL00139C 9.23 2.800e-10 275-285
142	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE	PR00704C 11.88 6.162e-09 132-149
143	BL01019	ADP-ribosylation factors family proteins.	BL01019B 19.49 9.757e-34 106-161 BL01019A 13.20 6.351e-31 62-102 BL01019C 12.52 8.091e-19 165-191
143	BL01020	SAR1 family proteins.	BL01020C 15.35 3.494e-18 90-141
143	PR00328	GTP-BINDING SAR1 PROTEIN SIGNATURE	PR00328A 10.62 4.638e-11 26-50 PR00328C 13.16 4.170e-10 89-115
144	BL50007	Phosphatidylinositol-specific phospholipase X-box domain proteins prof.	BL50007E 25.63 2.761e-18 173-210
144	PR00390	PHOSPHOLIPASE C SIGNATURE	PR00390F 12.03 4.176e-11 187-198
144	PR00399	SYNAPTOTAGMIN SIGNATURE	PR00399D 14.48 4.490e-09 177-188
144	PR00360	C2 DOMAIN	PR00360B 13.61 5.909e-11 144-158

SEQ ID NO:	Accession No.	Description	Results*
		SIGNATURE	PR00360C 8.77 1.321e-09 166-175 PR00360A 14.59 5.500e-09 114-127
149	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 8.636e-11 715-729
149	PR00390	PHOSPHOLIPASE C SIGNATURE	PR00390A 15.09 5.390e-20 342-361 PR00390E 14.63 9.357e-20 608-627 PR00390D 15.76 3.250e-17 587-609 PR00390C 12.52 5.714e-14 471-489 PR00390B 12.57 1.269e-11 373-394 PR00390F 12.03 5.333e-10 758-769
149	PF01140	Matrix protein (MA), p15.	PF01140D 15.54 8.535e-09 498-533
149	BL50007	Phosphatidylinositol-specific phospholipase X-box domain proteins prof.	BL50007D 19.54 7.698e-35 582-624 BL50007B 20.90 6.571e-30 407-445 BL50007A 19.61 4.671e-21 343-389 BL50007E 25.63 7.585e-20 744-781 BL50007C 8.97 4.522e-14 472-489 BL50007A 19.61 8.946e-09 348-394
153	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00720B 16.57 6.595e-15 996-1020
153	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791C 20.98 6.011e-12 606-645
153	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYN.	PD00289 9.97 5.050e-11 625-639
153	PR00834	HTRA/DEGQ PROTEASE FAMILY SIGNATURE	PR00834F 10.91 2.946e-09 621-634
153	BL00888	Cyclic nucleotide-binding domain proteins.	BL00888B 14.79 4.682e-09 355-379
154	PR00826	FANCONI ANAEMIA GROUP A PROTEIN SIGNATURE	PR00826G 13.17 1.143e-30 1346-1370 PR00826B 11.56 1.150e-29 1123-1146 PR00826A 10.40 1.161e-27 1105-1124 PR00826E 14.92 1.141e-24 1294-1313 PR00826D 6.81 1.132e-23 1253-1272 PR00826F 9.90 1.136e-23 1323-1341 PR00826C 7.00 1.110e-13 1238-1248
154	PR00723	SUBTILISIN SERINE PROTEASE FAMILY (S8) SIGNATURE	PR00723C 10.64 3.340e-09 772-789
155	PR00826	FANCONI ANAEMIA GROUP A PROTEIN SIGNATURE	PR00826G 13.17 1.143e-30 1303-1327 PR00826B 11.56 1.150e-29 1080-1103 PR00826A 10.40 1.161e-27 1062-1081 PR00826E 14.92 1.141e-24 1251-1270 PR00826D 6.81 1.132e-23 1210-1229 PR00826F 9.90 1.136e-23 1280-1298 PR00826C 7.00 1.110e-13 1195-1205
155	PR00723	SUBTILISIN SERINE PROTEASE FAMILY (S8) SIGNATURE	PR00723C 10.64 3.340e-09 772-789
157	PR00267	INTERFERON REGULATORY FACTOR	PR00267D 13.82 3.118e-29 36-59 PR00267C 14.28 4.857e-21 13-31

SEQ ID NO:	Accession No.	Description	Results*
		SIGNATURE	
157	BL00601	Tryptophan pentad repeat proteins (IRF family) proteins.	BL00601B 20.92 4.500e-31 32-61 BL00601C 19.42 7.429e-09 72-85
159	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00720B 16.57 7.677e-17 137-161
160	PR00209	ALPHA/BETA GLIADIN FAMILY SIGNATURE	PR00209B 4.88 7.457e-10 1-20
160	PD02699	PROTEIN DNA-BINDING BINDING DNA.	PD02699A 8.91 4.143e-21 144-173 PD02699B 18.28 5.655e-09 173-197
162	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 6.671e-15 219-267
163	BL50007	Phosphatidylinositol-specific phospholipase X-box domain proteins prof.	BL50007A 19.61 1.000e-40 675-721 BL50007B 20.90 3.872e-27 734-772 BL50007D 19.54 5.105e-27 1056-1098 BL50007C 8.97 3.935e-14 802-819 BL50007E 25.63 5.661e-14 1217-1254
163	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 4.545e-11 1191-1205
163	PR00390	PHOSPHOLIPASE C SIGNATURE	PR00390B 12.57 5.974e-20 700-721 PR00390A 15.09 6.049e-20 674-693 PR00390E 14.63 7.070e-16 1082-1101 PR00390D 15.76 7.107e-16 1061-1083 PR00390C 12.52 1.000e-13 801-819 PR00390F 12.03 5.500e-09 1231-1242
164	BL00250	TGF-beta family proteins.	BL00250A 21.24 1.500e-31 303-339 BL00250B 27.37 8.200e-30 371-407
164	PR00671	INHIBIN BETA B CHAIN SIGNATURE	PR00671G 5.35 3.250e-27 184-206 PR00671C 4.18 1.173e-26 40-60 PR00671H 13.45 1.000e-25 231-252 PR00671B 4.29 1.474e-25 20-40 PR00671E 8.84 1.115e-23 124-142 PR00671A 8.36 1.429e-22 2-21 PR00671F 13.86 1.105e-21 149-166 PR00671D 3.47 1.100e-20 61-77
164	PR00672	INHIBIN BETA C CHAIN SIGNATURE	PR00672E 10.40 1.419e-10 142-165
164	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 3.874e-11 28-43 PR00049D 0.00 9.319e-11 30-45 PR00049D 0.00 9.319e-11 31-46 PR00049D 0.00 2.983e-09 34-49
164	PR00669	INHIBIN ALPHA CHAIN SIGNATURE	PR00669F 5.57 8.483e-09 320-338
164	PR00438	GROWTH FACTOR CYSTINE KNOT SUPERFAMILY SIGNATURE	PR00438A 13.54 1.000e-08 328-338
165	PR00785	NUCLEAR TRANSLOCATOR SIGNATURE	PR00785I 13.44 5.957e-10 284-302
165	BL00038	Myc-type, 'helix-loop-helix' dimerization domain proteins.	BL00038B 16.97 3.930e-09 92-113
166	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 5.408e-11 268-289 PR00211B 0.86 9.048e-10 274-295 PR00211B 0.86

SEQ ID NO:	Accession No.	Description	Results*
			2.167e-09 280-301
166	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.407e-09 235-250
166	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.186e-09 212-245 DM00215 19.43 6.949e-09 243-276 DM00215 19.43 7.559e-09 227-260 DM00215 19.43 9.085e-09 217-250
167	BL00240	Receptor tyrosine kinase class III proteins.	BL00240F 17.74 2.105e-36 533-581 BL00240E 11.56 5.875e-33 481-519 BL00240D 23.07 9.882e-22 403-458 BL00240C 22.58 8.962e-20 352-401 BL00240G 28.45 4.770e-19 580-633
167	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 4.938e-21 495-526 BL00107B 13.31 6.400e-15 562-578
167	BL00239	Receptor tyrosine kinase class II proteins.	BL00239E 17.14 9.400e-39 534-584 BL00239F 28.15 2.765e-22 588-633 BL00239B 25.15 6.958e-15 414-462 BL00239C 18.75 3.211e-13 482-505 BL00239D 16.81 9.118e-13 507-533
167	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109D 17.04 5.091e-27 563-586 PR00109B 12.27 5.846e-21 495-514 PR00109E 14.41 8.500e-21 607-630 PR00109C 12.85 1.000e-13 544-555 PR00109A 15.00 8.364e-12 443-457
167	BL00790	Receptor tyrosine kinase class V proteins.	BL00790Q 7.68 1.889e-17 541-574 BL00790Q 15.61 4.529e-12 599-648 BL00790M 8.74 7.831e-11 486-508 BL00790N 13.25 4.411e-10 508-535
167	BL50001	Src homology 2 (SH2) domain proteins profile.	BL50001B 17.40 2.714e-11 492-513 BL50001D 11.00 5.500e-10 562-573
167	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 6.211e-10 221-231
167	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870D 15.74 9.617e-09 213-248
169	PR00711	ATRIAL NATRIURETIC PEPTIDE SIGNATURE	PR00711A 12.00 9.769e-20 11-30
170	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007A 19.33 1.000e-16 158-185 PR00007C 15.60 8.200e-15 229-251 PR00007B 14.16 5.846e-14 185-205 PR00007D 9.64 5.250e-10 264-275
170	BL01113	C1q domain proteins.	BL01113B 18.26 1.581e-29 164-200 BL01113C 13.18 3.077e-15 229-249 BL01113A 17.99 1.243e-13 50-77 BL01113A 17.99 6.108e-13 35-62 BL01113A 17.99 3.077e-12 41-68 BL01113A 17.99 1.574e-10 38-65 BL01113A 17.99 9.617e-10 44-71 BL01113A 17.99 7.577e-09 59-86 BL01113A 17.99 7.577e-09 110-137
170	BL00420	Speract receptor repeat proteins domain proteins.	BL00420A 20.42 5.154e-12 44-73 BL00420A 20.42 1.655e-11 86-115 BL00420A 20.42 2.328e-10 101-130 BL00420A 20.42 4.185e-09 47-76 BL00420A 20.42 9.031e-09 50-79
171	BL00284	Serpins proteins.	BL00284A 15.64 5.500e-21 26-50
172	PR00749	LYSOZYME G	PR00749C 7.26 4.600e-16 84-103 PR00749F

SEQ ID NO:	Accession No.	Description	Results*
		SIGNATURE	13.63 2.364e-13 157-174 PR00749D 13.61 1.222e-12 103-124 PR00749E 18.92 5.061e-10 124-143 PR00749B 16.54 6.589e-09 60-82 PR00749H 8.22 7.368e-09 191-212
173	PR00678	PI3 KINASE P85 REGULATORY SUBUNIT SIGNATURE	PR00678H 9.13 4.960e-14 406-429
173	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 6.748e-11 78-93
173	PR00401	SH2 DOMAIN SIGNATURE	PR00401A 14.00 8.800e-11 400-415
173	PR00239	MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE	PR00239E 1.58 2.518e-10 86-98
173	PR00021	SMALL PROLINE-RICH PROTEIN SIGNATURE	PR00021A 4.31 4.214e-11 181-194 PR00021A 4.31 2.823e-09 180-193 PR00021A 4.31 3.848e-09 182-195 PR00021A 4.31 6.582e-09 183-196 PR00021A 4.31 9.430e-09 178-191 PR00021A 4.31 9.886e-09 179-192
178	PR00343	SELECTIN SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE	PR00343C 16.85 4.906e-12 10-29 PR00343C 16.85 4.098e-10 125-144 PR00343C 16.85 5.636e-09 68-87 PR00343C 16.85 7.818e-09 418-437
178	PF00084	Sushi domain proteins (SCR repeat proteins).	PF00084B 9.45 7.188e-10 351-363 PF00084B 9.45 5.950e-09 59-71 PF00084C 11.25 7.353e-09 199-209 PF00084B 9.45 7.750e-09 174-186 PF00084C 11.25 9.471e-09 434-444
182	BL01019	ADP-ribosylation factors family proteins.	BL01019B 19.49 5.200e-39 90-145 BL01019A 13.20 1.973e-31 46-86 BL01019C 12.52 1.857e-25 147-173
182	BL01020	SAR1 family proteins.	BL01020C 15.35 7.798e-14 74-125
182	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 6.365e-10 17-39
182	PR00440	G-PROTEIN ALPHA SUBUNIT GROUP 12 SIGNATURE	PR00440C 9.54 3.143e-09 62-80
182	PR00328	GTP-BINDING SAR1 PROTEIN SIGNATURE	PR00328A 10.62 5.883e-11 18-42 PR00328C 13.16 5.065e-09 73-99
183	PF00094	von Willebrand factor type D domain proteins.	PF00094B 10.43 3.935e-18 596-614 PF00094B 10.43 8.286e-14 1060-1078
183	PD02576	PRECURSOR GLYCOPROTEIN SIGNAL CELL.	PD02576A 27.60 6.118e-34 894-943 PD02576A 27.60 9.182e-25 424-473 PD02576A 27.60 8.147e-10 791-840
183	BL01253	Type I fibronectin domain proteins.	BL01253G 11.34 8.989e-09 1151-1165
184	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243H 17.53 4.375e-10 1190-1216
184	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.508e-11 1195-1214 PR00011B 13.08 4.522e-10 1195-1214

SEQ ID NO:	Accession No.	Description	Results*
			PR00011A 14.06 2.479e-09 1195-1214
184	DM00191	w SPAC8A4.04C RESISTANCE SPAC8A4.05C DAUNORUBICIN.	DM00191D 13.94 6.009e-09 438-477
184	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 7.485e-09 232-281
184	PF00624	Flocculin repeat proteins.	PF00624J 6.21 9.782e-10 256-311 PF00624F 11.04 1.218e-09 726-762 PF00624G 10.91 3.032e-09 69-124 PF00624J 6.21 4.488e-09 257-312 PF00624J 6.21 6.512e-09 633-688 PF00624J 6.21 7.279e-09 270-325 PF00624G 10.91 8.476e-09 643-698 PF00624J 6.21 8.744e-09 161-216 PF00624J 6.21 9.233e-09 74-129
184	PF00997	Kappa casein.	PF00997D 9.95 9.894e-09 136-171
185	BL00122	Carboxylesterases type- B serine proteins.	BL00122E 22.02 2.862e-20 25-66 BL00122D 12.53 4.000e-11 1-17
186	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 8.181e-10 151-197
186	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243I 31.77 2.141e-09 8-51
186	PR00451	CHITIN-BINDING DOMAIN SIGNATURE	PR00451A 6.49 5.355e-09 44-53
186	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 5.592e-09 35-75
186	BL01185	C-terminal cystine knot proteins.	BL01185D 23.45 9.258e-09 50-103
186	BL00246	Wnt-1 family proteins.	BL00246E 20.32 5.553e-09 55-101 BL00246E 20.32 9.788e-09 11-57

* Results include in order: Accession No., subtype, e-value, and amino acid position of the signature in the corresponding polypeptide

TABLE 4

SEQ ID NO:	Pfam Model	Description	E-value	Score	No: of Pfam Domains	Position of the Domain
94	LRR	Leucine Rich Repeat	7.5e-36	132.5	8	58-81:82-105:106-130:131-154:155-178:179-202:203-226:227-250
96	UBX	UBX domain	7e-25	96.1	1	330-409
97	UBX	UBX domain	9.8e-25	95.6	1	299-378
100	AMP-binding	AMP-binding enzyme	2.1e-86	300.5	2	91-230:236-503
101	FG-GAP	FG-GAP repeat	2.2e-07	37.9	1	38-94
102	A2M	Alpha-2-macroglobulin family	1.1e-21	73.0	1	15-152
104	trypsin	Trypsin	3.5e-74	236.2	1	22-240
105	ig	Immunoglobulin	6.3e-24	82.1	3	46-115:148-214:250-

SEQ ID NO:	Pfam Model	Description	E-value	Score	No: of Pfam Domains	Position of the Domain
		domain				307
106	EGF	EGF-like domain	3.7e-89	309.6	19	124-151:159-185:190-217:290-326:453-488:494-528:534-570:758-786:861-897:903-939:945-979:1082-1116:1185-1221:1302-1338:1344-1381:1387-1423:1429-1465:1471-1506:1512-1548
106	TB	TB domain	3.5e-65	230.0	6	233-275:341-372:802-844:994-1031:1131-1174:1236-1277
107	7tm_2	7 transmembrane receptor (Secretin family)	0.00044	-68.4	1	2-119
108	lectin_c	Lectin C-type domain	9e-24	92.4	1	52-178
108	Xlink	Extracellular link domain	2.2e-05	13.8	1	47-70
109	vwc	von Willebrand factor type C domain	3.6e-18	73.8	2	337-391:404-457
110	ig	Immunoglobulin domain	2.2e-05	22.4	1	29-106
111	ig	Immunoglobulin domain	2.2e-05	22.4	1	26-103
112	7tm_1	7 transmembrane receptor (rhodopsin family)	5.2e-59	189.6	1	55-305
113	PX	PX domain	1.6e-15	65.0	1	23-164
115	ank	Ank repeat	2e-54	194.2	8	35-67:69-102:127-160:161-194:195-228:229-262:263-295:296-327
115	WH2	WH2 motif	0.0015	25.2	1	703-720
116	ank	Ank repeat	2e-54	194.2	8	35-67:69-102:127-160:161-194:195-228:229-262:263-295:296-327
116	WH2	WH2 motif	0.0015	25.2	1	645-662
119	AAA	ATPase family associated with various cellul	2.8e-71	250.2	1	436-621
120	Peptidase C1	Papain family cysteine protease	2.3e-123	412.6	1	114-332
121	PI-PLC-X	Phosphatidylinositol-specific phospholipase	9.8e-71	248.4	1	338-488
121	PI-PLC-Y	Phosphatidylinositol-specific phospholipase	2.4e-53	190.6	1	532-649

SEQ ID NO:	Pfam Model	Description	E-value	Score	No: of Pfam Domains	Position of the Domain
		itol-specific phospholipase				
121	C2	C2 domain	6.7e-23	89.5	1	667-757
121	PH	PH domain	0.00021	20.7	1	64-172
122	ig	Immunoglobulin domain	0.00088	17.2	1	52-135
123	cNMP_binding	Cyclic nucleotide-binding domain	7.9e-15	62.7	1	180-280
124	Sema	Sema domain	3.6e-118	406.0	1	64-328
126	7tm_1	7 transmembrane receptor (rhodopsin family)	4e-07	24.8	1	1-103
127	SLT	Transglycosylase SLT domain	0.0029	17.5	1	82-202
128	sushi	Sushi domain (SCR repeat)	1.3e-34	128.4	3	29-79:87-140:147-201
129	vwd	von Willebrand factor type D domain	7.9e-114	391.6	3	112-260:465-619:935-1083
129	TIL	Trypsin Inhibitor like cysteine rich domain	7.5e-14	59.5	4	369-425:735-792:834-895:1204-1258
131	lectin_c	Lectin C-type domain	2e-46	167.7	1	201-309
132	sushi	Sushi domain (SCR repeat)	1.3e-106	367.6	10	1-35:40-93:98-146:155-208:213-267:272-327:332-385:390-443:448-502:507-559
133	RhoGEF	RhoGEF domain	1.7e-18	74.9	1	791-976
133	PDZ	PDZ domain (Also known as DHR or GLGF)	1.5e-09	45.1	1	72-147
133	PH	PH domain	0.00089	18.5	1	1020-1132
134	TPR	TPR Domain	1.2e-16	68.8	6	64-97:107-140:153-186:263-296:352-385:449-482
135	PX	PX domain	1.6e-15	65.0	1	23-164
138	Zn_carbOpept	Zinc carboxypeptidase	2.3e-118	406.6	1	19-227
139	ank	Ank repeat	3.9e-18	73.7	2	462-494:495-527
139	VPS9	Vacuolar sorting protein 9 (VPS9) domain	1.9e-12	54.8	1	264-369
142	Peptidase_C1	Papain family cysteine protease	2.3e-123	412.6	1	114-332
143	arf	ADP-ribosylation factor family	1.5e-43	158.1	1	8-197
143	ras	Ras family	0.00027	-88.1	1	27-208
144	C2	C2 domain	2.3e-30	114.3	1	96-186
144	PI-PLC-Y	Phosphatidylinositol-specific	7.6e-14	53.7	1	42-76

SEQ ID NO:	Pfam Model	Description	E-value	Score	No: of Pfam Domains	Position of the Domain
		phospholipase				
147	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	4.5e-06	33.6	1	13-39
147	rrm	RNA recognition motif.	0.014	22.0	1	32-103
148	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	3.4e-06	34.0	1	13-39
148	rrm	RNA recognition motif.	0.00011	29.0	1	67-142
149	PI-PLC-X	Phosphatidylinositol-specific phospholipase	9.8e-71	248.4	1	338-488
149	PI-PLC-Y	Phosphatidylinositol-specific phospholipase	2.4e-53	190.6	1	532-649
149	C2	C2 domain	6.7e-23	89.5	1	667-757
149	PH	PH domain	0.00021	20.7	1	64-172
153	RasGEF	RasGEF domain	1e-47	172.0	1	907-1092
153	PDZ	PDZ domain (Also known as DHR or GLGF)	5.4e-17	69.9	1	580-661
153	cNMP_binding	Cyclic nucleotide-binding domain	3.6e-13	57.2	1	345-435
153	RA	Ras association (RalGDS/AF-6) domain	1.3e-05	32.1	1	799-885
157	IRF	Interferon regulatory factor transcription f	7.6e-43	155.8	1	1-76
159	RasGEF	RasGEF domain	7e-50	179.1	1	47-238
159	PH	PH domain	1.9e-15	59.9	1	390-493
160	RFX_DNA_binding	RFX DNA-binding domain	3.5e-30	113.7	1	95-173
161	rrm	RNA recognition motif.	0.0041	23.8	1	84-157
162	cadherin	Cadherin domain	5.3e-27	103.1	3	27-124:140-227:241-336
163	PI-PLC-X	Phosphatidylinositol-specific phospholipase	3.5e-69	243.2	1	670-818
163	PI-PLC-Y	Phosphatidylinositol-specific phospholipase	9.6e-43	155.4	2	941-954:1031-1123
163	C2	C2 domain	1.8e-08	41.6	1	1148-1230
163	RA	Ras association (RalGDS/AF-6) domain	0.085	3.0	1	1410-1515
164	TGF-beta	Transforming growth factor beta like	1.8e-58	207.7	1	300-407
164	TGFb_propeptide	TGF-beta propeptide	1.1e-40	148.5	1	62-280
165	PAS	PAS domain	1.3e-07	33.3	2	140-192:294-337

SEQ ID NO:	Pfam Model	Description	E-value	Score	No: of Pfam Domains	Position of the Domain
166	rrm	RNA recognition motif.	9.4e-08	39.2	1	84-157
167	pkinese	Protein kinase domain	3.1e-89	309.9	1	360-636
167	ig	Immunoglobulin domain	3.7e-20	70.0	3	54-111:169-230:268-289
170	Clq	Clq domain	1.3e-40	148.4	1	149-273
170	Collagen	Collagen triple helix repeat (20 copies)	6.9e-08	39.6	2	20-79:80-139
171	serpin	Serpin (serine protease inhibitor)	2.4e-50	172.8	1	1-145
172	SLT	Transglycosylase SLT domain	0.0029	17.5	1	82-202
173	SH2	SH2 domain	2.4e-16	50.8	1	400-453
178	sushi	Sushi domain (SCR repeat)	1.3e-106	367.6	10	1-35:40-93:98-146:155-208:213-267:272-327:332-385:390-443:448-502:507-559
178	EGF	EGF-like domain	7.8e-15	62.7	3	559-590:595-622:627-654
185	COesterase	Carboxylesterase	6e-27	94.9	1	3-56

TABLE 5

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
94	1a4y	A	60	249	6.5e-22	0.29	-0.02		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPIPOPE MAPPING, LEUCINE-RICH 3 REPEATS
94	1a9n	A	126	242	1.3e-20	0.51	0.15		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
94	1a9n	A	161	249	1e-10	0.25	0.19		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
94	1a9n	A	60	207	1.3e-18	0.43	0.96		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
94	1a9n	A	88	231	3.9e-22	0.72	0.86		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
94	1a9n	C	126	242	1.3e-20	0.60	0.40		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
94	1a9n	C	60	207	2.6e-18	0.39	0.72		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
94	1a9n	C	88	231	1.3e-22	0.74	0.77		U2 RNA HAIRPIN IV;	COMPLEX (NUCLEAR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	PROTEIN/RNA COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
94	1fqv	A	64	249	3.9e-12	0.17	-0.11		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2- ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE- RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
94	1fs2	A	60	239	3.9e-19	0.29	0.10		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
96	1a2y	B	40	74	0.0065	-0.84	0.10		MONOCLONAL ANTIBODY D1.3; CHAIN: A, B; LYSOZYME; CHAIN: C;	COMPLEX (IMMUNOGLOBULIN/HYDROLASE) COMPLEX (IMMUNOGLOBULIN/HYDROLASE), IMMUNOGLOBULIN V 2 REGION, SIGNAL, HYDROLASE, GLYCOSIDASE, BACTERIOLYTIC 3 ENZYME, EGG WHITE
97	1a2y	B	40	74	0.0065	-0.84	0.10		MONOCLONAL ANTIBODY D1.3; CHAIN: A, B; LYSOZYME; CHAIN: C;	COMPLEX (IMMUNOGLOBULIN/HYDROLASE) COMPLEX (IMMUNOGLOBULIN/HYDROLASE), IMMUNOGLOBULIN V 2 REGION, SIGNAL, HYDROLASE, GLYCOSIDASE, BACTERIOLYTIC 3 ENZYME, EGG WHITE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
100	1amu	A	37	579	0			154.59	GRAMICIDIN SYNTHETASE I; CHAIN: A, B; PHENYLALANINE; CHAIN: C, D;	PEPTIDE SYNTHETASE GRSA; PEPTIDE SYNTHETASE, GRSA, ADENYLATE FORMING
100	1amu	A	50	578	0	0.51	1.00		GRAMICIDIN SYNTHETASE I; CHAIN: A, B; PHENYLALANINE; CHAIN: C, D;	PEPTIDE SYNTHETASE GRSA; PEPTIDE SYNTHETASE, GRSA, ADENYLATE FORMING
100	1lei		41	577	0			186.29	LUCIFERASE; CHAIN: NULL;	OXIDOREDUCTASE OXIDOREDUCTASE, MONOOXYGENASE, PHOTOPROTEIN, LUMINESCENCE
100	1lei		50	576	0	0.78	1.00		LUCIFERASE; CHAIN: NULL;	OXIDOREDUCTASE OXIDOREDUCTASE, MONOOXYGENASE, PHOTOPROTEIN, LUMINESCENCE
102	1c3d		1	50	5.1e-20	-0.41	0.31		C3D; CHAIN: NULL;	COMPLEMENT COMPLEMENT, C3, C3D, ALPHA-ALPHA BARREL
102	1qqf	A	1	49	5.1e-19	-0.06	0.23		COMPLEMENT C3DG; CHAIN: A;	IMMUNE SYSTEM ALPHA-ALPHA BARREL, COMPLEMENT
104	1a0j	A	22	247	1.7e-98			210.73	TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
104	1a0j	A	22	248	1.7e-98	0.83	1.00		TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
104	1a0l	A	22	253	1.7e-76			137.52	BETA-TRYPTASE; CHAIN: A, B, C, D;	SERINE PROTEINASE TRYPSIN-LIKE SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA
104	1aht	H	22	254	1e-69			137.36	ALPHA-THROMBIN;	COMPLEX (SERINE)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									1AHT 4 CHAIN: L, H; 1AHT 5 HIRUGEN; 1AHT 8 CHAIN: I; 1AHT 9	PROTEINASE/INHIBITOR
104	1aks	B	154	236	3.9e-33	0.16	1.00		ALPHA TRYPSIN; CHAIN: A, B;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE
104	1ao5	A	22	253	1.7e-82			193.53	GLANDULAR KALLIKREIN-13; CHAIN: A, B;	SERINE PROTEASE PRORENIN CONVERTING ENZYME (PRECE), EPIDERMAL GLANDULAR KALLIKREIN, SERINE PROTEASE, PROTEIN MATURATION
104	1aut	C	22	252	1e-69			146.28	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO- MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
104	1bio		22	236	1.3e-76			161.35	COMPLEMENT FACTOR D; CHAIN: NULL;	SERINE PROTEASE SERINE PROTEASE, HYDROLASE, COMPLEMENT, FACTOR D, CATALYTIC 2 TRIAD, SELF- REGULATION
104	1bqy	A	22	253	8.5e-83			190.92	PLASMINOGEN ACTIVATOR; CHAIN: A, B; GLU- GLY-ARG- CHLOROMETHYLKE TONE INHIBITOR; CHAIN: E, F;	BLOOD CLOTTING TSV-PA; FIBRINOLYSIS, PLASMINOGEN ACTIVATOR, SERINE PROTEINASE, 2 SNAKE VENOM, COMPLEX (HYDROLASE/INHIBITOR), BLOOD CLOTTING
104	1bru	P	22	249	3.4e-85			148.11	ELASTASE; CHAIN: P;	SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE
104	1dpo		22	253	3.4e-95			208.46	TRYPSIN; CHAIN:	SERINE PROTEASE HYDROLASE,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									NULL;	SERINE PROTEASE, DIGESTION, PANCREAS, ZYMOGEN, 2 SIGNAL, MULTIGENE FAMILY
104	1fxy	A	22	249	5.1e-87	0.94	1.00		COAGULATION FACTOR XA-TRYPSIN CHIMERA; CHAIN: A; D-PHE-PRO-ARG-CHLOROMETHYLKETONE (PPACK) WITH CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) TRYPSIN, COAGULATION FACTOR XA, CHIMERA, PROTEASE, PPACK, 2 CHLOROMETHYLKETONE, COMPLEX (PROTEASE/INHIBITOR)
104	1fxy	A	22	250	5.1e-87			189.85	COAGULATION FACTOR XA-TRYPSIN CHIMERA; CHAIN: A; D-PHE-PRO-ARG-CHLOROMETHYLKETONE (PPACK) WITH CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) TRYPSIN, COAGULATION FACTOR XA, CHIMERA, PROTEASE, PPACK, 2 CHLOROMETHYLKETONE, COMPLEX (PROTEASE/INHIBITOR)
104	1gct	A	12	249	6.8e-76			142.82	HYDROLASE (SERINE PROTEINASE) GAMMA-CHYMOTRYPSIN *A (E.C.3.4.21.1) (SP*H 7.0) 1GCT 3	
104	1mct	A	22	247	5.1e-100			217.46	COMPLEX(PROTEINASE/INHIBITOR) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH INHIBITOR FROM BITTER 1MCT 3 GOURD 1MCT 4	
104	1mct	A	22	248	5.1e-100	0.95	1.00		COMPLEX(PROTEIN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									ASE/(INHIBITOR) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH INHIBITOR FROM BITTER IMCT 3 GOURD IMCT 4	
104	1nrm	A	22	245	3.4e-87	0.99	1.00		NEUROPSIN; CHAIN: A, B;	SERINE PROTEINASE SERINE PROTEINASE, GLYCOPROTEIN
104	1nrm	A	22	252	3.4e-87			233.14	NEUROPSIN; CHAIN: A, B;	SERINE PROTEINASE SERINE PROTEINASE, GLYCOPROTEIN
104	1pfx	C	22	247	1e-77			136.25	FACTOR IXA; CHAIN: C, L;; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
104	1sgf	A	31	253	3.4e-68			147.35	NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)
104	1sgf	G	22	248	3.4e-91	0.87	1.00		NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)
104	1sgf	G	22	253	3.4e-91			204.41	NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
104	1slw	B	22	248	6.8e-95	0.97	1.00		ECOTIN; CHAIN: A; ANIONIC TRYPSIN; CHAIN: B;	COMPLEX (SERINE PROTEASE/INHIBITOR) TRYPSIN INHIBITOR; SERINE PROTEASE, INHIBITOR, COMPLEX, METAL BINDING SITES, 2 PROTEIN ENGINEERING, PROTEASE- SUBSTRATE INTERACTIONS, 3 METALLOPROTEINS
104	1slw	B	22	253	6.8e-95			198.58	ECOTIN; CHAIN: A; ANIONIC TRYPSIN; CHAIN: B;	COMPLEX (SERINE PROTEASE/INHIBITOR) TRYPSIN INHIBITOR; SERINE PROTEASE, INHIBITOR, COMPLEX, METAL BINDING SITES, 2 PROTEIN ENGINEERING, PROTEASE- SUBSTRATE INTERACTIONS, 3 METALLOPROTEINS
104	1ton		22	253	6.8e-83			183.92	HYDROLASE(SERIN E PROTEINASE) TONIN (E.C. NUMBER NOT ASSIGNED) 1TON 4	
104	1tm	A	22	249	3.4e-98	0.86	1.00		HYDROLASE (SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR 1TRN 3 DIISOPROPYL- FLUOROPHOSPHO LUORIDATE (DFP) 1TRN 4 HUMAN TRYPSIN, DFP INHIBITED 1TRN 6	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
104	1tm	A	22	250	3.4e-98			200.17	HYDROLASE (SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR ITRN 3 DIISOPROPYL-FLUOROPHOSPHORYL FLUORIDATE (DFP) ITRN 4 HUMAN TRYPSIN, DFP INHIBITED ITRN 6	
104	1uvu	H	22	242	3.4e-63			142.38	THROMBIN; CHAIN: L, H;	SERINE PROTEASE FACTOR II; SERINE PROTEASE, HYDROLASE, THROMBIN, BLOOD COAGULATION
104	2tbs		22	246	5.1e-94	0.85	1.00		HYDROLASE(SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH BENZAMIDINE INHIBITOR 2TBS 3	
104	2tbs		22	254	5.1e-94			205.95	HYDROLASE(SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH BENZAMIDINE INHIBITOR 2TBS 3	
104	5ptp		22	247	8.5e-95			212.27	BETA TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL
104	5ptp		22	248	8.5e-95	0.90	1.00		BETA TRYPSIN;	SERINE PROTEASE HYDROLASE,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: NULL;	SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL
105	1ad0	A	135	319	5.1e-20	-0.09	0.49		FAB FRAGMENT, ANTIBODY A5B7; CHAIN: A, B, C, D;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB FRAGMENT
105	1adq	L	35	231	5.1e-24			70.41	IGG4 REA; CHAIN: A; RF-AN IGM/LAMBDA; CHAIN: H, L;	COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN), RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
105	1axt	H	37	226	1.5e-29	-0.26	0.11		IMMUNOGLOBULIN IGG2A; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY FAB; CATALYST, ALDOLASE REACTION
105	1b2w	L	31	232	3.4e-19			70.24	ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X- RAY STRUCTURE, THREE- DIMENSIONAL STRUCTURE, GAMMA-3 INTERFERON, IMMUNE SYSTEM
105	1b6d	A	31	228	1e-18			66.53	IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT- CHAIN DIMER HEADER
105	1bbj	L	31	228	1.7e-19			70.26	IMMUNOGLOBULIN FAB' FRAGMENT OF MONOCLONAL ANTIBODY B72.3 1BBJ3 (MURINE/HUMAN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
105	1bih	A	32	402	1.5e-40	-0.19	0.15		CHIMERA) IBBJ 4 HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
105	1bih	A	34	403	1.5e-40			105.99	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
105	1bih	A	4	312	1e-33	-0.32	0.01		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
105	1bog	A	31	232	1.7e-19			69.73	ANTIBODY (CB 4-1); CHAIN: A, B; PEPTIDE; CHAIN: C;	COMPLEX (ANTIBODY/PEPTIDE) POLYSPECIFICITY, CROSS REACTIVITY, FAB-FRAGMENT, PEPTIDE, 2 HIV-1, COMPLEX (ANTIBODY/PEPTIDE)
105	1cel	L	31	228	6.8e-19			66.53	CAMPATH-1H:LIGHT CHAIN; CHAIN: L; CAMPATH-1H:HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P; AXONIN-1; CHAIN: A;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
105	1cs6	A	32	403	1.7e-48	-0.09	0.07			CELL ADHESION NEURAL CELL ADHESION
105	1ct8	B	36	232	3.4e-31	0.06	0.28		7C8 FAB FRAGMENT; SHORT CHAIN; CHAIN: A, C; 7C8 FAB FRAGMENT; LONG CHAIN; CHAIN: B, D	IMMUNE SYSTEM ABZYME TRANSITION STATE ANALOG, IMMUNE SYSTEM
105	1cvs	C	138	322	3.4e-37	-0.19	0.09		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR
105	1cvs	D	138	322	8.5e-39	-0.07	0.09		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
105	1cvs	D	243	402	3.4e-25	0.14	0.27		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
105	1dfb	L	137	319	5.1e-20	-0.19	0.28		IMMUNOGLOBULIN 3D6 FAB IDFB 3	
105	1dfb	L	31	232	1.7e-18			67.12	IMMUNOGLOBULIN 3D6 FAB IDFB 3	
105	1dgi	R	33	322	6.8e-32	-0.38	0.19		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
105	1dn2	A	133	312	3.4e-25	0.08	0.13		IMMUNOGLOBULIN LAMBDA HEAVY CHAIN; CHAIN: A, B; ENGINEERED PEPTIDE; CHAIN: E, F;	IMMUNE SYSTEM FC IGG PHAGE DISPLAY PEPTIDE
105	1dn2	A	235	404	1.7e-50	0.03	-0.11		IMMUNOGLOBULIN	IMMUNE SYSTEM FC IGG PHAGE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									LAMBDA HEAVY CHAIN; CHAIN: A, B; ENGINEERED PEPTIDE; CHAIN: E, F;	DISPLAY PEPTIDE
105	1e4k	A	133	312	1e-24	0.11	0.06		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR CHAIN: C; FC FRAGMENT OF HUMAN IGG1; CHAIN: A, B;	COMPLEX CD16; IGG1-FC COMPLEX, FC FRAGMENT, IGG, FC, RECEPTOR, CD16, GAMMA
105	1e4k	A	235	404	5.1e-50	0.16	-0.07		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR CHAIN: C; FC FRAGMENT OF HUMAN IGG1; CHAIN: A, B;	COMPLEX CD16; IGG1-FC COMPLEX, FC FRAGMENT, IGG, FC, RECEPTOR, CD16, GAMMA
105	1epf	A	145	312	2.6e-23	0.04	0.99		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
105	1ev2	E	130	322	1.5e-34	-0.07	0.06		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
105	1ev2	G	138	326	1.4e-37	0.16	0.15		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									RECEPTOR 2; CHAIN: E, F, G, H;	DOMAINS, B-TREFOIL FOLD
105	1fc2	D	128	322	1e-24			66.62	IMMUNOGLOBULIN IMMUNOGLOBULIN FC AND FRAGMENT B OF PROTEIN A COMPLEX 1FC2 4	
105	1fc2	D	133	312	1e-24	0.04	0.07		IMMUNOGLOBULIN IMMUNOGLOBULIN FC AND FRAGMENT B OF PROTEIN A COMPLEX 1FC2 4	
105	1fcg	A	133	322	1.3e-22	0.19	0.42		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
105	1fsk	C	33	232	8.5e-33	-0.14	0.12		MAJOR POLLEN ALLERGEN BET V 1- A; CHAIN: A, D, G, J; IMMUNOGLOBULIN KAPPA LIGHT CHAIN; CHAIN: B, E, H, K; ANTIBODY HEAVY CHAIN FAB; CHAIN: C, F, I, L;	IMMUNE SYSTEM BET V 1-A, BETVI ALLERGEN; BV16 FAB-FRAGMENT, KAPPA MOPC21 CODING SEQUENCE; HEAVY CHAIN OF THE MONOCLONAL ANTIBODY MST2; BET V 1, BV16 FAB FRAGMENT, ANTIBODY ALLERGEN COMPLEX
105	1fvd	A	31	232	1.2e-19			69.02	IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
105	1gc1	L	34	228	3.4e-18			70.37	ENVELOPE PROTEIN GP120; CHAIN: G; CD4; CHAIN: C; ANTIBODY 17B;	COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB) COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB), HIV-1 EXTERIOR 2 ENVELOPE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: L, H;	GP120, T-CELL SURFACE GLYCOPROTEIN CD4, 3 ANTIGEN-BINDING FRAGMENT OF HUMAN IMMUNOGLOBULIN 17B, 4 GLYCOSYLATED PROTEIN
105	1gpo	H	36	231	3.4e-30	-0.06	0.00		ANTIBODY M41; CHAIN: L, H, M, I;	IMMUNOGLOBULIN PROTEIN ENGINEERING, ANTIBODY DESIGN, IMMUNOGLOBULIN 2 STRUCTURE, ANTIGEN-BINDING SITE, CANONICAL CONFORMATION, 3 COMPLEMENTARITY - DETERMINING REGION
105	1hyx	H	36	232	1.7e-29	0.02	-0.06		IMMUNOGLOBULIN 6D9; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY 6D9 CATALYTIC ANTIBODY, ESTER HYDROLYSIS, ESTEROLYTIC, FAB, 2 IMMUNOGLOBULIN
105	ligc	L	31	232	3.4e-16			66.36	COMPLEX (ANTIBODY/BINDIN G PROTEIN) IGG1 FAB FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN III) IIGC 5 PROTEIN G, STREPTOCOCCUS IIGC 15	
105	ligy	B	19	403	3.4e-76			72.79	IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION
105	ligy	B	36	404	3.4e-76	-0.25	0.05		IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
105	1itb	B	41	326	2.6e-27			68.50	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
105	1iil	A	34	231	3.4e-23			69.16	LAMBDA III BENCE JONES PROTEIN CLE; CHAIN: A, B	IMMUNOGLOBULIN IMMUNOGLOBULIN, BENCE JONES PROTEIN
105	1mam	H	36	227	6.8e-30	-0.23	0.03		IMMUNOGLOBULIN ANTIGEN-BINDING FRAGMENT (FAB) (JGG2B, KAPPA) IMAM 3	
105	1mco	H	18	404	1.5e-82			76.87	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (JGG1) (MCG) WITH A HINGE DELETION 1MCO 3	
105	1mco	H	32	404	1.5e-82	-0.27	0.40		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (JGG1) (MCG) WITH A HINGE DELETION 1MCO 3	
105	1mco	H	5	312	1.4e-49	-0.11	0.07		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (JGG1) (MCG) WITH A HINGE DELETION 1MCO 3	
105	1mfb	L	243	404	6.8e-15	0.15	-0.19		IMMUNOGLOBULIN FAB FRAGMENT (MURINE SE155-4) COMPLEX WITH	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									HEPTASACCHARIDE 1MFB 3 B: GAL(1-2)MAN(1-4)RAM(1-3)GAL(1-2)[ABE(1-3)]MAN(1-4)RAM 1MFB 4	
105	1mnu	H	36	226	5.1e-29	0.03	0.16		IGG2A-KAPPA ANTIBODY MN12H2 (LIGHT CHAIN); CHAIN: L; IGG2A-KAPPA ANTIBODY MN12H2 (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM MURINE IMMUNOGLOBULIN IGG2A KAPPA, BACTERICIDAL ANTIBODY, 2 EPI TOPE P1.16 OF POR A FROM NEISSERIA MENINGITIDIS, 3 UNLIGANDED, IMMUNE SYSTEM
105	1sm3	H	33	229	1.7e-31	-0.01	0.09		SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPI TOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPI TOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPI TOPE)
105	2feb	A	133	325	2.6e-25	0.08	0.16		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
105	2hlp	H	36	229	8.5e-29	-0.01	0.03		2H1; CHAIN: L, H; PA1; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE) ANTIBODY STRUCTURE, CRYPTOCOCCUS, PEPTIDE, PHAGE LIBRARY, 2 POLYSACCHARIDE, COMPLEX (ANTIBODY/PEPTIDE)
105	2hmi	D	37	226	1e-28	0.06	0.06		HIV-1 REVERSE TRANSCRIPTASE; CHAIN: A, B; MONOCLONAL ANTIBODY 28; CHAIN: C, D; DNA; CHAIN: E, F;	COMPLEX (RT/DNA/FAB) HIV-1 RT; FAB 28; AIDS, HIV-1, RT, POLYMERASE
105	32c2	B	33	226	3.4e-31	-0.22	0.06		IGG1 ANTIBODY 32C2; CHAIN: A;	IMMUNE SYSTEM FAB, ANTIBODY, AROMATASE, P450

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
105	3ft	A	34	231	1.4e-18			67.63	IGG1 ANTIBODY 32C2; CHAIN: B; METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: A, C; METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: B, D;	IMMUNE SYSTEM METAL CHELATASE, CATALYTIC ANTIBODY, FAB FRAGMENT, IMMUNE 2 SYSTEM
105	6fab	L	31	232	1.7e-16			70.37	IMMUNOGLOBULIN ANTIGEN-BINDING FRAGMENT OF THE MURINE ANTI-PHENYLARSONATE 6FAB 3 ANTIBODY 36-71, FAB 36-71 6FAB 4	
105	8fab	A	34	226	1.2e-23			70.63	IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HIL) 8FAB 3	
106	lapj		1221	1284	2.6e-14	0.49	0.98		FIBRILLIN; CHAIN: NULL;	EXTRACELLULAR MATRIX FIBRILLIN FRAGMENT, MICROFIBRIL, TB MODULE, MARFAN SYNDROME, 2 CONNECTIVE TISSUE, NOVEL FOLD, EXTRACELLULAR MATRIX
106	lapj		786	857	3.9e-16	0.71	0.99		FIBRILLIN; CHAIN: NULL;	EXTRACELLULAR MATRIX FIBRILLIN FRAGMENT, MICROFIBRIL, TB MODULE,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										MARFAN SYNDROME, 2 CONNECTIVE TISSUE, NOVEL FOLD, EXTRACELLULAR MATRIX
106	1apj		979	1043	1.2e-10	0.31	0.55		FIBRILLIN; CHAIN: NULL;	EXTRACELLULAR MATRIX FIBRILLIN FRAGMENT, MICROFIBRIL, TB MODULE, MARFAN SYNDROME, 2 CONNECTIVE TISSUE, NOVEL FOLD, EXTRACELLULAR MATRIX
106	1apq		1508	1548	1e-10	-0.15	0.12		COMPLEMENT PROTEASE C1r; CHAIN: NULL;	COMPLEMENT COMPLEMENT, EGF, CALCIUM BINDING, SERINE PROTEASE
106	1aut	L	1133	1229	5.2e-13	-0.17	0.23		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
106	1aut	L	115	200	5.2e-10	0.05	-0.01		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
106	1aut	L	1338	1441	1e-20	0.48	0.71		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	1aut	L	1423	1522	2.6e-23	0.18	0.68		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO- MAI; CHAIN: P;	COAGULATION/INHIBITOR) COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
106	1aut	L	1449	1555	1.2e-15	-0.06	0.05		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO- MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
106	1aut	L	174	290	2.6e-10	0.01	0.10		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO- MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
106	1aut	L	487	575	2.6e-23	0.14	0.74		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO- MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
106	1aut	L	816	914	2.6e-14	0.17	0.11		ACTIVATED PROTEIN C; CHAIN:	COMPLEX (BLOOD COAGULATION/INHIBITOR)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									C, L; D-PHE-PRO-MAI; CHAIN: P;	AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
106	1aut	L	859	950	6.5e-19	0.16	0.27		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
106	1aut	L	897	987	9.1e-18	0.26	0.22		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
106	1dan	L	1039	1124	6.8e-12	0.01	-0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
106	1dan	L	1137	1230	3.4e-12	-0.05	0.07		BLOOD COAGULATION FACTOR VIIA;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKE TONE (DFFRCMK) WITH CHAIN: C;	GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
106	1dan	L	941	1032	3.4e-10	-0.17	0.04		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKE TONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
106	1dqb	A	1423	1511	1e-19	0.30	-0.07		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION
106	1dqb	A	488	570	9.1e-19	0.12	0.10		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION
106	1dqb	A	897	981	5.2e-15	0.28	0.10		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION
106	1dva	L	1039	1124	6.8e-12	0.16	-0.18		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	1dva	L	286	379	1e-13	0.25	-0.05		PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y; DES-GLA FACTOR VIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
106	1dva	L	941	1032	3.4e-10	-0.29	0.16		DES-GLA FACTOR VIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
106	1dx5	I	1181	1338	3.9e-14	0.05	0.19		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, 2 ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
106	1dx5	I	124	217	3.9e-12	0.23	0.11		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; N; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L- GLY-L-ARM; CHAIN: E, F, G, H;	FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
106	1dx5	I	1266	1381	7.8e-16	-0.18	0.12		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; N; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L- GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
106	1dx5	I	1340	1465	1.3e-22	-0.33	0.40		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; N; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L- GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
106	1dx5	I	1383	1506	9.1e-27	0.19	0.21		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									THROMBOMODULI N; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
106	1dx5	I	1424	1548	1e-23	0.32	0.88		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULI N; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
106	1dx5	I	1466	1598	8.5e-12	0.10	0.00		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULI N; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
106	1dx5	I	185	320	1.3e-15	0.13	0.05		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULI N; CHAIN: I, J, K, L;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	ANTIFIBRINOLYTIC COMPLEX
106	1dx5	I	448	570	1.3e-23	0.07	0.53		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULI N; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
106	1dx5	I	489	612	1.7e-16	0.19	-0.13		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULI N; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
106	1dx5	I	857	979	1e-23	-0.02	0.64		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULI N; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	1emn		1145	1212	1.7e-12	0.05	0.29		GLY-L-ARM; CHAIN: E, F, G, H; FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1emn		1178	1224	6.5e-13	0.11	0.98		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1emn		1181	1265	1e-12	-0.33	0.78		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1emn		1337	1402	3.9e-19	0.08	0.88		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1emn		1465	1527	3.9e-19	0.18	0.72		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									NULL;	EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1emn		1506	1551	1.3e-11	0.28	0.78		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1emn		410	489	3.4e-13	0.05	-0.19		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1emn		488	549	6.5e-20	-0.58	0.62		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1emn		530	615	1e-15	0.12	0.19		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	1emn		711	777	6.8e-13	-0.64	0.12		FIBRILLIN; CHAIN: NULL;	SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1f5y	A	76	148	1.7e-10	0.09	-0.18		LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: A;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
106	1fak	L	1039	1124	6.8e-12	0.07	-0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
106	1fak	L	1137	1230	3.4e-12	-0.18	0.03		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	1fak	L	1336	1443	2.6e-23	0.25	0.28		CHAIN: I; BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
106	1fak	L	1423	1526	2.6e-23	-0.10	0.23		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
106	1fak	L	163	271	1.3e-08	0.05	-0.15		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
106	1fak	L	286	379	1e-13	-0.28	0.07		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
106	1fak	L	481	575	2.6e-22	0.02	0.99		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
106	1fak	L	857	957	1.3e-20	0.09	0.55		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
106	1fak	L	897	987	7.8e-19	-0.07	0.07		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	1fak	L	941	1032	3.4e-10	-0.08	0.06		CHAIN: I; BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
106	1god	A	158	290	1.3e-09	0.21	-0.19		PHOSPHOLIPASE A2; CHAIN: A;	HYDROLASE GODMT-II; LYS49-PHOSPHOLIPASE A2, SNAKE VENOM, BOTHROPS
106	1hae		157	201	5.2e-10	0.80	-0.05		HERGULIN-ALPHA; CHAIN: NULL;	GROWTH FACTOR NEU DIFFERENTIATION FACTOR (RAT), ACETYLCHOLINE GROWTH FACTOR
106	1igr	A	122	291	3.9e-10	-0.17	0.04		INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A;	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY
106	1jia	A	1309	1429	1.2e-22	0.10	-0.20		PHOSPHOLIPASE A2; CHAIN: A, B;	PHOSPHOLIPASE PHOSPHOLIPASE A2, AGKISTRODON HALYS PALLAS CRYSTAL 2 STRUCTURE
106	1klo		129	246	1.3e-13	0.06	-0.18		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
106	1klo		1352	1533	6.5e-21	0.01	-0.13		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
106	1klo		163	327	2.6e-18	0.27	0.78		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
106	1klo		294	447	1.7e-08	0.30	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
106	1klo		735	898	3.4e-11	0.12	-0.18		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	1klo		771	930	5.2e-14	0.14	0.05		NULL; LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
106	1klo		868	1027	2.6e-12	-0.03	0.03		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
106	1pfx	L	1084	1229	2.6e-18	0.08	-0.03		FACTOR IXA; CHAIN: C, L,; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
106	1pfx	L	1296	1408	1.3e-22	-0.05	0.30		FACTOR IXA; CHAIN: C, L,; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
106	1pfx	L	129	249	3.9e-16	0.17	-0.15		FACTOR IXA; CHAIN: C, L,; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
106	1pfx	L	1352	1491	2.6e-32	-0.02	0.03		FACTOR IXA; CHAIN: C, L,; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
106	1pfx	L	1391	1535	6.5e-30	-0.03	0.16		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
106	1pfx	L	1436	1550	6.5e-24	-0.03	0.12		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
106	1pfx	L	159	312	2.6e-21	0.02	-0.18		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
106	1pfx	L	286	379	1.5e-11	0.08	-0.07		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	1pfx	L	455	575	2.6e-31	-0.44	0.40		FACTOR IXA; CHAIN: C, L;; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
106	1pfx	L	868	987	1.2e-24	0.13	-0.03		FACTOR IXA; CHAIN: C, L;; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
106	1pp2	R	1252	1387	7.8e-19	0.08	-0.19		HYDROLASE CALCIUM-FREE PHOSPHOLIPASE A=2= (E.C.3.1.1.4) 1PP2 4	
106	1qfk	L	1471	1550	8.5e-13	0.18	0.65		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
106	1tpg		119	190	3.9e-10	0.02	0.19		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN:	PLASMINOGEN ACTIVATION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	1tpg		1320	1430	1e-23	0.28	-0.18		NULL; ITPG 8	PLASMINOGEN ACTIVATION
106	1tpg		1405	1512	5.2e-20	0.04	-0.05		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
106	1tpg		140	220	7.8e-16	0.60	0.40		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
106	1tpg		471	570	3.9e-22	-0.20	0.34		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
106	1tpg		879	969	2.6e-19	0.03	-0.13		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
106	1whe		148	222	2.6e-12	0.14	-0.07		COAGULATION FACTOR X; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN, HYDROLASE, SERINE PROTEASE, PLASMA, BLOOD 2 COAGULATION FACTOR
106	1whe		906	984	6.5e-15	-0.07	0.17		COAGULATION FACTOR X; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN, HYDROLASE, SERINE PROTEASE, PLASMA, BLOOD 2 COAGULATION FACTOR
106	9wga	A	1081	1250	6.8e-13	0.05	-0.14		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2)	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
106	9wga	A	586	749	3.4e-11	0.09	-0.19		9WGA 3 LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
108	1b08	A	211	312	3.4e-18	0.04	-0.19		LUNG SURFACTANT PROTEIN D; CHAIN: A, B, C;	SUGAR BINDING PROTEIN C-TYPE LECTIN, CRD, SP-D, COLECTIN, ALPHA-HELICAL COILED-2 COIL, LUNG SURFACTANT, SUGAR BINDING PROTEIN
108	1bj3	A	29	178	8.5e-33			69.74	COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-BINDING PROTEIN B; CHAIN: B;	COLLAGEN BINDING PROTEIN IX-BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
108	1bj3	A	32	177	8.5e-33	0.40	1.00		COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-BINDING PROTEIN B; CHAIN: B;	COLLAGEN BINDING PROTEIN IX-BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
108	1c3a	B	32	180	5.1e-31	0.38	0.81		FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT;	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
108	1dv8	A	211	309	6.8e-21	0.00	-0.19		CHAIN: B ASIALOGLYCOPROTEIN RECEPTOR 1; CHAIN: A;	SIGNALING PROTEIN HEPATIC LECTIN HI; C-TYPE LECTIN CRD
108	1dv8	A	33	177	5.1e-29	0.30	0.57		ASIALOGLYCOPROTEIN RECEPTOR 1; CHAIN: A;	SIGNALING PROTEIN HEPATIC LECTIN HI; C-TYPE LECTIN CRD
108	1egg	A	33	177	3.4e-30	0.26	1.00		MACROPHAGE MANNOSE RECEPTOR; CHAIN: A, B;	SUGAR BINDING PROTEIN C-TYPE LECTIN, MANNOSE RECEPTOR
108	1egg	B	31	184	6.8e-31	0.14	0.98		MACROPHAGE MANNOSE RECEPTOR; CHAIN: A, B;	SUGAR BINDING PROTEIN C-TYPE LECTIN, MANNOSE RECEPTOR
108	1esl		45	187	3.4e-27	0.71	0.93		CELL ADHESION PROTEIN E-SELECTIN (LECTIN AND EGF DOMAINS, RESIDUES 1 - 157) IESL 3 (FORMERLY KNOWN AS ELAM-1) IESL 4	
108	1esl		46	214	3.4e-27			62.46	CELL ADHESION PROTEIN E-SELECTIN (LECTIN AND EGF DOMAINS, RESIDUES 1 - 157) IESL 3 (FORMERLY KNOWN AS ELAM-1) IESL 4	
108	1htm		15	181	3.4e-26			61.20	TETRALECTIN; CHAIN: NULL; IESL 4	LECTIN TETRALECTIN, PLASMINOGEN BINDING, KRINGLE 4, ALPHA-HELICAL 2 COILED COIL,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
108	1ixx	A	32	177	8.5e-31	0.38	1.00		COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	C-TYPE LECTIN, CARBOHYDRATE RECOGNITION DOMAIN
108	1ixx	A	33	178	8.5e-31			63.16	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
108	1ixx	B	32	180	3.4e-31	0.29	0.48		COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
108	1ixx	B	34	180	3.4e-31			55.73	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
108	1lit		33	179	1e-32	0.56	0.90		LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR, PANCREATIC STONE INHIBITOR, LECTIN
108	1lit		33	180	1e-32			76.77	LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR, PANCREATIC STONE INHIBITOR, LECTIN
108	1qdd	A	20	180	5.1e-34			80.98	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN, PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
108	1qdd	A	210	313	5.1e-19	0.20	-0.15		LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN, PANCREATIC STONE PROTEIN, PSP;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
108	1qdd	A	26	179	5.1e-34	0.42	0.99		LITHOSTATHINE;	PANCREATIC STONE INHIBITOR, LITHOSTATHINE
108	1m3		29	181	3.4e-26			68.02	TETRALECTIN; CHAIN: NULL;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
108	2afp	A	210	309	3.4e-18	0.12	-0.15		SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	LECTIN TETRALECTIN, PLASMINOGEN BINDING, KRINGLE 4, C-TYPE LECTIN, 2 CARBOHYDRATE RECOGNITION DOMAIN ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C-2 TYPE LECTIN, ANTIFREEZE PROTEIN
109	1emn		243	328	3.4e-14	0.09	-0.17		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
109	1f7e	A	38	72	5.1e-07	-0.02	0.04		BLOOD COAGULATION FACTOR VII; CHAIN: A;	BLOOD CLOTTING FACTOR VII, BLOOD COAGULATION, EGF-LIKE DOMAIN, BLOOD 2 CLOTTING
109	1kdo		239	374	3.4e-17	0.09	-0.19		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
109	1klo		247	404	3.9e-10	0.09	0.10		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
109	1klo		247	406	3.4e-17			76.67	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
109	1qfk	L	39	110	8.5e-10	0.07	-0.13		NULL; COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
109	1qub	A	146	470	1.3e-14			91.30	HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
109	1xka	L	73	148	1.7e-08	0.08	-0.17		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
109	4mt2		276	339	6.8e-09	0.13	-0.17		METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2 3	
109	9wga	A	64	232	3.4e-18	0.00	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
110	1ac6	A	16	123	8.5e-29			52.19	T-CELL RECEPTOR ALPHA; CHAIN: A;	RECEPTOR RECEPTOR, V ALPHA DOMAIN, SITE-DIRECTED

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									B;	MUTAGENESIS, 2 THREE-DIMENSIONAL STRUCTURE, GLYCOPROTEIN, SIGNAL
110	1b0w	A	14	123	1.7e-34			51.99	BENCE-JONES KAPPA I PROTEIN BRE; CHAIN: A, B, C; IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNE SYSTEM BENCE-JONES; IMMUNOGLOBULIN, AMYLOID, IMMUNE SYSTEM
110	1b6d	A	16	122	3.4e-36	0.49	0.62		IMMUNOGLOBULIN	IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
110	1bj1	L	16	122	5.1e-38	0.33	0.83		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
110	1bw w	A	13	122	8.5e-35			50.58	IG KAPPA CHAIN V-I REGION REI; CHAIN: A, B;	IMMUNE SYSTEM REIV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENCE-JONES 2 PROTEIN, IMMUNE SYSTEM
110	1dee	A	16	122	5.1e-39	0.74	0.82		IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A; CHAIN: G, H;	IMMUNE SYSTEM FAB-IBP COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3 SPECIFICITY
110	1dfb	L	16	122	5.1e-36	0.65	0.83		IMMUNOGLOBULIN 3D6 FAB 1DFB 3	
110	1dql	L	16	122	3.4e-38	0.64	0.88		IGM MEZ IMMUNOGLOBULIN; CHAIN: L; IGM MEZ IMMUNOGLOBULIN; CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD, ANTIBODY, IGM, FV
110	1fgv	L	14	122	8.5e-37			52.50	IMMUNOGLOBULIN FV FRAGMENT OF A	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									HUMANIZED VERSION OF THE ANTI-CD18 IFGV 3 ANTIBODY 'H52' (HUH52-AA.FV) IFGV 4	
110	1fgv	L	16	122	8.5e-37	0.30	0.63		IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 IFGV 3 ANTIBODY 'H52' (HUH52-AA.FV) IFGV 4	
110	1fvc	A	16	122	8.5e-37	0.11	0.77		IMMUNOGLOBULIN FV FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 8 IFVC 3	
110	1fvd	A	16	122	3.4e-37	0.20	0.64		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 IFVD 3	
110	1kb5	A	15	123	1.7e-38	0.46	0.84		KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T- CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
110	1kb5	A	17	123	1.7e-38			55.34	KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T- CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
110	1nmb	L	14	123	1.4e-30			51.23	H; N9 NEURAMINIDASE; INMB 4 CHAIN: N; INMB 5 FAB NC10; INMB 9 CHAIN: L, H; INMB 10	(IMMUNOGLOBULIN/RECEPTOR) COMPLEX (HYDROLASE/IMMUNOGLOBULIN)
110	2fgw	L	16	122	5.1e-37	0.32	0.92		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	
111	1ac6	A	14	120	1e-26			50.92	T-CELL RECEPTOR ALPHA; CHAIN: A, B;	RECEPTOR RECEPTOR, V ALPHA DOMAIN, SITE-DIRECTED MUTAGENESIS, 2 THREE- DIMENSIONAL STRUCTURE, GLYCOPROTEIN, SIGNAL
111	1b0w	A	11	120	3.4e-35			51.25	BENCE-JONES KAPPA I PROTEIN BRE; CHAIN: A, B, C; IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNE SYSTEM BENCE-JONES; IMMUNOGLOBULIN, AMYLOID, IMMUNE SYSTEM
111	1b6d	A	12	119	1.7e-37	0.60	0.98			IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT- CHAIN DIMER HEADER
111	1b88	A	13	120	5.1e-36			50.11	T CELL RECEPTOR V-ALPHA DOMAIN; CHAIN: A, B;	T CELL RECEPTOR TCR; T CELL RECEPTOR, MHC CLASS I, HUMAN IMMUNODEFICIENCY VIRUS, 2 MOLECULAR RECOGNITION
111	1bj1	L	12	119	3.4e-39	0.37	1.00		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN),

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	ANGIOGENIC FACTOR
111	1bw w	A	9	119	1e-36			52.25	IG KAPPA CHAIN V-1 REGION REI; CHAIN: A, B;	IMMUNE SYSTEM REIV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENICE-JONES 2 PROTEIN, IMMUNE SYSTEM
111	1dee	A	12	119	1.7e-40	0.72	0.96		IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A; CHAIN: G, H;	IMMUNE SYSTEM FAB-IBP COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3 SPECIFICITY
111	1dfb	L	12	119	3.4e-37	0.42	0.77		IMMUNOGLOBULIN 3D6 FAB 1DFB 3	
111	1dql	L	12	119	1.2e-39	0.53	0.98		IGM MEZ IMMUNOGLOBULIN; CHAIN: L; IGM MEZ IMMUNOGLOBULIN; CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD, ANTIBODY, IGM, FV
111	1fgv	L	11	119	6.8e-38			51.87	IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 1FGV 3 ANTIBODY 'H52' (HUH52-AA FV) 1FGV 4	
111	1fgv	L	12	119	6.8e-38	0.77	0.96		IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 1FGV 3 ANTIBODY 'H52'	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									(HUH52-AA FV) 1FGV 4	
111	1fvc	A	12	119	1.2e-37	0.29	0.74		IMMUNOGLOBULIN FV FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 8 1FVC 3	
111	1fvd	A	12	119	3.4e-38	0.23	0.39		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
111	1kb5	A	13	120	1.7e-38	0.51	0.90		KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T-CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
111	1kb5	A	14	120	1.7e-38			54.13	KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T-CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
111	1nmb	L	11	120	5.1e-32			50.60	N9 NEURAMINIDASE; 1NMB 4 CHAIN: N; 1NMB 5 FAB NC10; 1NMB 9 CHAIN: L, H; 1NMB 10	COMPLEX (HYDROLASE/IMMUNOGLOBULIN)
111	2fgw	L	12	119	3.4e-38	0.35	0.94		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	
114	1elr	A	371	442	0.00026	-0.21	0.27		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
114	1elr	A	371	442	0.00026	-0.21	0.27		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
114	1elw	A	374	440	0.0052	-0.23	0.40		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
114	1elw	A	374	440	0.0052	-0.23	0.40		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
114	1fch	A	131	445	0.00013	-0.40	0.28		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1- CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
114	1fch	A	131	445	0.00013	-0.40	0.28		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1- CONTAINING PEPTIDE; CHAIN: C,	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
114	1fch	A	275	518	9.1e-09	-0.34	0.57		D; PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
114	1fch	A	275	518	9.1e-09	-0.34	0.57		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
115	1a5e		6	147	5.1e-14	0.04	-0.05		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
115	1awc	B	166	315	1.2e-31	0.93	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
115	1awc	B	195	349	1e-40	0.57	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
115	lawc	B	268	420	1.4e-36	-0.00	-0.06		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
115	lawc	B	40	215	3.4e-28	0.29	0.98		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
115	lawc	B	69	249	1.3e-35	0.30	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
115	lawc	B	6	181	5.1e-28	0.08	0.71		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
115	lbd8		237	386	3.4e-29	0.22	0.47		P19INK4D CDK4/6	TUMOR SUPPRESSOR TUMOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
115	1bd8		9	181	1e-26	0.10	0.03		INHIBITOR; CHAIN: NULL; P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
115	1bi7	B	6	147	3.4e-14	-0.20	0.05		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
115	1biX	B	132	287	5.2e-40	0.81	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
115	1biX	B	166	320	7.8e-39	0.44	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
115	1biX	B	198	348	5.2e-36	0.73	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
115	1biX	B	4	184	5.2e-27	0.44	1.00		CYCLIN-DEPENDENT	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
115	1blx	B	72	251	1.3e-36	0.59	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
115	1bu9	A	234	392	6.8e-31	0.37	0.28		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
115	1bu9	A	6	186	1.7e-29	0.12	0.59		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
115	1d9s	A	124	252	3.9e-29	0.37	0.99		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
115	1d9s	A	6	147	3.4e-14	0.08	-0.02		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
115	1d9s	A	9	151	1.3e-18	0.44	0.43		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
115	1ez3	A	804	880	3.9e-08	0.14	-0.19		CHAIN: A; SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
115	1ez3	A	817	880	1.3e-08	0.38	-0.05		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
115	1iib	A	234	391	3.4e-30	0.24	0.87		CYCLIN- DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
115	1iib	A	6	185	1e-28	0.03	0.77		CYCLIN- DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
115	1iib	A	80	215	1.7e-28	0.23	1.00		CYCLIN- DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
115	1ikn	D	161	348	3.4e-38	0.41	0.99		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
115	1ikn	D	2	202	1.7e-28	-0.15	0.24		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
115	likn	D	35	233	8.5e-35	0.04	0.70		I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
115	lmyo		2	56	1e-11	0.07	0.66		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLTATION, NMR, ANK-REPEAT COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
115	lnfi	E	159	348	3.4e-38	0.67	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF- KAPPA-B P50; CHAIN: B, D; I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
115	lnfi	E	159	354	1.3e-47	0.48	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF- KAPPA-B P50; CHAIN: B, D; I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
115	lnfi	E	261	453	3.4e-37	0.07	-0.14		NF-KAPPA-B P65; CHAIN: A, C; NF- KAPPA-B P50; CHAIN: B, D; I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
115	lnfi	E	34	233	3.4e-35	0.17	0.98		NF-KAPPA-B P65; CHAIN: A, C; NF- KAPPA-B P50; CHAIN: B, D; I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
115	1nfi	E	39	250	3.9e-36	0.41	0.99		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
115	1nfi	E	4	165	5.1e-27	0.28	0.83		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
115	1nfi	E	69	289	1.2e-40	0.64	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
115	1ycs	B	2	57	3.4e-14	0.39	0.70		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) ONCOGENE/ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
116	1awc	B	166	315	1.7e-34	0.79	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
116	lawc	B	195	349	1e-40	0.57	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	TRANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
116	lawc	B	200	348	1.7e-36	0.73	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
116	lawc	B	234	382	5.1e-34	0.43	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
116	lawc	B	268	399	1.7e-34	0.20	0.29		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
116	lawc	B	69	249	1.3e-35	0.30	1.00		GA BINDING PROTEIN ALPHA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
116	lawc	B	6	181	1.4e-27	0.09	0.68		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
116	lawc	B	76	215	1.7e-29	0.26	0.99		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
116	lbd8		101	249	1.7e-27	0.28	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
116	lbd8		237	385	3.4e-31	0.50	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
116	lbd8		2	113	5.1e-12	0.10	0.17		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
116	lbdx	B	101	249	1e-25	0.57	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									P19INK4D; CHAIN: B;	KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
116	1blx	B	132	287	5.2e-40	0.81	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR
116	1blx	B	166	320	7.8e-39	0.44	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
116	1blx	B	198	348	5.2e-36	0.73	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR
116	1blx	B	237	385	1.4e-31	0.56	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
116	1blx	B	4	184	5.2e-27	0.44	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR
116	1blx	B	72	251	1.3e-36	0.59	1.00		CYCLIN-	PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
116	1bu9	A	132	288	1.5e-30	0.84	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
116	1bu9	A	234	387	1.4e-35	0.29	0.66		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
116	1bu9	A	6	186	5.1e-28	0.15	0.64		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
116	1d9s	A	9	151	1.3e-18	0.44	0.43		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
116	1ez3	A	746	822	3.9e-08	0.14	-0.19		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
116	1ez3	A	759	822	1.3e-08	0.38	-0.05		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
116	1ihb	A	132	287	6.8e-30	0.61	1.00		CYCLIN-	CELL CYCLE INHIBITOR P18-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
116	1ihb	A	234	386	5.1e-35	0.46	0.94		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
116	1ihb	A	6	185	1.7e-27	0.03	0.58		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
116	1ikn	D	127	299	6.8e-34	0.35	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
116	1ikn	D	161	348	1.5e-37	0.29	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
116	1ikn	D	229	399	1.7e-33	0.15	0.19		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
116	1ikn	D	2	199	5.1e-28	0.05	0.22		NF-KAPPA-B P65 SUBUNIT; CHAIN: A;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	IKB/NFKB COMPLEX
116	1myo		2	58	3.4e-12	-0.09	0.87		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
116	1nfi	E	125	299	1.7e-34	0.76	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF- KAPPA-B P50; CHAIN: B, D; I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
116	1nfi	E	159	356	7.8e-48	0.72	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF- KAPPA-B P50; CHAIN: B, D; I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
116	1nfi	E	161	348	8.5e-38	0.58	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF- KAPPA-B P50; CHAIN: B, D; I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
116	1nfi	E	228	399	3.4e-33	0.38	0.51		NF-KAPPA-B P65; CHAIN: A, C; NF- KAPPA-B P50; CHAIN: B, D; I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
116	1nfi	E	263	444	1.4e-33	0.10	-0.14		NF-KAPPA-B P65; CHAIN: A, C; NF- KAPPA-B P50; CHAIN: B, D; I-	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT),

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									KAPPA-B-ALPHA; CHAIN: E, F;	ANKYRIN 2 REPEAT HELIX
116	1nfi	E	2	199	3.4e-28	0.28	0.19		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
116	1nfi	E	39	250	3.9e-36	0.41	0.99		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
116	1nfi	E	69	289	1.2e-40	0.64	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
116	1ycs	B	2	57	1.2e-13	0.39	0.70		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
117	1a5t		150	455	6.8e-14	0.25	-0.05		DELTA PRIME; CHAIN: NULL;	ZINC FINGER HOLB; ZINC FINGER, DNA REPLICATION
119	1d2n	A	401	566	3.4e-29	0.55	0.65		N-	HEXAMERIZATION DOMAIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									ETHYLMALIMIDE-SENSITIVE FUSION PROTEIN; CHAIN: A;	HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT
119	1e94	E	388	489	5.1e-13	-0.54	0.21		HEAT SHOCK PROTEIN HSLV; CHAIN: A, B, C, D; HEAT SHOCK PROTEIN HSLU; CHAIN: E, F;	CHAPERONE HSLV; HSLU CHAPERONE, HSLVU, CLPQY, AAA-ATPASE, ATP-DEPENDENT 2 PROTEOLYSIS, PROTEASOME
119	1e94	E	496	577	3.4e-05	-0.30	0.31		HEAT SHOCK PROTEIN HSLV; CHAIN: A, B, C, D; HEAT SHOCK PROTEIN HSLU; CHAIN: E, F;	CHAPERONE HSLV; HSLU CHAPERONE, HSLVU, CLPQY, AAA-ATPASE, ATP-DEPENDENT 2 PROTEOLYSIS, PROTEASOME
119	1g41	A	388	656	1.7e-18	-0.06	0.13		HEAT SHOCK PROTEIN HSLU; CHAIN: A;	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS
119	1shk	A	437	466	0.0024	-0.62	0.06		SHIKIMATE KINASE; CHAIN: A, B;	TRANSFERASE SHIKIMATE KINASE, PHOSPHORYL TRANSFER, ADP, SHIKIMATE 2 PATHWAY, P-LOOP PROTEIN, TRANSFERASE
119	3adk		434	599	3.9e-05	0.09	0.01		TRANSFERASE(PHOTRANSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	
120	1cs8	A	19	333	0			497.56	HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
120	1cs8	A	19	333	0			497.56	HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
120	1cs8	A	21	333	0	0.83	1.00		HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
120	1cs8	A	21	333	0	0.83	1.00		HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
120	1icf	B	292	333	1.7e-17	-0.53	0.90		CATHEPSIN L; HEAVY CHAIN; CHAIN: A, C; CATHEPSIN L; LIGHT CHAIN; CHAIN: B, D; INVARIANT CHAIN; CHAIN: I, J;	HYDROLASE II FRAGMENT, CD74 FRAGMENT CYSTEINE PROTEINASE, CATHEPSIN, MHC CLASS II, INVARIANT 2 CHAIN, THYROGLOBULIN TYPE-1 DOMAIN
120	1icf	B	292	333	1.7e-17	-0.53	0.90		CATHEPSIN L; HEAVY CHAIN; CHAIN: A, C; CATHEPSIN L; LIGHT CHAIN; CHAIN: B, D; INVARIANT CHAIN; CHAIN: I, J;	HYDROLASE II FRAGMENT, CD74 FRAGMENT CYSTEINE PROTEINASE, CATHEPSIN, MHC CLASS II, INVARIANT 2 CHAIN, THYROGLOBULIN TYPE-1 DOMAIN
121	1djx	A	242	793	0			519.97	PHOSPHOINOSITIDE -SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
121	1djx	A	242	793	0			519.97	PHOSPHOINOSITIDE -SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI- BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
121	1dix	A	259	792	0	0.65	1.00		PHOSPHOINOSITIDE -SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
121	1dix	A	259	792	0	0.68	1.00		PHOSPHOINOSITIDE -SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
121	1dix	B	200	793	0			571.84	PHOSPHOINOSITIDE -SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
121	1dix	B	200	793	0			571.84	PHOSPHOINOSITIDE -SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
121	1dix	B	201	792	0	0.65	1.00		PHOSPHOINOSITIDE -SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										CALCIUM-BINDING, PHOSPHOLIPASE C, 3
121	1djx	B	201	792	0	0.66	1.00		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	PHOSPHOINOSITIDE-SPECIFIC LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3
121	1exr	A	177	322	5.1e-36	0.18	0.07		CALMODULIN; CHAIN: A;	PHOSPHOINOSITIDE-SPECIFIC METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
121	1exr	A	177	322	5.1e-36	0.18	0.07		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
121	1mai		55	170	9.1e-29	0.89	1.00		PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN PLECKSTRIN, PHOSPHOLIPASE, INOSITOL TRISPHOSPHATE, 2 SIGNAL TRANSDUCTION PROTEIN, HYDROLASE
121	1mai		55	170	9.1e-29	0.89	1.00		PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN PLECKSTRIN, PHOSPHOLIPASE, INOSITOL TRISPHOSPHATE, 2 SIGNAL TRANSDUCTION PROTEIN, HYDROLASE
121	1mai		55	170	9.1e-29			110.09	PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN PLECKSTRIN, PHOSPHOLIPASE, INOSITOL TRISPHOSPHATE, 2 SIGNAL TRANSDUCTION PROTEIN, HYDROLASE
121	1mai		55	170	9.1e-29			110.09	PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN PLECKSTRIN, PHOSPHOLIPASE, INOSITOL TRISPHOSPHATE, 2 SIGNAL TRANSDUCTION PROTEIN, HYDROLASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
121	1tnx		179	320	3.4e-34	0.07	0.09		TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
121	1tnx		179	320	3.4e-34	0.07	0.09		TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
121	1top		179	320	1.4e-34	0.26	0.84		CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
121	1top		179	320	1.4e-34	0.26	0.84		CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
121	1vrk	A	176	323	3.4e-36	0.07	0.33		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
121	1vrk	A	176	323	3.4e-36	0.07	0.33		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
122	12e8	H	35	247	5.1e-27			64.22	2E8 (IGG1=KAPPA=) ANTIBODY; CHAIN: L, H, M, P;	IMMUNOGLOBULIN IMMUNOGLOBULIN
122	1a0q	H	40	245	5.1e-24			63.99	29G11 FAB; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, ESTERASE COMPLEX
122	1a3r	H	40	247	1.5e-27			68.09	IGG2A; CHAIN: L, H; HUMAN RHINOVIRUS CAPSID PROTEIN VP2; CHAIN: P;	(IMMUNOGLOBULIN/VIRAL PEPTIDE) ANTIBODY 8F5; IMMUNOGLOBULIN, ANTIBODY, RHINOVIRUS, NEUTRALIZATION, 2 CONTINUOUS EPTOPE, COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
122	1a3r	H	41	242	1.5e-27	0.10	0.48		IGG2A; CHAIN: L, H; HUMAN RHINOVIRUS CAPSID PROTEIN VP2; CHAIN: P;	COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE) ANTIBODY 8F5; IMMUNOGLOBULIN, ANTIBODY, RHINOVIRUS, NEUTRALIZATION, 2 CONTINUOUS EPI TOPE, COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE)
122	1a5f	H	39	245	1.7e-25			63.45	MONOCLONAL ANTI-B-SELECTIN 7A9 ANTIBODY; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB, ANTIBODY, ANTI-E-SELECTIN
122	1ae6	H	35	245	6.8e-25			63.32	ANTIBODY CTM01; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB FRAGMENT, HUMANISATION
122	1aif	L	37	231	1e-17	-0.20	0.42		ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN IMMUNOGLOBULIN, C REGION, V REGION
122	1axt	H	37	247	5.1e-27			65.91	IMMUNOGLOBULIN IGG2A; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY FAB, CATALYST, ALDOLASE REACTION
122	1ay1	H	35	247	1e-26			67.40	TP7 FAB; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY, FAB, ENZYME INHIBITOR, PCR, 2 HOT START
122	1baf	H	35	247	1e-24			63.28	IMMUNOGLOBULIN FAB FRAGMENT OF MURINE MONOCLONAL ANTIBODY AN02 COMPLEX 1BAF 3 WITH ITS HAPTEN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									(2,2,6,6-TETRAMETHYL-1-PIPERIDINYLOXY-1BAF 4 DINITROPHENYL) 1BAF 5	
122	1bog	B	35	247	3.4e-24			64.40	ANTIBODY (CB 4-1); CHAIN: A, B; PEPTIDE; CHAIN: C;	COMPLEX (ANTIBODY/PEPTIDE) POLYSPECIFICITY, CROSS REACTIVITY, FAB-FRAGMENT, PEPTIDE, 2 HIV-1, COMPLEX (ANTIBODY/PEPTIDE)
122	1bql	H	36	246	3.4e-24			64.73	COMPLEX (ANTIBODY/ANTIGEN) HYHEL-5 FAB COMPLEXED WITH BOBWHITE QUAIL LYSOZYME 1BQL 3 1BQL 95	
122	1ce1	H	37	242	1.5e-27	0.09	0.34		CAMPATH-1H: LIGHT CHAIN; CHAIN: L; CAMPATH-1H: HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
122	1cf8	H	35	247	5.1e-27			64.05	CATALYTIC ANTIBODY 19A4 (LIGHT CHAIN); CHAIN: L; CATALYTIC ANTIBODY 19A4 (HEAVY CHAIN); CHAIN: H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, TERPENOID SYNTHASE, CARBOXYLATION, 2 CYCLIZATION CASCADE
122	1cf8	H	44	242	5.1e-27	0.08	0.16		CATALYTIC ANTIBODY 19A4	CATALYTIC ANTIBODY CATALYTIC ANTIBODY,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									(LIGHT CHAIN); CHAIN: L; CATALYTIC ANTIBODY 19A4 (HEAVY CHAIN); CHAIN: H;	TERPENOID SYNTHASE, CARBOCATION, 2 CYCLIZATION CASCADE
122	1cf8	L	40	231	1.4e-17	-0.19	0.31		CATALYTIC ANTIBODY 19A4 (LIGHT CHAIN); CHAIN: L; CATALYTIC ANTIBODY 19A4 (HEAVY CHAIN); CHAIN: H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, TERPENOID SYNTHASE, CARBOCATION, 2 CYCLIZATION CASCADE
122	1cf9	H	41	242	6.8e-30	0.20	0.57		FAB ANTIBODY LIGHT CHAIN; CHAIN: L; FAB ANTIBODY HEAVY CHAIN; CHAIN: H;	IMMUNE SYSTEM ANTI-PRION FAB 3F4; ANTI-PRION FAB 3F4 ANTI-PRION ANTIBODY, FAB 3F4
122	1cf8	B	37	247	3.4e-24			62.70	7C8 FAB FRAGMENT; SHORT CHAIN; CHAIN: A, C; 7C8 FAB FRAGMENT; LONG CHAIN; CHAIN: B, D	IMMUNE SYSTEM ABZYME TRANSITION STATE ANALOG, IMMUNE SYSTEM
122	1dqq	B	44	242	6.8e-28	-0.13	0.07		ANTI-LYSOZYME ANTIBODY HYHEL-63 (LIGHT CHAIN); CHAIN: A, C; ANTI-LYSOZYME ANTIBODY HYHEL-63 (HEAVY CHAIN); CHAIN: B, D;	IMMUNE SYSTEM ANTI-LYSOZYME ANTIBODY, HYHEL-63, HEN EGG WHITE LYSOZYME
122	1e6o	L	40	231	8.5e-18	-0.17	0.06		IMMUNOGLOBULIN LIGHT CHAIN;	IMMUNOGLOBULIN FAB, ANTIBODY, ANTIGEN, HIV-1, P24,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: L; IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H;	CA
122	1f5w	A	35	150	1.3e-24	0.36	0.98		COXSACKIE VIRUS AND ADENOVIRUS RECEPTOR; CHAIN: A, B;	VIRUS/VIRAL PROTEIN RECEPTOR IMMUNOGLOBULIN V DOMAIN FOLD, SYMMETRIC DIMER
122	1f5w	A	37	152	3.4e-22	0.22	0.92		COXSACKIE VIRUS AND ADENOVIRUS RECEPTOR; CHAIN: A, B;	VIRUS/VIRAL PROTEIN RECEPTOR IMMUNOGLOBULIN V DOMAIN FOLD, SYMMETRIC DIMER
122	1fig	H	35	244	-8.5e-24			71.28	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (KAPPA LIGHT CHAIN) FAB' FRAGMENT IFIG 3	
122	1fms	L	37	231	1.7e-18	-0.07	0.06		IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A:ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN , BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE
122	1fsk	B	41	231	1e-17	0.03	0.00		MAJOR POLLEN ALLERGEN BET V 1- A; CHAIN: A, D, G, J; IMMUNOGLOBULIN KAPPA LIGHT CHAIN; CHAIN: B, E, H, K; ANTIBODY HEAVY CHAIN FAB; CHAIN: C, F, I, L;	IMMUNE SYSTEM BET V I-A, BETVI ALLERGEN; BV16 FAB-FRAGMENT, KAPPA MOPC21 CODING SEQUENCE; HEAVY CHAIN OF THE MONOCLONAL ANTIBODY MST2; BET V 1, BV16 FAB FRAGMENT, ANTIBODY ALLERGEN COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
122	1ghf	H	40	245	1.7e-23			66.93	ANTI-ANTI-IDIO TYPE GH1002 FAB FRAGMENT; CHAIN: L, H	ANTIBODY FAB FRAGMENT ANTIBODY FAB FRAGMENT
122	1gpo	H	44	242	1.7e-28	0.04	-0.09		ANTIBODY M41; CHAIN: L, H, M, I;	IMMUNOGLOBULIN PROTEIN ENGINEERING, ANTIBODY DESIGN, IMMUNOGLOBULIN 2 STRUCTURE, ANTIGEN-BINDING SITE, CANONICAL CONFORMATION, 3 COMPLEMENTARITY- DETERMINING REGION
122	1igj	B	36	246	1.7e-22			65.63	IMMUNOGLOBULIN FAB (GG2A,KAPPA) FRAGMENT (26-10) COMPLEX WITH DIGOXIN IIGJA 1 IIGJA 2	
122	1kb5	H	35	247	6.8e-25			68.30	KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T- CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
122	1kb5	L	37	231	1.7e-19	0.15	0.88		KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T- CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
122	1mfe	H	37	247	1.5e-22			64.30	IMMUNOGLOBULIN FAB FRAGMENT (MURINE SE155-4) COMPLEX WITH DODECASACCHARI DE 1MFE 3 {-	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									3)ALPHA-D-GALACTOSE(1-2)[ALPHA-D-ABEQUOSE(1-3)]ALPHA-1MFE 4 D-MANNOSE(1-4)ALPHA-L-RHAMNOSE(1-} (PART OF THE IMFE 5 CELL SURFACE CARBOHYDRATE OF PATHOGENIC SALMONELLA) IMFE 6	
122	1nid	H	35	246	1.2e-26			68.87	FAB1583; CHAIN: L, H	IMMUNOGLOBULIN FAB FRAGMENT, IMMUNOGLOBULIN
122	1nsn	H	39	244	1.7e-26			63.71	IGG FAB (IGG1, KAPPA); INSN 4 CHAIN: L, H; INSN 5 STAPHYLOCOCCAL NUCLEASE; INSN 9 CHAIN: S; INSN 10	COMPLEX (IMMUNOGLOBULIN/HYDROLASE) N10 FAB IMMUNOGLOBULIN; INSN 7 STAPHYLOCOCCAL NUCLEASE RIBONUCLEASE, INSN 11 IMMUNOGLOBULIN, STAPHYLOCOCCAL NUCLEASE INSN 25
122	1psk	H	35	240	5.1e-23			62.61	ANTIBODY; CHAIN: L, H;	IMMUNOGLOBULIN FAB, GD2-GANGLIOSIDE, CARBOHYDRATE, MELANOMA, IMMUNOGLOBULIN
122	1sm3	H	35	247	6.8e-29			63.77	SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPITOPE)
122	1sm3	H	37	242	6.8e-29	0.00	0.35		SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE;	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: P;	2 COMPLEX (ANTIBODY/PEPTIDE EPTIPE)
122	1tet	H	35	247	6.8e-25			62.73	IMMUNOGLOBULIN IGG1 MONOCLONAL FAB FRAGMENT (TE33) COMPLEX WITH CHOLERA 1TET 3 TOXIN PEPTIDE 3 (CTP3) 1TET 4	
122	1wej	H	35	253	1.7e-25			66.09	E8 ANTIBODY; CHAIN: L, H; CYTOCHROME C; CHAIN: F;	COMPLEX (ANTIBODY/ELECTRON TRANSPORT) FAB E8; CYT C, ANTIGEN; IMMUNOGLOBULIN, IGG1 KAPPA, FAB FRAGMENT, HORSE 2 CYTOCHROME C, COMPLEX (ANTIBODY/ELECTRON TRANSPORT)
122	1wej	L	37	231	8.5e-19	-0.30	0.81		E8 ANTIBODY; CHAIN: L, H; CYTOCHROME C; CHAIN: F;	COMPLEX (ANTIBODY/ELECTRON TRANSPORT) FAB E8; CYT C, ANTIGEN; IMMUNOGLOBULIN, IGG1 KAPPA, FAB FRAGMENT, HORSE 2 CYTOCHROME C, COMPLEX (ANTIBODY/ELECTRON TRANSPORT)
122	25c8	H	35	245	1.2e-26			71.71	IGG 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION
122	3hfm	H	35	247	1.4e-28			65.83	COMPLEX(ANTIBODY-ANTIGEN) IGG1 FAB FRAGMENT (HY/HEL-10) AND LYSOZYME (E.C.3.2.1.17) 3HFM 4 COMPLEX 3HFM 5	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
122	3hfm	H	44	242	1.4e-28	0.00	0.28		COMPLEX(ANTIBODY-ANTIGEN) IG*G1 FAB FRAGMENT (HY/HEL\$-10) AND LYSOZYME (E.C.3.2.1.17) 3HFM 4 COMPLEX 3HFM 5	
123	1fr9	A	176	303	2.6e-06	-0.08	0.06		CARBON MONOXIDE OXIDATION SYSTEM TRANSCRIPTION CHAIN: A, B;	TRANSCRIPTION COOA GENE PRODUCT; CARBON MONOXIDE, HEME SENSOR, CATABOLITE GENE ACTIVATOR 2 PROTEIN
123	1fr9	A	181	319	3.4e-05	-0.21	0.05		CARBON MONOXIDE OXIDATION SYSTEM TRANSCRIPTION CHAIN: A, B;	TRANSCRIPTION COOA GENE PRODUCT; CARBON MONOXIDE, HEME SENSOR, CATABOLITE GENE ACTIVATOR 2 PROTEIN
123	1rgs		135	288	1.4e-27	0.33	0.62		CAMP DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE RI(ALPHA); REGULATORY SUBUNIT, KINASE
123	2cgp	A	171	319	1.7e-26	-0.25	0.23		CATABOLITE GENE ACTIVATOR PROTEIN; CHAIN: A; DNA (5'-D(*Gp*Tp*CP*Ap*C P*Ap*Tp*Tp*Ap*Ap*T)-3'); CHAIN: B; DNA (5'- CHAIN: C;	TRANSCRIPTION/DNA COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, CAMP-2 BINDING, ACTIVATOR
127	1531		36	212	1e-47	0.70	1.00		HYDROLASE(O-GLYCOSYL)	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									LYSOZYME (E.C.3.2.1.17) 153L 3	
127	153l		36	212	1e-47	0.70	1.00		HYDROLASE(O-GLYCOSYL) LYSOZYME (E.C.3.2.1.17) 153L 3	
127	153l		36	212	1e-47			186.19	HYDROLASE(O-GLYCOSYL) LYSOZYME (E.C.3.2.1.17) 153L 3	
127	153l		36	212	1e-47			186.19	HYDROLASE(O-GLYCOSYL) LYSOZYME (E.C.3.2.1.17) 153L 3	
128	1ckl	A	147	267	2.6e-11	0.10	0.87		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
128	1ckl	A	29	145	5.1e-18	0.05	-0.15		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
128	1ckl	A	87	201	1e-18	0.40	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
128	1ckl	A	87	204	1e-18			58.04	CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									C, D, E, F;	COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
128	1e5g	A	29	141	1.7e-15	0.19	0.65		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
128	1e5g	A	87	201	7.8e-25	0.65	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
128	1e5g	A	87	202	1.4e-24	0.43	0.98		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
128	1hcc		147	202	6.5e-16	0.55	1.00		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN (CCPS) OF FACTOR H 1HCC 3	
128	1hcc		87	141	1.3e-10	0.44	0.90		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN (CCPS) OF FACTOR H 1HCC 3	
128	1hfh		143	266	3.4e-14	0.19	0.52		GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
128	1hfh	28	141	1.7e-13	0.19	0.05			STRUCTURE) 1HFH 4 1HFHA 5	
									GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
128	1hfh	83	202	3.4e-17				93.95	GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
									GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
128	1hfh	87	202	3.4e-17	0.28	0.82			GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
									GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED 1HFHA 1 STRUCTURE) 1HFH 4 1HFHA 5	
128	1hfi	147	201	3.9e-16	0.68	0.98			GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED 1HFHA 1 STRUCTURE) 1HFH 4 1HFHA 5	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
128	1hfi		87	140	5.2e-10	0.57	1.00		IHFIA 5 GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED IHFIA 1 STRUCTURE) IHFIA 4 IHFIA 5	
128	1pfx	L	104	192	5.1e-10	0.15	0.10		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
128	1qub	A	3	266	6.8e-39			95.32	HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
128	1qub	A	8	266	6.8e-39	0.07	0.87		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
128	1vvc		145	266	3.4e-24	-0.22	0.21		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
128	1vvc		29	142	1.5e-17	0.07	-0.05		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
128	1vvc		86	203	3.4e-20			82.91	CHAIN: NULL; VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
128	1vvc		87	202	3.4e-20	0.30	1.00		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
129	1ata		834	896	5.2e-12	0.29	0.09		PROTEINASE INHIBITOR (TRYPSIN) TRYPSIN INHIBITOR (PH 4.75) IATA 3 (NMR, MINIMIZED AVERAGE STRUCTURE) IATA 4	
129	1aut	L	845	940	5.1e-11	0.29	-0.19		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO- MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
129	1dan	L	819	898	1.7e-10	0.49	-0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	PROTEASE/COFACTOR/LIGAND)
129	1dan	L	851	943	3.4e-12	0.08	-0.15		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
129	1dan	L	939	1020	1.7e-10	0.01	-0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
129	1dva	L	330	427	8.5e-14	0.20	-0.18		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
129	1dva	L	819	898	1.7e-10	0.65	-0.12		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
129	1dva	L	851	943	3.4e-12	0.30	-0.14		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
129	1dx5	I	1167	1294	3.4e-11	0.02	-0.20		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CDI41 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
129	1dx5	I	1167	1294	3.4e-11	0.02	-0.20		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CDI41 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									N; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
129	1fak	L	819	898	1.7e-10	0.27	-0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
129	1fak	L	819	898	1.7e-10	0.27	-0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
129	1fak	L	851	943	3.4e-12	0.05	-0.14		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
129	1fak	L	851	943	3.4e-12	0.10	-0.15		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
129	1klo		333	472	1e-09	0.21	-0.15		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
129	1klo		755	902	3.4e-15	0.20	-0.18		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
129	1klo		755	902	3.4e-15	0.20	-0.18		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
129	1pfx	L	330	438	1.4e-10	0.15	-0.14		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
129	1pfx	L	772	920	2.6e-08	0.03	-0.18		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
129	1pfx	L	819	898	1.7e-09	0.09	-0.19		FACTOR IXA; CHAIN: C, L; D-PHE-	COMPLEX (BLOOD COAGULATION/INHIBITOR)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PRO-ARG; CHAIN: I;	CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
129	1qfk	L	1263	1339	5.1e-11	0.16	-0.19		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
129	1qfk	L	334	427	5.1e-13	0.32	-0.18		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
129	1qfk	L	822	898	6.8e-10	0.31	-0.18		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN);	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	
129	1qub	A	379	488	3.9e-08	0.20	-0.15		HUMAN BETA2- GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI- DOMAIN, MEMBRANE ADHESION
129	1xka	L	334	427	3.4e-10	0.22	-0.07		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
129	1xka	L	822	898	1e-10	0.22	-0.13		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
129	1xka	L	855	940	3.4e-09	0.11	-0.19		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
129	9wga	A	1219	1364	5.1e-11	0.02	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
129	9wga	A	1219	1364	5.1e-11	0.02	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
129	9wga	A	277	420	5.1e-14	0.08	-0.19		(ISOLECTIN 2) 9WGA 3	
									LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
129	9wga	A	277	420	5.1e-14	0.08	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
129	9wga	A	318	544	1.5e-11	0.31	-0.18		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
129	9wga	A	318	544	1.5e-11	0.31	-0.18		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
129	9wga	A	757	907	3.4e-12	0.13	-0.17		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
129	9wga	A	757	907	3.4e-12	0.13	-0.17		LECTIN (AGGLUTININ)	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
129	9wga	A	777	975	5.1e-13	0.29	-0.12		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
129	9wga	A	777	975	5.1e-13	0.29	-0.12		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
130	1apo		1210	1245	1.3e-06	0.37	0.53		COAGULATION FACTOR EGF-LIKE MODULE OF BLOOD COAGULATION FACTOR X (N-TERMINAL, 1APO 3 APO FORM) (NMR, 13 STRUCTURES) 1APO 4	
130	1apo		1210	1245	1.3e-06	0.37	0.53		COAGULATION FACTOR EGF-LIKE MODULE OF BLOOD COAGULATION FACTOR X (N-TERMINAL, 1APO 3 APO FORM) (NMR, 13 STRUCTURES) 1APO 4	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
130	1ciu		39	385	5.2e-34	0.05	-0.19		CYCLODEXTRIN GLYCOSYLTRANSF ERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
130	1ciu		39	385	5.2e-34	0.05	-0.19		CYCLODEXTRIN GLYCOSYLTRANSF ERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
130	1ciu		404	783	1.3e-32	0.01	-0.18		CYCLODEXTRIN GLYCOSYLTRANSF ERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
130	1ciu		404	783	1.3e-32	0.01	-0.18		CYCLODEXTRIN GLYCOSYLTRANSF ERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
130	1ciu		669	1044	1.3e-26	0.05	-0.19		CYCLODEXTRIN GLYCOSYLTRANSF ERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
130	1ciu		669	1044	1.3e-26	0.05	-0.19		CYCLODEXTRIN GLYCOSYLTRANSF ERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
130	1ciu		863	1177	3.9e-22	0.03	-0.15		CYCLODEXTRIN GLYCOSYLTRANSF ERASE; 1CIU 6 CHAIN: NULL; 1CIU	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
130	1ciu		863	1177	3.9e-22	0.03	-0.15		7 CYCLODEXTRIN GLYCOSYLTRANSF ERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
130	1cwv	A	264	749	9.1e-60	0.05	-0.20		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
130	1cwv	A	264	749	9.1e-60	0.05	-0.20		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
130	1cwv	A	521	996	1.2e-61			101.45	INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
130	1cwv	A	521	996	1.2e-61			101.45	INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
130	1cwv	A	561	1082	1e-56	0.04	-0.19		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
130	1cwv	A	561	1082	1e-56	0.04	-0.19		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
130	1dan	L	1210	1282	8.5e-10	0.15	0.04		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMETHYLKE TONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
130	1dan	L	1210	1282	8.5e-10	0.15	0.04		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T,	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									U; D-PHE-PHE-ARG-CHLOROMETHYLKE TONE (DFRCMK) WITH CHAIN: C;	
130	1edm	B	1210	1242	5.1e-07	0.32	0.76		FACTOR IX; CHAIN: B, C;	COAGULATION FACTOR CRYSTAL STRUCTURE, EPIDERMAL GROWTH FACTOR, EGF, 2 CALCIUM-BINDING, EGF-LIKE DOMAIN, STRUCTURE AND FUNCTION, 3 HUMAN FACTOR IX, COAGULATION FACTOR
130	1edm	B	1210	1242	5.1e-07	0.32	0.76		FACTOR IX; CHAIN: B, C;	COAGULATION FACTOR CRYSTAL STRUCTURE, EPIDERMAL GROWTH FACTOR, EGF, 2 CALCIUM-BINDING, EGF-LIKE DOMAIN, STRUCTURE AND FUNCTION, 3 HUMAN FACTOR IX, COAGULATION FACTOR
130	1fak	L	1210	1282	8.5e-10	-0.03	0.00		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
130	1fak	L	1210	1282	8.5e-10	-0.03	0.00		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
130	1pfx	L	1189	1242	5.2e-10	0.04	-0.11		FACTOR IXA; CHAIN: C, L,; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
130	1pfx	L	1189	1242	5.2e-10	0.04	-0.11		FACTOR IXA; CHAIN: C, L,; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
130	1pfx	L	1210	1273	1e-08	0.15	0.11		FACTOR IXA; CHAIN: C, L,; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
130	1pfx	L	1210	1273	1e-08	0.15	0.11		FACTOR IXA; CHAIN: C, L,; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
130	1qfk	L	1214	1282	3.4e-09	0.04	-0.13		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVILA; FVILA; BLOOD COAGULATION, SERINE PROTEASE
130	1qfk	L	1214	1282	3.4e-09	0.04	-0.13		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVILA; FVILA; BLOOD COAGULATION, SERINE PROTEASE
130	1tpg		1189	1242	2.6e-10	0.44	0.07		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
130	1tpg		1189	1242	2.6e-10	0.44	0.07		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
130	1tpg		1197	1246	1.7e-07	-0.12	0.03		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
130	1tpg		1197	1246	1.7e-07	-0.12	0.03		T-PLASMINOGEN	PLASMINOGEN ACTIVATION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	
130	1whe		1189	1245	3.9e-10	0.29	-0.14		COAGULATION FACTOR X; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN, HYDROLASE, SERINE PROTEASE, PLASMA, BLOOD 2 COAGULATION FACTOR
130	1whe		1189	1245	3.9e-10	0.29	-0.14		COAGULATION FACTOR X; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN, HYDROLASE, SERINE PROTEASE, PLASMA, BLOOD 2 COAGULATION FACTOR
130	9wga	A	1191	1293	5.1e-08	0.22	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
130	9wga	A	1191	1293	5.1e-08	0.22	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
131	1b08	A	153	308	6.5e-42	0.45	0.89		LUNG SURFACTANT PROTEIN D; CHAIN: A, B, C;	SUGAR BINDING PROTEIN C-TYPE LECTIN, CRD, SP-D, COLECTIN, ALPHA-HELICAL COILED-2 COIL, LUNG SURFACTANT, SUGAR BINDING PROTEIN
131	1dv8	A	184	311	1e-39	1.03	1.00		ASIALOGLYCOPROT EIN RECEPTOR I; CHAIN: A;	SIGNALING PROTEIN HEPATIC LECTIN HI; C-TYPE LECTIN CRD
132	1aut	L	292	374	1e-11	-0.03	0.03		ACTIVATED	COMPLEX (BLOOD)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
132	1ckl	A	155	267	2.6e-16	0.71	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1ckl	A	213	330	6.5e-20	0.10	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1ckl	A	272	387	1.3e-25	0.62	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1ckl	A	284	388	5.1e-12	0.53	0.99		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1ckl	A	2	80	1.4e-09	-0.18	0.23		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1ckl	A	332	445	9.1e-28	0.86	0.99		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1ckl	A	390	505	7.8e-23	0.40	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1ckl	A	40	145	5.2e-20	0.43	0.99		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1ckl	A	448	562	2.6e-21	0.20	0.99		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1ckl	A	4	93	6.5e-22	0.63	0.77		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1ckl	A	97	211	5.1e-10	0.38	0.66		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
132	1e5g	A	154	260	3.9e-21	0.71	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	154	266	8.5e-18	0.48	0.98		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	212	321	5.2e-18	0.53	0.51		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	270	386	7.8e-27	0.75	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	331	444	6.5e-31	0.82	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	332	443	1.4e-16	0.75	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	388	501	1.7e-17	0.19	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	3	80	8.5e-10	-0.08	0.99		COMPLEMENT CONTROL PROTEIN;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: A;	MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	40	145	9.1e-24	0.63	0.99		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	40	151	3.4e-11	0.70	0.72		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	448	560	1.2e-14	0.15	0.93		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	448	560	1.3e-26	0.26	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	4	93	1.2e-23	0.46	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	506	566	2.6e-12	0.68	0.42		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	97	209	6.5e-20	0.53	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
132	1e5g	A	97	210	3.4e-15	0.54	0.75		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
132	1emn		289	370	5.1e-12	0.18	-0.19		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
132	1emn		503	585	6.8e-12	-0.23	0.04		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
132	155y	A	376	452	1e-10	0.37	-0.17		LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: A;	LIPID BINDING PROTEIN LDL RECEPTOR; BETA HAIRPIN, 3-10 HELIX, CALCIUM BINDING
132	1hcc		154	208	5.2e-09	-0.09	0.47		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN (/CCPS) OF FACTOR H 1HCC 3	
132	1hcc		330	385	6.5e-13	0.16	0.46		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN (/CCPS) OF FACTOR H 1HCC 3	
132	1hcc		38	94	3.9e-12	0.71	0.70		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN (/CCPS) OF FACTOR H 1HCC 3	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
132	lhcc		4	35	1.2e-07	-0.64	0.01		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN (CCPS) OF FACTOR H 1HCC 3	
132	lhcc		503	559	2.6e-15	0.10	0.13		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN (CCPS) OF FACTOR H 1HCC 3	
132	lhfh		151	267	5.1e-12	0.47	0.31		GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
132	lhfh		328	444	3.4e-11			83.97	GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
132	lhfh		444	559	6.8e-12	0.30	0.76		GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SqFold Score	Compound	PDB annotation
132	1hfh		97	208	1e-09	0.32	0.75		STRUCTURE) 1HFH 4 1HFHA 5	
									GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
132	1hfi		154	209	1.3e-10	0.55	0.95		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HFIA 1 STRUCTURE) 1HFI 4 1HFIA 5	
132	1hfi		330	386	1.3e-13	0.74	0.96		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HFIA 1 STRUCTURE) 1HFI 4 1HFIA 5	
132	1hfi		38	93	6.5e-12	0.87	0.68		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HFIA 1 STRUCTURE) 1HFI 4 1HFIA 5	
132	1hfi		4	36	1e-07	0.24	0.18		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									(NMR, MINIMIZED AVERAGED 1HFIA 1 STRUCTURE) 1HFI 4 1HFIA 5	
132	1hfi		503	559	1e-16	0.24	0.59		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HFIA 1 STRUCTURE) 1HFI 4 1HFIA 5	
132	1klo		275	426	1e-13	0.00	-0.18		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
132	1qub	A	111	329	1.7e-28	0.29	0.96		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
132	1qub	A	210	522	6.5e-39			189.59	HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
132	1qub	A	212	489	6.8e-28	0.41	1.00		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
132	1qub	A	288	503	1e-31	0.37	1.00		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
132	1qub	A	2	270	1.7e-35	0.06	0.86		HUMAN BETA2-	MEMBRANE ADHESION SHORT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									GLYCOPROTEIN I; CHAIN: A;	CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
132	1qub	A	331	576	1.7e-41	0.53	1.00		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
132	1qub	A	388	589	6.8e-22	0.30	1.00		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
132	1vvc		153	267	1.7e-14	0.48	1.00		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
132	1vvc		211	327	5.1e-14	0.28	0.75		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
132	1vvc		271	385	1.7e-12	0.44	0.34		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
132	1vvc		330	444	5.1e-17	0.53	0.92		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
132	1vvc		388	502	5.1e-15	0.33	1.00		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
132	1vvc		388	504	5.2e-21			91.84	VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
132	1vvc		446	559	6.8e-14	-0.10	0.35		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
132	1vvc		505	584	2.6e-15	0.02	0.18		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
132	1vvc		505	589	1.7e-10	-0.14	0.01		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
132	1vvc		97	208	3.4e-14	0.40	0.82		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
132	1xka	L	180	260	3.4e-09	0.17	-0.17		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
132	9wga	A	369	547	1.4e-11	0.06	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	GROWTH FACTOR LIKE DOMAIN
132	9wga	A	7	178	1.7e-10	0.07	-0.20		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
133	1b8q	A	76	167	0.0026	-0.04	0.45		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
133	1be9	A	67	164	3.4e-12	0.48	0.69		PSD-95; CHAIN: A; CRIP1; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
133	1by1	A	775	987	3.4e-30	-0.15	0.75		PIX; CHAIN: A;	TRANSPORT PROTEIN RHO-GTPASE EXCHANGE FACTOR, TRANSPORT PROTEIN
133	1by1	A	787	992	2.6e-42	0.03	0.93		PIX; CHAIN: A;	TRANSPORT PROTEIN RHO-GTPASE EXCHANGE FACTOR, TRANSPORT PROTEIN
133	1dbh	A	800	1129	5.1e-36	0.18	1.00		HUMAN SOS 1; CHAIN: A;	GENE REGULATION SON OF SEVENLESS PROTEIN; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GENE REGULATION
133	1f5x	A	785	979	3.4e-34	0.37	1.00		RHO-GEF VAV; CHAIN: A;	SIGNALING PROTEIN 11 ALPHA-HELICES

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
133	1i16		71	157	2.6e-17	0.61	0.55		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CEMOATTRACTANT FACTOR, PDZ DOMAIN
133	1kwa	A	71	148	1.3e-16	0.58	0.92		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
133	1pdr		69	153	6.8e-12	0.65	0.93		HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT
133	1pls		1021	1144	0.0034	0.01	0.33		PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOGY DOMAIN) MUTANT IPLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS IPLS 4 (INS(G105-LEHHHHH)) (NMR, 25 STRUCTURES) IPLS 5	
133	1qav	A	67	147	5.1e-07	0.77	0.83		ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA-FINGER, HETERODIMER
133	1qlc	A	73	149	1.4e-08	0.90	0.99		POSTSYNAPTIC	PEPTIDE RECOGNITION PSD-95; PDZ

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									DENSITY PROTEIN 95; CHAIN: A;	DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING
133	3pdz	A	73	151	3.4e-10	0.75	0.99		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTPIE, PTP-BAS, SPECIFICITY 2 OF BINDING
134	1a17		104	249	6.8e-10	-0.12	0.00		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
134	1a17		149	283	6.8e-14	0.10	0.47		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
134	1a17		185	335	5.1e-13	0.16	0.25		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
134	1a17		227	343	1e-17	0.14	0.77		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
134	1a17		235	396	1.3e-07	-0.37	0.09		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
134	1a17		262	381	1e-09	-0.09	0.28		SERINE/THREONINE	HYDROLASE TETRATRICOPEPTIDE,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PROTEIN PHOSPHATASE 5; CHAIN: NULL;	TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
134	1a17		63	213	6.8e-10	0.04	-0.14		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRAPOLYPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
134	1d8d	A	150	422	5.1e-10	0.06	-0.08		FARNESYLTRANSFERASE (ALPHA SUBUNIT); CHAIN: A; FARNESYLTRANSFERASE (BETA SUBUNIT); CHAIN: B; K-RAS4B PEPTIDE SUBSTRATE; CHAIN: P;	TRANSFERASE FTASE; FTASE; FTASE, PFT, PFTASE, FARNESYLTRANSFERASE, FARNESYL 2 TRANSFERASE, CAAAX, RAS, CANCER
134	1e96	B	114	239	0.0026	-0.23	0.15		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
134	1e96	B	152	340	3.4e-11	0.03	-0.15		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
134	1e96	B	229	389	3.4e-14	-0.02	0.13		RAS-RELATED C3 BOTULINUM TOXIN	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
134	1e96	B	315	481	5.1e-06	-0.24	0.12		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
134	1e96	B	34	204	3.4e-10	-0.15	0.04		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
134	1elr	A	105	216	1.7e-10	0.17	0.12		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
134	1elr	A	117	242	1.3e-05	-0.13	0.21		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
134	1elr	A	151	256	5.1e-14	-0.08	0.52		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
134	1elr	A	167	291	5.2e-10	0.25	0.10		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
134	1elr	A	227	343	3.4e-20	0.12	0.87		MEEVD; CHAIN: B; TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	BINDING CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
134	1elr	A	269	389	1.7e-12	-0.30	0.33		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
134	1elr	A	35	140	1e-11	-0.05	0.00		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
134	1elr	A	70	183	1.2e-12	-0.05	0.18		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
134	1elw	A	151	275	3.4e-12	0.22	0.77		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
134	1elw	A	214	303	1.5e-10	0.55	0.80		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
134	1elw	A	232	335	3.4e-17	0.13	0.63		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
134	1elw	A	274	398	3.4e-12	-0.50	0.06		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
134	1elw	A	440	486	6.8e-06	-0.40	0.04		TPR1-DOMAIN OF	CHAPERONE HOP, TPR-DOMAIN,

SEQ ID NO;	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
134	1fch	A	130	424	3.4e-23	0.04	0.54		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOME RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRA TRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
134	1fch	A	156	476	6.5e-32	-0.17	0.34		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOME RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRA TRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
134	1fch	A	233	485	5.1e-28	-0.14	0.54		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOME RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRA TRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
134	1fch	A	2	280	5.1e-26	-0.20	0.19		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOME RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRA TRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
134	1fch	A	45	336	5.1e-34	0.07	0.37		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-	SIGNALING PROTEIN PEROXISOME RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CONTAINING PEPTIDE; CHAIN: C, D;	TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
134	1qge	A	130	385	3.4e-07	-0.18	0.11		VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	PROTEIN TRANSPORT HELIX-TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT
137	1elr	A	371	442	0.00026	-0.21	0.27		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
137	1elr	A	371	442	0.00026	-0.21	0.27		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
137	1elw	A	374	440	0.0052	-0.23	0.40		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
137	1elw	A	374	440	0.0052	-0.23	0.40		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
137	1fch	A	131	445	0.00013	-0.40	0.28		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
137	1fch	A	131	445	0.00013	-0.40	0.28		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
137	1fch	A	275	518	9.1e-09	-0.34	0.57		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
137	1fch	A	275	518	9.1e-09	-0.34	0.57		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
138	1aye		1	244	1.4e-95			207.01	PROCARBOXYPEPTIDASE A2; CHAIN: NULL;	SERINE PROTEASE PCPA2; SERINE PROTEASE, ZYMOGEN, HYDROLASE
138	1aye		3	244	1.4e-95	0.61	1.00		PROCARBOXYPEPTIDASE A2; CHAIN: NULL;	SERINE PROTEASE PCPA2; SERINE PROTEASE, ZYMOGEN, HYDROLASE
138	1dtd	A	3	244	3.4e-94	0.66	1.00		CARBOXYPEPTIDASE A2; CHAIN: A; METALLOCARBOXY PEPTIDASE INHIBITOR; CHAIN: B	HYDROLASE/HYDROLASE INHIBITOR CARBOXYPEPTIDASE A2, LEECH CARBOXYPEPTIDASE INHIBITOR
138	1pca		1	244	3.4e-89			228.73	HYDROLASE(C-TERMINAL PEPTIDASE)	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
138	1pca	3	242	3.4e-89	0.62	1.00			PROCARBOXYPEPTIDASE A (E.C.3.4.12.2) 1PCA 3	
138	2ctc	1	242	6.8e-95				292.46	HYDROLASE(C-TERMINAL PEPTIDASE) CARBOXYPEPTIDASE A (E.C.3.4.17.1) COMPLEX WITH L-PHENYL 2CTC 3 LACTATE (L-O-PHE) 2CTC 4	
138	2ctc	3	242	6.8e-95	0.61	1.00			HYDROLASE(C-TERMINAL PEPTIDASE) CARBOXYPEPTIDASE A (E.C.3.4.17.1) COMPLEX WITH L-PHENYL 2CTC 3 LACTATE (L-O-PHE) 2CTC 4	
139	1a5e	401	515	3.4e-24	0.10	0.99			TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
139	1awc	B	401	535	6.8e-40	0.11	1.00		GA BINDING PROTEIN ALPHA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D; E; ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	GAPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
139	1bd8		371	518	8.5e-31	-0.36	0.16		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
139	1bd8		404	536	3.4e-31	0.10	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
139	1bi7	B	401	515	1.7e-25	-0.07	0.94		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
139	1biX	B	350	485	1.5e-27	-0.09	0.11		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
139	1biX	B	371	518	3.4e-29	-0.40	0.04		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
139	1biX	B	404	536	3.4e-31	0.03	1.00		CYCLIN-	COMPLEX (INHIBITOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
139	1bu9	A	368	520	1.7e-37	-0.33	0.11		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
139	1bu9	A	401	538	1e-34	0.15	0.99		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
139	1d9s	A	401	521	5.1e-25	0.09	0.99		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
139	1d9s	A	434	536	1.7e-19	0.10	0.49		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
139	1ihb	A	347	486	6.8e-29	-0.14	0.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
139	1ihb	A	368	519	1e-36	-0.32	0.13		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
139	1ihb	A	401	538	1e-34	0.11	0.99		A, B; CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	INHIBITOR CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
139	1ikn	D	342	535	1.7e-41	-0.38	0.22		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
139	1myo		435	533	8.5e-26	0.13	0.19		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
139	1sw6	A	389	537	1e-19	-0.25	0.10		REGULATORY PROTEIN SWI6; CHAIN: A, B;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE
139	1yes	B	401	515	3.4e-21	-0.21	0.80		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
139	1yes	B	434	534	6.8e-23	-0.18	0.78		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										ONCOGENE/ANKYRIN REPEATS)
141	1e5d	A	15	95	5.1e-09	0.14	0.12		RUBREDOXIN:OXY GEN OXIDOREDUCTASE; OXYGENREDUCTASE, DIIRON- CENTRE, 2 FLAVOPROTEINS, LACTAMASE-FOLD	OXIDOREDUCTASE OXIDOREDUCTASE, OXYGENREDUCTASE, DIIRON- CENTRE, 2 FLAVOPROTEINS, LACTAMASE-FOLD
141	1qh5	A	5	96	6.8e-12	-0.03	0.27		HYDROXYACYLGL UTATHIONE HYDROLASE; CHAIN: A, B;	HYDROLASE GLYOXALASE II; METALLO-HYDROLASE
141	2bc2	A	12	100	1.4e-12	-0.03	0.01		METALLO BETA- LACTAMASE II; CHAIN: A, B;	HYDROLASE HYDROLASE, BETA- LACTAMASE, ANTIBIOTIC, METALLOENZYME
142	1cs8	A	19	333	0			497.56	HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
142	1cs8	A	19	333	0			497.56	HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
142	1cs8	A	21	333	0	0.83	1.00		HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
142	1cs8	A	21	333	0	0.83	1.00		HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
142	1icf	B	292	333	1.7e-17	-0.53	0.90		CATHEPSIN L; HEAVY CHAIN; CHAIN: A, C; CATHEPSIN L; LIGHT CHAIN; CHAIN: B, D; INVARIANT CHAIN;	HYDROLASE II FRAGMENT, CD74 FRAGMENT CYSTEINE PROTEINASE, CATHEPSIN, MHC CLASS II, INVARIANT 2 CHAIN, THYROGLOBULIN TYPE-1 DOMAIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
142	1icf	B	292	333	1.7e-17	-0.53	0.90		CHAIN: I, J; CATHEPSIN L: HEAVY CHAIN; CHAIN: A, C; CATHEPSIN L: LIGHT CHAIN; CHAIN: B, D; INVARIANT CHAIN; CHAIN: I, J;	HYDROLASE II FRAGMENT, CD74 FRAGMENT CYSTEINE PROTEINASE, CATHEPSIN, MHC CLASS II, INVARIANT 2 CHAIN, THYROGLOBULIN TYPE-1 DOMAIN
143	1ctq	A	22	197	6.8e-46			53.49	TRANSFORMING PROTEIN P21/H-RAS- 1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
143	1ctq	A	24	197	6.8e-46	0.44	0.89		TRANSFORMING PROTEIN P21/H-RAS- 1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
143	1d5c	A	24	194	5.1e-48	0.80	1.00		RAB6 GTPASE; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G- PROTEIN, GTPASE, RAB6, VESICULAR TRAFFICKING
143	1e0s	A	14	190	8.5e-53	0.90	1.00		ADP- RIBOSYLATION FACTOR 6; CHAIN: A;	G PROTEIN G PROTEIN, RAS, ARF, ARF6, MEMBRANE TRAFFIC
143	1ek0	A	26	197	3.4e-47	0.34	0.63		GTP-BINDING PROTEIN YPT51; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G PROTEIN, VESICULAR TRAFFIC, GTP HYDROLYSIS, YPT/RAB 2 PROTEIN, ENDOCYTOSIS, HYDROLASE
143	1fzq	A	23	194	1.7e-45	1.00	1.00		ADP- RIBOSYLATION FACTOR-LIKE PROTEIN 3; CHAIN: A;	SIGNALING PROTEIN ARF-LIKE PROTEIN 3, ARL3; PROTEIN-GDP COMPLEX WITHOUT MAGNESIUM, ARF FAMILY, RAS 2 SUPERFAMILY,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
143	1hur	A	10	199	1e-58			118.41	A; HUMAN ADP-RIBOSYLATION FACTOR 1; 1HUR 5 CHAIN: A, B; 1HUR 7	G-DOMAIN PROTEIN TRANSPORT GDP-BINDING, MEMBRANE TRAFFICKING, NON-MYRISTOYLATED 1HUR 16
143	1hur	A	9	196	1e-58	0.64	1.00		HUMAN ADP-RIBOSYLATION FACTOR 1; 1HUR 5 CHAIN: A, B; 1HUR 7	PROTEIN TRANSPORT GDP-BINDING, MEMBRANE TRAFFICKING, NON-MYRISTOYLATED 1HUR 16
143	1zbd	A	13	200	1.7e-56	0.52	0.27		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
143	1zbd	A	21	202	1.7e-56			51.86	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
143	3rab	A	16	197	3.4e-56	0.15	0.51		RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
143	3rab	A	16	197	3.4e-56			59.67	RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
144	1dix	A	1	222	3.4e-69	0.29	1.00		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
144	1dix	B	1	222	3.4e-69	0.09	1.00		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
147	1b7f	A	11	98	1e-17	-0.14	0.62		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(*GP*UP*UP*GP* UP*UP*UP*UP*UP*U P*UP*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
147	1evj	A	33	122	1.7e-17	-0.06	0.43		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*A P*AP*AP*AP*AP*AP *A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
147	1evj	A	7	112	5.1e-21	-0.32	0.13		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*A	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Coumpound	PDB annotation
									P*AP*AP*AP*AP*AP* A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	
147	1cvj	B	33	122	1.7e-17	0.18	0.58		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP P*AP*AP*AP*AP*AP A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
147	1cvj	F	33	122	1.7e-17	0.31	0.78		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP P*AP*AP*AP*AP*AP A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
147	1cvj	H	33	122	1.7e-17	0.25	0.80		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP P*AP*AP*AP*AP*AP A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
147	1d8z	A	32	108	3.4e-18	0.35	0.71		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
147	1ha1		26	104	3.4e-21	0.06	0.00		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Coumpound	PDB annotation
147	1hd1	A	32	101	5.1e-19	0.04	0.07		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
147	2up1	A	23	109	1.4e-22	0.06	0.11		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UPI; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
148	1b7f	A	68	150	1.5e-15	0.38	0.98		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(p*Gp*Up*Up*Gp*Up*Up*Up*Up*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRANSCRIPTION PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
148	1b7f	A	7	145	8.5e-26	0.06	0.06		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(p*Gp*Up*Up*Gp*Up*Up*Up*Up*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRANSCRIPTION PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
148	1cvj	B	71	155	3.4e-17	0.21	0.88		POLYDENTYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*A P*AP*AP*AP*AP*A*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
148	1evj	F	71	155	3.4e-17	0.39	0.90		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
148	1evj	H	71	155	3.4e-17	0.37	0.94		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
148	1d8z	A	67	147	1.5e-15	0.19	0.35		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
148	1d9a	A	71	145	1.7e-15	0.21	0.34		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
148	1fht		64	146	5.1e-12	0.20	0.12		U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	RIBONUCLEOPROTEIN U1A117; RIBONUCLEOPROTEIN, RNP DOMAIN, SPLICEOSOME
148	1fjc	A	70	153	1.7e-13	0.29	0.18		NUCLEOLIN RBD2; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
148	1hd1	A	71	145	1.2e-19	0.33	0.47		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN DQ; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
148	1sxl		61	149	1.7e-17	-0.14	0.23		RNA-BINDING PROTEIN SEX-LETHAL PROTEIN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									(C-TERMINUS, OR SECOND RNA-BINDING DOMAIN ISXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) ISXL 4 (NMR, 17 STRUCTURES) ISXL 5	
148	2mss	A	71	145	5.1e-20	0.56	0.31		MUSASHI1; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
148	2sxl		68	150	1.5e-15	0.29	0.66		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPLICING
148	2u2f	A	70	145	1.7e-12	-0.09	0.00		SPLICING FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN
149	1dix	A	242	793	0			519.97	PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
149	1dix	A	242	793	0			519.97	PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
149	1dix	A	259	792	0	0.65	1.00		PHOSPHOINOSITIDE-SPECIFIC	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PHOSPHOLIPASE C, CHAIN: A, B;	HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSUDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
149	1dix	A	259	792	0	0.68	1.00		PHOSPHOINOSITIDE -SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSUDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
149	1dix	B	200	793	0			571.84	PHOSPHOINOSITIDE -SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSUDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
149	1dix	B	200	793	0			571.84	PHOSPHOINOSITIDE -SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSUDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
149	1dix	B	201	792	0	0.65	1.00		PHOSPHOINOSITIDE -SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSUDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
149	1dix	B	201	792	0	0.66	1.00		PHOSPHOINOSITIDE -SPECIFIC	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PHOSPHOLIPASE C, CHAIN: A, B;	HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3
149	1exr	A	177	322	5.1e-36	0.18	0.07		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
149	1exr	A	177	322	5.1e-36	0.18	0.07		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
149	1mai		55	170	9.1e-29	0.89	1.00		PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN PLECKSTRIN, PHOSPHOLIPASE, INOSITOL TRISPHOSPHATE, 2
149	1mai		55	170	9.1e-29	0.89	1.00		PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN, HYDROLASE
149	1mai		55	170	9.1e-29			110.09	PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN PLECKSTRIN, PHOSPHOLIPASE, INOSITOL TRISPHOSPHATE, 2
149	1mai		55	170	9.1e-29			110.09	PHOSPHOLIPASE C DELTA-1; CHAIN: NULL;	SIGNAL TRANSDUCTION PROTEIN, HYDROLASE
149	1mx		179	320	3.4e-34	0.07	0.09		TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
149	1mx		179	320	3.4e-34	0.07	0.09		TROPONIN C; 1TNX 4 CHAIN: NULL;	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
149	1top		179	320	1.4e-34	0.26	0.84		1TNX 5 CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
149	1top		179	320	1.4e-34	0.26	0.84		CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
149	1vrk	A	176	323	3.4e-36	0.07	0.33		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
149	1vrk	A	176	323	3.4e-36	0.07	0.33		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
151	1qbj	A	32	89	0.0046	0.47	0.96		DOUBLE- STRANDED RNA SPECIFIC ADENOSINE DEAMINASE CHAIN: A, B, C; DNA (5'- D(*TP*CP*GP*CP*G P*CP*G)-3'); CHAIN: D, E, F;	HYDROLASE/DNA PROTEIN/Z-DNA COMPLEX, HYDROLASE/DNA
151	1qgp	A	32	89	0.0046	0.28	1.00		DOUBLE STRANDED RNA ADENOSINE DEAMINASE; CHAIN: A;	HYDROLASE Z-ALPHA-Z-DNA BINDING DOMAIN, RNA-EDITING, Z-DNA 2 RECOGNITION, ADAR1, HELIX-TURN-HELIX, HYDROLASE
153	1bkd		S451	606	2.6e-28	0.23	0.77		H-RAS; CHAIN: R; SON OF SEVENLESS- 1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
153	1bkd		S900	1116	1e-64	0.53	1.00		H-RAS; CHAIN: R; SON OF SEVENLESS-1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR
153	1f9	A	86	168	0.00065	-0.35	0.19		CARBON MONOXIDE OXIDATION SYSTEM TRANSCRIPTION CHAIN: A, B;	TRANSCRIPTION COOA GENE PRODUCT; CARBON MONOXIDE, HEME SENSOR, CATABOLITE GENE ACTIVATOR 2 PROTEIN
153	1i16		579	650	3.9e-14	0.24	0.98		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CEMOATTRACTANT FACTOR, PDZ DOMAIN
153	1kwa	A	577	659	2.6e-16	0.60	1.00		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
153	1pdr		579	640	9.1e-12	0.72	0.80		HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT
153	1rgs		256	414	6.8e-12	0.02	0.19		CAMP DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE R(1ALPHA); REGULATORY SUBUNIT, KINASE
153	2cgp	A	339	480	1.2e-16	-0.13	0.00		CATABOLITE GENE ACTIVATOR PROTEIN; CHAIN: A; DNA (5'-D(*GP*TP*CP*AP*CP*AP*TP*TP*AP*AP*T)-3'); CHAIN: B; DNA (5'-CHAIN: C;	TRANSCRIPTION/DNA COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, CAMP-2 BINDING, ACTIVATOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
157	2irf	G	1	75	6.8e-32	0.23	1.00		INTERFERON REGULATORY FACTOR 2; CHAIN: G, H, I, J, K, L; DNA (5'-D(P*AP*AP*GP*TP*GP*AP*AP*AP*GP*(I DO) CHAIN: A, B, C; DNA (5'-D(*TP*TP*CP*AP*CP*TP*TP*TP*CP*AP*C P*(IDO) CHAIN: D, E, F;	GENE REGULATION/DNA IRF-2; TRANSCRIPTION FACTOR, IFN INDUCTION, IRF FAMILY
157	2irf	G	1	75	6.8e-32			103.26	INTERFERON REGULATORY FACTOR 2; CHAIN: G, H, I, J, K, L; DNA (5'-D(P*AP*AP*GP*TP*GP*AP*AP*AP*GP*(I DO) CHAIN: A, B, C; DNA (5'-D(*TP*TP*CP*AP*CP*TP*TP*TP*CP*AP*C P*(IDO) CHAIN: D, E, F;	GENE REGULATION/DNA IRF-2; TRANSCRIPTION FACTOR, IFN INDUCTION, IRF FAMILY
158	2irf	G	1	29	1.7e-11	-0.33	0.96		INTERFERON REGULATORY FACTOR 2; CHAIN: G, H, I, J, K, L; DNA (5'-D(P*AP*AP*GP*TP*GP*AP*AP*AP*GP*(I DO) CHAIN: A, B, C;	GENE REGULATION/DNA IRF-2; TRANSCRIPTION FACTOR, IFN INDUCTION, IRF FAMILY

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									DNA (5'-D(*TP*TP*CP*AP*CP*TP*TP*TP*CP*AP*CP*(IDO) CHAIN: D, E, F;	
159	1bkd		S1	315	2.6e-76			74.57	H-RAS; CHAIN: R; SON OF SEVENLESS-1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR
159	1bkd		S23	293	2.6e-76	0.37	1.00		H-RAS; CHAIN: R; SON OF SEVENLESS-1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR
159	1bkd		S31	199	3.4e-52	0.05	1.00		H-RAS; CHAIN: R; SON OF SEVENLESS-1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR
159	1btn		392	491	9.1e-21	0.43	0.94		BETA-SPECTRIN; 1BTN 4 CHAIN: NULL; 1BTN 5	SIGNAL TRANSDUCTION PROTEIN
159	1fao	A	388	488	3.9e-07	0.31	0.59		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
159	1fb8	A	385	496	6.5e-09	0.31	0.53		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
159	1fgy	A	391	467	5.2e-06	0.23	0.75		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
159	1pms		399	491	2.6e-10	0.18	0.16		SOS 1; CHAIN: NULL;	GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
159	1qgg	A	391	511	3.9e-12	0.18	-0.13		INSULIN RECEPTOR SUBSTRATE 1; CHAIN: A, B;	SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION
160	1dp7	P	108	183	6.8e-33	0.61	1.00		MHC CLASS II TRANSCRIPTION FACTOR HRFX1; CHAIN: P; DNA (5'-D(*CP*GP*(BRO)UP*TP*AP*CP*CP*AP*(BRO) CHAIN: D;	TRANSCRIPTION/DNA REGULATORY FACTOR X; WINGED HELIX, MHC CLASS II TRANSCRIPTION FACTOR, PROTEIN-2 DNA COCRYSTAL STRUCTURE, NOVEL MODE OF DNA RECOGNITION
161	1b7f	A	74	152	5.1e-18	0.43	0.12		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(p*Gp*Up*Up*Gp*Up*Up*Up*Up*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
161	1cvj	A	70	154	3.4e-19	0.36	0.28		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*A P*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
161	1d8z	A	79	153	5.1e-18	0.38	0.69		HU ANTIGEN C;	RNA BINDING PROTEIN RNA-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
161	1hal		77	153	1e-26	0.57	0.57		CHAIN: A; HNRNP A1; CHAIN: NULL;	BINDING DOMAIN NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
161	1hd1	A	83	154	5.1e-24	0.87	0.86		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN IN D0; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
161	1sxl		74	152	5.1e-18	0.17	0.12		RNA-BINDING PROTEIN SEX-LETHAL PROTEIN (C-TERMINUS, OR SECOND RNA-BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	
161	2mss	A	83	154	5.1e-19	0.72	0.46		MUSASHI1; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
161	2sxl		80	154	6.8e-17	0.34	0.59		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPLICING
161	2up1	A	76	153	6.8e-27	0.68	0.40		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN IN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
161	3sxl	A	72	153	1.7e-18	0.49	0.54		TELOMETRIC DNA; CHAIN: B;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
162	1edh	A	122	337	8.5e-30			75.74	E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
162	1edh	A	142	337	8.5e-30	0.39	0.94		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
162	1edh	A	243	351	8.5e-09	0.36	-0.01		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
162	1ncg		142	226	0.0029	0.57	0.11		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
162	1ncg		267	335	0.00068	0.11	0.49		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
162	1nci	B	176	228	0.0037	-0.12	0.45		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
162	1nci	B	270	337	0.00012	-0.15	0.37		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
162	1ncj	A	122	336	5.1e-31			79.80	N-CADHERIN;	CELL ADHESION PROTEIN CELL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
162	Incj	A	142	337	5.1e-31	0.39	1.00		CHAIN: A; N-CADHERIN; CHAIN: A;	ADHESION PROTEIN CELL ADHESION PROTEIN CELL ADHESION PROTEIN
162	Incj	A	243	345	8.5e-10	0.22	0.47		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
162	Incj	A	30	228	1.7e-26	0.18	-0.14		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
162	Isuh		142	232	1.2e-06	0.01	0.17		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
162	Isuh		243	341	1e-05	-0.01	0.42		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
163	1a25	A	1142	1217	5.2e-10	-0.28	0.18		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN
163	1byn	A	1150	1251	3.9e-15	-0.21	0.13		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
163	1dix	A	1029	1261	9.1e-76	0.36	1.00		PHOSPHOINOSITIDE -SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSUDER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
163	1dix	A	605	807	2.6e-76	0.19	1.00		PHOSPHOINOSITIDE -SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSUDER,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
163	1dix	B	1029	1261	1.3e-75	0.21	1.00		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
163	1dix	B	526	781	1.4e-10	-0.14	0.92		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
163	1dix	B	605	807	5.2e-76	0.24	1.00		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
163	1rsy		1151	1250	9.1e-13	-0.41	0.13		CALCIUM/PHOSPHO LIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
164	lagq	B	299	406	1.2e-13	-0.42	0.28		GLIAL CELL-DERIVED NEUROTROPIC	GROWTH FACTOR GDNF; GROWTH FACTOR, NEUROTROPIC FACTOR, CYSTINE KNOT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
164	1bmp		301	406	3.4e-45	0.01	1.00		FACTOR; CHAIN: A, B, C, D; BONE MORPHOGENETIC PROTEIN-7; CHAIN: NULL;	TRANSFORMING GROWTH FACTOR OSTEOGENIC PROTEIN-1, HOP-1, BMP-7; MORPHOGEN, TRANSFORMING GROWTH FACTOR, CYTOKINE, BONE, 2 CARTILAGE, GLYCOPROTEIN
164	1bmp		301	407	3.4e-45			88.97	BONE MORPHOGENETIC PROTEIN-7; CHAIN: NULL;	TRANSFORMING GROWTH FACTOR OSTEOGENIC PROTEIN-1, HOP-1, BMP-7; MORPHOGEN, TRANSFORMING GROWTH FACTOR, CYTOKINE, BONE, 2 CARTILAGE, GLYCOPROTEIN
164	1kla	A	290	407	1.3e-37			73.65	TRANSFORMING GROWTH FACTOR-BETA 1; CHAIN: A, B;	GROWTH FACTOR TGF-B1; GROWTH FACTOR, MITOGEN, GLYCOPROTEIN
164	1kla	A	296	407	1.3e-37	0.05	0.70		TRANSFORMING GROWTH FACTOR-BETA 1; CHAIN: A, B;	GROWTH FACTOR TGF-B1; GROWTH FACTOR, MITOGEN, GLYCOPROTEIN
164	1kla	A	302	407	1.7e-31	0.21	0.87		TRANSFORMING GROWTH FACTOR-BETA 1; CHAIN: A, B;	GROWTH FACTOR TGF-B1; GROWTH FACTOR, MITOGEN, GLYCOPROTEIN
164	1tgj		290	407	1.3e-37			77.32	TRANSFORMING GROWTH FACTOR-BETA 3; CHAIN: NULL;	GROWTH FACTOR TGF-BETA3; GROWTH FACTOR, MITOGEN, GLYCOPROTEIN, SIGNAL
164	1tgj		296	407	1.3e-37	0.38	0.81		TRANSFORMING GROWTH FACTOR-BETA 3; CHAIN: NULL;	GROWTH FACTOR TGF-BETA3; GROWTH FACTOR, MITOGEN, GLYCOPROTEIN, SIGNAL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
164	1tgi		298	407	1.4e-31	0.13	0.96		TRANSFORMING GROWTH FACTOR-BETA 3; CHAIN: NULL;	GROWTH FACTOR TGF-BETA3; GROWTH FACTOR, MITOGEN, GLYCOPROTEIN, SIGNAL
164	2tgi		290	407	6.8e-31			69.00	GROWTH FACTOR TRANSFORMING GROWTH FACTOR-BETA TWO (TGF-B2) 2TGI 3	
164	2tgi		302	407	6.8e-31	0.12	0.59		GROWTH FACTOR TRANSFORMING GROWTH FACTOR-BETA TWO (TGF-B2) 2TGI 3	
164	3bmp	A	300	406	3.4e-48	0.42	0.99		BONE MORPHOGENETIC PROTEIN 2 (BMP-2); CHAIN: A;	CYTOKINE CYTOKINE, BONE MORPHOGENETIC PROTEIN, CYSTIN-KNOT, TGFB- 2 FAMILY
165	1a0a	A	58	113	1.7e-09	-0.45	0.11		PHOSPHATE SYSTEM POSITIVE REGULATORY PROTEIN CHAIN: A; B; DNA; CHAIN: C; D;	COMPLEX (TRANSCRIPTION FACTOR/DNA) BHLH; UASP2(17); TRANSCRIPTION FACTOR, BASIC HELIX LOOP HELIX, 2 COMPLEX (TRANSCRIPTION FACTOR/DNA)
165	1drm	A	141	206	0.00026	0.04	0.17		SENSOR PROTEIN FIXL; CHAIN: A;	TRANSFERASE FIXL, HEME DOMAIN, CRYSTAL STRUCTURE, PAS FAMILY, TWO-2 COMPONENT SYSTEM, HISTIDINE KINASE
165	1mdy	A	51	116	1.2e-14	-0.50	0.04		TRANSCRIPTION ACTIVATION/DNA MYOD BASIC-HELIX-LOOP-HELIX (BHLH) DOMAIN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									IMDY 3 (RESIDUES 102 - 166) MUTANT WITH CYS 135 REPLACED BY SER IMDY 4 (C135S) COMPLEXED WITH DNA IMDY 5 (5'-D(*TP*CP*AP*AP*C P*AP*GP*CP*TP*GP *TP*TP*GP*A)-3') IMDY 6	
166	1b7f	A	80	227	5.1e-27	0.34	0.87		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(*Gp*UP*UP*Gp*UP*UP*UP*UP*U P*UP*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
166	1cvj	A	84	224	6.8e-23	0.45	0.72		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*A P*AP*AP*AP*AP*AP *A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
166	1d8z	A	79	168	1.5e-22	0.67	0.99		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
166	1ha1		1	160	5.1e-35	-0.43	0.07		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
166	1ha1		77	221	6.8e-29	0.22	0.19		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
166	1hd1	A	83	160	3.4e-22	0.69	0.87		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN IN D0; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
166	2up1	A	1	166	5.1e-38	-0.15	0.15		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN IN A1; CHAIN: A; 12- NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
166	2up1	A	76	221	3.4e-31	-0.01	0.45		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN IN A1; CHAIN: A; 12- NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
166	3sx1	A	82	227	8.5e-26	0.26	0.59		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
167	1cs6	A	11	307	2.6e-34	0.12	-0.01		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
167	1cs6	A	29	127	1.7e-08	0.15	-0.14		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
167	1cvs	C	150	277	1.2e-17	0.01	1.00		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
167	1cvs	C	35	246	1.4e-52	0.09	0.59		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
167	1cvs	D	150	277	1.2e-17	0.38	1.00		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
167	1cvs	D	150	293	5.2e-43	0.18	1.00		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
167	1cvs	D	35	246	5.1e-52	0.17	0.70		FIBROBLAST GROWTH FACTOR 2;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
167	1epf	A	54	232	2.6e-18	0.36	0.94		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
167	1ev2	E	34	246	3.4e-49	0.14	0.84		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
167	1ev2	G	150	297	6.8e-19	0.14	1.00		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
167	1ev2	G	34	247	1.7e-52	0.04	0.86		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
167	1evt	C	150	277	1.7e-17	0.19	1.00		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
167	1evt	C	35	246	1e-49	-0.01	0.84		RECEPTOR 1; CHAIN: C, D; FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	DOMAINS, B-TREFOIL FOLD GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
167	1f2q	A	45	126	7.8e-08	0.20	0.55		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
167	1f2q	A	54	247	9.1e-15	0.46	0.42		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
167	1fcg	A	54	245	1.3e-16	0.26	0.92		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
167	1fgk	A	346	644	0	1.00	1.00		FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
167	1fgk	A	346	644	0			412.56	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
167	1fgk	B	343	643	0	0.82	1.00		FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
167	1fgk	B	343	643	0			390.85	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
167	1fmk		289	646	0	0.39	1.00		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
167	1itb	B	11	245	2.6e-21	0.09	0.13		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
167	1itb	B	42	321	9.1e-38	0.19	0.40		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
167	1itb	B	42	367	9.1e-38			89.43	INTERLEUKIN-1 RECEPTOR; CHAIN: B;	TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR) COMPLEX
167	1nct		46	127	8.5e-09	0.00	-0.17		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	(IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
167	1qcf	A	291	649	0	0.43	1.00		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
167	1tnm		46	127	8.5e-09	0.13	-0.18		HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
167	1twit		54	110	2.6e-07	0.29	0.41		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
167	2dli	A	54	247	2.6e-17	0.12	0.46		TWITCHIN 18TH IGSF MODULE; CHAIN: NULL; MHC CLASS I NK CELL RECEPTOR	MUSCLE PROTEIN IMMUNOGLOBULIN SUPERFAMILY, I SET, MUSCLE PROTEIN IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									PRECURSOR; CHAIN: A;	NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
167	2fcb	A	54	249	2.6e-19	0.21	0.90		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
167	3ncm	A	54	110	1.3e-07	0.05	0.35		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN- BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
170	1c28	A	145	277	2.6e-45	0.76	1.00		30 KD ADIPOCYTE COMPLEMENT- RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
170	1c28	A	145	277	2.6e-45			110.60	30 KD ADIPOCYTE COMPLEMENT- RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
170	1c28	A	149	277	1.2e-26	0.71	1.00		30 KD ADIPOCYTE COMPLEMENT- RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
170	1c28	B	145	276	2.6e-39	0.57	0.99		30 KD ADIPOCYTE COMPLEMENT- RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
170	1c28	B	145	276	2.6e-39			92.47	30 KD ADIPOCYTE COMPLEMENT- RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
170	1c28	B	159	276	6.8e-23	0.71	0.82		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
170	1c28	C	145	276	1.3e-32	0.50	0.90		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
170	1c28	C	145	276	1.3e-32			73.47	30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
170	1c28	C	164	276	3.4e-16	0.35	1.00		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
171	1as4	A	4	167	1e-47	0.35	0.89		ANTICHYMOTRYPSIN; CHAIN: A, B;	SERPIN ACT; SERPIN, SERINE PROTEASE INHIBITOR, ANTICHYMOTRYPSIN
171	1by7	A	2	168	1.7e-43	0.64	0.99		PLASMINOGEN ACTIVATOR INHIBITOR-2; CHAIN: A;	PROTEIN BINDING PAI-2; SERPIN, PROTEIN BINDING
171	1ezx	A	4	167	8.5e-48	0.31	0.95		ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1-ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1-ANTITRYPSIN, 2 TRYPSIN
171	1hle	A	1	167	8.5e-48	0.43	1.00		HYDROLASE INHIBITOR(SERINE PROTEINASE) HORSE LEUKOCYTE	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									ELASTASE INHIBITOR (HLEI) IHLE 3	
171	1ova	A	3	167	3.4e-40	0.45	0.99		SERPIN OVALBUMIN (EGG ALBUMIN) IOVA 3	
171	1qlp	A	4	167	8.5e-48	0.43	0.92		ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR; ALPHA-1-ANTIPROTEINASE; SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE
171	1qmn	A	4	167	6.8e-46	0.02	0.70		ALPHA-1-ANTICHYMOTRYPSIN; CHAIN: A;	SERPIN AACT SERPIN, SERINE PROTEINASE INHIBITOR, PARTIAL LOOP 2 INSERTION, LOOP-SHEET POLYMERIZATION, EMPHYSEMA, DISEASE 3 MUTATION, ACUTE PHASE PROTEIN, CONFORMATIONAL DISEASE
171	2ant	I	4	145	1.3e-39	0.44	1.00		ANTITHROMBIN; CHAIN: L, I;	SERPIN SERPIN, HEPARIN, INHIBITOR
171	2ant	L	1	145	3.9e-40	0.22	0.95		ANTITHROMBIN; CHAIN: L, I;	SERPIN SERPIN, HEPARIN, INHIBITOR
171	2ant	L	3	167	5.1e-39	0.42	0.99		ANTITHROMBIN; CHAIN: L, I;	SERPIN SERPIN, HEPARIN, INHIBITOR
172	1531		36	212	1e-47	0.70	1.00		HYDROLASE(O-GLYCOSYL) LYSOZYME (E.C.3.2.1.17) 153L 3	
172	1531		36	212	1e-47	0.70	1.00		HYDROLASE(O-GLYCOSYL)	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
172	1531		36	212	1e-47				LYSOZYME (E.C.3.2.1.17) 153L 3	
172	1531		36	212	1e-47			186.19	HYDROLASE(O-GLYCOSYL) LYSOZYME (E.C.3.2.1.17) 153L 3	
172	1531		36	212	1e-47			186.19	HYDROLASE(O-GLYCOSYL) LYSOZYME (E.C.3.2.1.17) 153L 3	
173	1a09	A	393	493	8.5e-19	0.80	0.84		C-SRC TYROSINE KINASE; CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GLU-(N,N-DIPENTYL AMINE); CHAIN: C, D;	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)
173	1ab2		394	496	1.7e-17	0.55	0.87		TRANSFERASE(PHOSPHOTRANSFERASE) PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.12) 1AB2 3 (SRC HOMOLOG 2 DOMAIN) (ABELSON, SH2 ABL) 1AB2 4 (NMR, 20 STRUCTURES) 1AB2 5	
173	1aot	F	394	495	5.1e-18	0.88	0.46		FYN PROTEIN-TYROSINE KINASE; CHAIN: F; PHOSPHOTYROSYL PEPTIDE; CHAIN: P	COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN) SRC HOMOLOGY 2 DOMAIN; SH2 DOMAIN, SIGNAL TRANSDUCTION, PEPTIDE COMPLEX, 2 COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
173	1aya	A	400	510	2.6e-17	0.56	0.59		HYDROLASE(SH2 DOMAIN) TYROSINE PHOSPHATASE SYP (N-TERMINAL SH2 DOMAIN) 1AYA 3 (PTP1D, SHPTP2) (E.C.3.1.3.48) COMPLEXED WITH THE PEPTIDE 1AYA 4 PDGFR-1009 1AYA 5	(PROTO-ONCOGENE/EARLY PROTEIN)
173	1bfi		392	511	1.3e-19	0.36	0.49		P85 ALPHA; CHAIN: NULL;	SH2 DOMAIN PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY ALPHA SH2 DOMAIN, P85ALPHA, PI 3-KINASE, NMR, C TERMINAL SH2 2 DOMAIN
173	1bkl		398	498	8.5e-18	0.76	0.39		PP60 V-SRC TYROSINE KINASE TRANSFORMING PROTEIN; CHAIN: NULL;	V-SRC SH2 DOMAIN SRC SH2; V-SRC SH2 DOMAIN, PHOSPHOTYROSINE RECOGNITION DOMAIN, PP60 2 SRC SH2 DOMAIN
173	1blj		388	493	3.4e-17	0.40	0.45		P55 BLK PROTEIN TYROSINE KINASE; CHAIN: NULL;	PHOSPHORYLATION SIGNAL TRANSDUCTION, TYROSINE KINASE, TRANSFERASE, 2 PHOSPHOTRANSFERASE, PHOSPHORYLATION COMPLEX
173	1csy	A	387	511	2.6e-18	0.42	0.09		SYK PROTEIN TYROSINE KINASE; CHAIN: A; ACETYL-THR-PTR-GLU-THR-LEU-NH2; CHAIN: B;	(PHOSPHOTRANSFERASE/PEPTIDE) PROTEIN-TYROSINE KINASE SH2 DOMAIN, COMPLEX 2 (PHOSPHOTRANSFERASE/PEPTIDE)
173	1fhs		394	507	1.3e-17	0.38	0.07		GROWTH FACTOR	SH2 DOMAIN GRB2; GRB2, SH2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									RECEPTOR BOUND PROTEIN-2; CHAIN: NULL;	DOMAIN, PROTEIN NMR, SOLUTION STRUCTURES
173	1lck	A	374	493	5.1e-23	0.16	0.28		P56=LCK= TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSHOPEPTIDE TEGQ(PHOSPHO)YQ PQA; ILCK 14 CHAIN: B; ILCK 15	COMPLEX (KINASE/PEPTIDE)
173	1lkk	A	395	493	1.2e-16	0.75	0.96		HUMAN P56 TYROSINE KINASE; ILKK 7 CHAIN: A; ILKK 8 PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU-ILE; ILKK 11 CHAIN: B; ILKK 12	COMPLEX (TYROSINE KINASE/PEPTIDE)
173	1lkk	A	395	509	2.6e-18	0.32	-0.09		HUMAN P56 TYROSINE KINASE; ILKK 7 CHAIN: A; ILKK 8 PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU-ILE; ILKK 11 CHAIN: B; ILKK 12	COMPLEX (TYROSINE KINASE/PEPTIDE)
173	1sha	A	398	493	1.4e-17	0.88	0.40		PHOSPHOTRANSFERASE V-SRC TYROSINE KINASE TRANSFORMING PROTEIN (PHOSPHOTYROSIN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									E ISHA 3 RECOGNITION DOMAIN SH2) (E.C.2.7.1.112) COMPLEX WITH ISHA 4 PHOSHOPEPTIDE A (TYR-VAL-PRO- MET-LEU, PHOSPHORYLATED TYR) ISHA 5	
173	1tce	A	394	511	6.5e-17	0.74	0.88		SHC; CHAIN: A; PHOSHOPEPTIDE OF THE ZETA CHAIN OF T CELL CHAIN: B,	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) SH2 DOMAIN, COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)
173	2abl		379	492	1.7e-21	0.39	0.88		ABL TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN
173	2pna		395	512	2.6e-18	0.37	0.35		SIGNALLING PROTEIN PHOSPHATIDYLINO SITOL 3-KINASE (E.C.2.7.1.137) (N- TERMINAL 2PNA 3 SH2 DOMAIN OF P85-ALPHA SUBUNIT) (NMR, 22 STRUCTURES) 2PNA 4	
178	1aut	L	168	260	8.5e-09	0.16	-0.13		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO- MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
178	1aut	L	559	636	5.2e-16	-0.04	0.05		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR)
178	1ckl	A	113	211	3.4e-09	0.26	0.87		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1ckl	A	155	267	2.6e-16	0.71	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1ckl	A	213	330	6.5e-20	0.10	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1ckl	A	272	387	1.3e-25	0.62	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
178	1ckl	A	2	80	3.4e-10	0.32	0.65		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1ckl	A	332	445	3.4e-14	0.51	0.89		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1ckl	A	332	445	9.1e-28	0.86	0.99		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1ckl	A	390	505	7.8e-23	0.40	1.00		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1ckl	A	40	145	5.2e-20	0.43	0.99		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1ckl	A	448	562	2.6e-21	0.20	0.99		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
										COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1ckl	A	4	93	6.5e-22	0.63	0.77		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
178	1dx5	I	566	654	3.9e-19	0.01	-0.02		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
178	1e5g	A	154	260	3.9e-21	0.71	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	154	268	1.2e-17	0.66	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	212	321	5.2e-18	0.53	0.51		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	213	324	1.2e-11	0.35	0.93		COMPLEMENT CONTROL PROTEIN;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: A;	MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	270	386	7.8e-27	0.75	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	331	444	6.5e-31	0.82	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	332	444	5.1e-18	0.83	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	389	504	1.7e-17	0.44	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	3	80	3.4e-10	-0.08	0.99		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	40	145	9.1e-24	0.63	0.99		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	40	151	6.8e-11	0.55	0.74		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	448	560	1.3e-26	0.26	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
178	1e5g	A	4	93	1.2e-23	0.46	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	506	566	2.6e-12	0.68	0.42		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	97	209	6.5e-20	0.53	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1e5g	A	98	210	6.8e-18	0.81	1.00		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
178	1fak	L	566	633	1.3e-14	0.09	-0.08		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
178	1hcc		154	208	5.2e-09	-0.09	0.47		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN ((CCP5) OF FACTOR H 1HCC 3	
178	1hcc		330	385	6.5e-13	0.16	0.46		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									((CCPS) OF FACTOR H 1HCC 3	
178	lhcc		38	94	3.9e-12	0.71	0.70		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN ((CCPS) OF FACTOR H 1HCC 3	
178	lhcc		390	443	3.9e-11	0.27	0.95		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN ((CCPS) OF FACTOR H 1HCC 3	
178	lhcc		4	35	1.2e-07	-0.64	0.01		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN ((CCPS) OF FACTOR H 1HCC 3	
178	lhcc		503	559	2.6e-15	0.10	0.13		GLYCOPROTEIN 16TH COMPLEMENT CONTROL PROTEIN ((CCPS) OF FACTOR H 1HCC 3	
178	lhfh		151	267	1.7e-10	0.38	0.94		GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
178	lhfh		328	444	5.1e-13	0.46	0.92		GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
178	1hfn		328	444	5.1e-13			83.97	GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
178	1hfn		97	208	3.4e-11	0.60	0.86		GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	
178	1hfi		154	209	1.3e-10	0.55	0.95		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HFIA 1 STRUCTURE) 1HFI 4 1HFIA 5	
178	1hfi		330	386	1.3e-13	0.74	0.96		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
178	1hfi		38	93	6.5e-12	0.87	0.68		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HFI 1 STRUCTURE) 1HFI 4 1HFI 5	
178	1hfi		390	444	5.2e-12	0.59	0.65		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HFI 1 STRUCTURE) 1HFI 4 1HFI 5	
178	1hfi		4	36	1e-07	0.24	0.18		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HFI 1 STRUCTURE) 1HFI 4 1HFI 5	
178	1hfi		503	559	1e-16	0.24	0.59		GLYCOPROTEIN FACTOR H, 15TH C-MODULE PAIR (NMR, MINIMIZED AVERAGED 1HFI 1 STRUCTURE) 1HFI 4 1HFI 5	
178	1klo		532	639	6.5e-14	0.13	-0.18		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
178	1qub	A	116	329	1.7e-29	0.54	1.00		HUMAN BETA2-	MEMBRANE ADHESION SHORT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									GLYCOPROTEIN I; CHAIN: A;	CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
178	1qub	A	212	443	1e-27	0.74	1.00		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
178	1qub	A	272	503	3.4e-31	0.29	1.00		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
178	1qub	A	2	267	1.7e-34	0.06	0.99		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
178	1qub	A	329	631	8.5e-42			190.64	HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
178	1qub	A	331	586	8.5e-42	0.53	1.00		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
178	1qub	A	40	350	1.7e-25	0.49	1.00		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
178	1qub	A	448	659	6.8e-19	-0.01	0.19		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
178	1vvc		153	268	5.1e-16	0.60	1.00		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
178	1vvc		211	325	6.8e-13	0.19	0.65		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
178	1vvc		270	385	5.1e-13	0.81	0.98		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
178	1vvc		330	444	3.4e-15	0.34	0.82		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
178	1vvc		388	504	5.1e-16			91.05	VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
178	1vvc		390	502	5.1e-16	0.17	1.00		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
178	1vvc		40	152	3.4e-09	0.48	0.98		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	SUSHI DOMAIN, 2 MODULE PAIR COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
178	1vvc		448	560	1.7e-16	0.53	0.86		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
178	1vvc		505	624	3.4e-10	0.43	0.17		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
178	1vvc		97	208	3.4e-16	0.32	0.66		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
178	1xca	L	178	260	6.8e-10	0.40	-0.09		BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE L, C;
178	9wga	A	323	506	6.8e-12	0.27	-0.18		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	GROWTH FACTOR LIKE DOMAIN
178	9wga	A	503	655	3.4e-12	0.00	0.15		LECTIN (AGGLUTININ)	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
179	1btk	A	1765	1861	2.6e-10	0.42	0.47		BRUTON'S TYROSINE KINASE; CHAIN: A, B;	TRANSFERASE BRUTON'S AGAMMAGLOBULINEMIA TYROSINE KINASE, BTK; TRANSFERASE, PH DOMAIN, BTK MOTIF, ZINC BINDING, X-LINKED 2 AGAMMAGLOBULINEMIA, TYROSINE-PROTEIN KINASE
179	1btn		1765	1862	1.2e-07	0.01	0.57		BETA-SPECTRIN; IBTN 4 CHAIN: NULL; IBTN 5	SIGNAL TRANSDUCTION PROTEIN
179	1fao	A	1765	1865	1.3e-21	0.47	1.00		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	SIGNALING PROTEIN DAPPI1, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
179	1fb8	A	1765	1865	5.2e-22	0.73	1.00		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	SIGNALING PROTEIN DAPPI1, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
179	1fgy	A	1761	1865	1.2e-20	0.00	0.45		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
179	1pms		1739	1864	1.3e-12	0.29	0.11		SOS 1; CHAIN: NULL;	SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
180	1ctu	A	115	447	1e-69	0.25	0.93		SOLUBLE QUINOPROTEIN GLUCOSE DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE BETA-PROPELLER, SUPERBARREL, COMPLEX WITH THE COFACTOR PQQ 2 AND THE INHIBITOR METHYLHYDRAZINE, OXIDOREDUCTASE
181	1b8q	A	5	102	8.5e-13	-0.11	0.59		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
181	1be9	A	2	77	8.5e-20	0.73	1.00		PSD-95; CHAIN: A; CRIPT; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
181	1i16		2	71	6.8e-14	0.34	0.78		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CEMOATTRACTANT FACTOR, PDZ DOMAIN
181	1kwa	A	1	77	1.7e-09	-0.10	0.63		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
181	1kwa	A	2	73	1e-11	0.05	0.77		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
181	1pdr		2	91	1.5e-19	0.48	1.00		HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT
181	1qau	A	5	102	8.5e-13	0.30	0.86		NEURONAL NITRIC OXIDE SYNTHASE	OXIDOREDUCTASE BETA-FINGER

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									(RESIDUES 1-130); CHAIN: A;	
181	1qav	A	2	84	1e-18	0.59	0.98		ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA-FINGER, HETERODIMER
181	1qlc	A	4	80	1.2e-21	0.48	1.00		POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING
181	3pdz	A	2	77	1.7e-18	0.77	1.00		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTPIE, PTP-BAS, SPECIFICITY 2 OF BINDING
182	1e0s	A	8	177	3.4e-60	0.94	1.00		ADP-RIBOSYLATION FACTOR 6; CHAIN: A;	G PROTEIN G PROTEIN, RAS, ARF, ARF6, MEMBRANE TRAFFIC
182	1fzq	A	4	176	8.5e-51	0.95	1.00		ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3; CHAIN: A;	SIGNALING PROTEIN ARF-LIKE PROTEIN 3, ARL3; PROTEIN-GDP COMPLEX WITHOUT MAGNESIUM, ARF FAMILY, RAS 2 SUPERFAMILY, G-DOMAIN
182	1hur	A	2	177	8.5e-66	0.95	1.00		HUMAN ADP-RIBOSYLATION FACTOR 1; IHUR 5 CHAIN: A, B; IHUR 7	PROTEIN TRANSPORT GDP-BINDING, MEMBRANE TRAFFICKIN, NON-MYRISTOYLATED IHUR 16
182	1hur	A	2	179	8.5e-66			178.06	HUMAN ADP-RIBOSYLATION	PROTEIN TRANSPORT GDP-BINDING, MEMBRANE TRAFFICKIN,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									FACTOR I; 1HUR 5 CHAIN: A, B; 1HUR 7	NON-MYRISTOYLATED 1HUR 16
183	1ata		834	896	5.2e-12	0.29	0.09		PROTEINASE INHIBITOR(TRYPSIN) TRYPSIN INHIBITOR (PH 4.75) 1ATA 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1ATA 4	
183	1aut	L	845	940	5.1e-11	0.29	-0.19		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO- MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
183	1dan	L	819	898	1.7e-10	0.49	-0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMETHYLKE TONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
183	1dan	L	851	943	3.4e-12	0.08	-0.15		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C;	
183	1dan	L	939	1020	1.7e-10	0.01	-0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
183	1dva	L	330	427	8.5e-14	0.20	-0.18		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C; D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
183	1dva	L	819	898	1.7e-10	0.65	-0.12		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C; D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
183	1dva	L	851	943	3.4e-12	0.30	-0.14		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C; D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	COMPLEX
183	1dx5	I	1167	1294	3.4e-11	0.02	-0.20		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
183	1dx5	I	1167	1294	3.4e-11	0.02	-0.20		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
183	1fak	L	819	898	1.7e-10	0.27	-0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE(COFACTOR/LIGAND)), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
183	1fak	L	819	898	1.7e-10	0.27	-0.18		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
183	1fak	L	851	943	3.4e-12	0.05	-0.14		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
183	1fak	L	851	943	3.4e-12	0.10	-0.15		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
183	1kdo		333	472	1e-09	0.21	-0.15		LAMININ; CHAIN:	GLYCOPROTEIN GLYCOPROTEIN

SEQ ID NO;	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
183	1klo		755	902	3.4e-15	0.20	-0.18		NULL; LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
183	1klo		755	902	3.4e-15	0.20	-0.18		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
183	1pfx	L	330	438	1.4e-10	0.15	-0.14		FACTOR IXA; CHAIN: C, L; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
183	1pfx	L	772	920	2.6e-08	0.03	-0.18		FACTOR IXA; CHAIN: C, L; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
183	1pfx	L	819	898	1.7e-09	0.09	-0.19		FACTOR IXA; CHAIN: C, L; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
183	1qfk	L	1263	1339	5.1e-11	0.16	-0.19		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	
183	1qfk	L	334	427	5.1e-13	0.32	-0.18		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
183	1qfk	L	822	898	6.8e-10	0.31	-0.18		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
183	1qub	A	379	488	3.9e-08	0.20	-0.15		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
183	1xka	L	334	427	3.4e-10	0.22	-0.07		BLOOD COAGULATION	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									FACTOR XA; CHAIN: L, C;	COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
183	1xka	L	822	898	1e-10	0.22	-0.13		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
183	1xka	L	855	940	3.4e-09	0.11	-0.19		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
183	9wga	A	1219	1364	5.1e-11	0.02	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
183	9wga	A	1219	1364	5.1e-11	0.02	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
183	9wga	A	277	420	5.1e-14	0.08	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
183	9wga	A	277	420	5.1e-14	0.08	-0.19		LECTIN (AGGLUTININ) WHEAT GERM	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
183	9wga	A	318	544	1.5e-11	0.31	-0.18		AGGLUTININ (ISOLECTIN 2) 9WGA 3	
183	9wga	A	318	544	1.5e-11	0.31	-0.18		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
183	9wga	A	757	907	3.4e-12	0.13	-0.17		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
183	9wga	A	757	907	3.4e-12	0.13	-0.17		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
183	9wga	A	777	975	5.1e-13	0.29	-0.12		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
183	9wga	A	777	975	5.1e-13	0.29	-0.12		LECTIN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									(AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
184	lapo		1210	1245	1.3e-06	0.37	0.53		COAGULATION FACTOR EGF-LIKE MODULE OF BLOOD COAGULATION FACTOR X (N- TERMINAL, 1APO 3 APO FORM) (NMR, 13 STRUCTURES) 1APO 4	
184	lapo		1210	1245	1.3e-06	0.37	0.53		COAGULATION FACTOR EGF-LIKE MODULE OF BLOOD COAGULATION FACTOR X (N- TERMINAL, 1APO 3 APO FORM) (NMR, 13 STRUCTURES) 1APO 4	
184	lcu		39	385	5.2e-34	0.05	-0.19		CYCLODEXTRIN GLYCOSYLTRANSF ERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
184	lcu		39	385	5.2e-34	0.05	-0.19		CYCLODEXTRIN GLYCOSYLTRANSF ERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
184	1ciu		404	783	1.3e-32	0.01	-0.18		CYCLODEXTRIN GLYCOSYLTRANSF ERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
184	1ciu		404	783	1.3e-32	0.01	-0.18		CYCLODEXTRIN GLYCOSYLTRANSF ERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
184	1ciu		669	1044	1.3e-26	0.05	-0.19		CYCLODEXTRIN GLYCOSYLTRANSF ERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
184	1ciu		669	1044	1.3e-26	0.05	-0.19		CYCLODEXTRIN GLYCOSYLTRANSF ERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
184	1ciu		863	1177	3.9e-22	0.03	-0.15		CYCLODEXTRIN GLYCOSYLTRANSF ERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
184	1ciu		863	1177	3.9e-22	0.03	-0.15		CYCLODEXTRIN GLYCOSYLTRANSF ERASE; 1CIU 6 CHAIN: NULL; 1CIU 7	GLYCOSIDASE CGTASE; 1CIU 8 THERMOSTABLE 1CIU 14
184	1cwv	A	264	749	9.1e-60	0.05	-0.20		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN- BINDING PROTEIN, INV GENE
184	1cwv	A	264	749	9.1e-60	0.05	-0.20		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN- BINDING PROTEIN, INV GENE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
184	1cwv	A	521	996	1.2e-61			101.45	INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
184	1cwv	A	521	996	1.2e-61			101.45	INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
184	1cwv	A	561	1082	1e-56	0.04	-0.19		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
184	1cwv	A	561	1082	1e-56	0.04	-0.19		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN-BINDING PROTEIN, INV GENE
184	1dan	L	1210	1282	8.5e-10	0.15	0.04		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
184	1dan	L	1210	1282	8.5e-10	0.15	0.04		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
184	1edm	B	1210	1242	5.1e-07	0.32	0.76		FACTOR IX; CHAIN: B, C;	COAGULATION FACTOR CRYSTAL STRUCTURE, EPIDERMAL GROWTH FACTOR, EGF, 2 CALCIUM-BINDING, EGF-LIKE DOMAIN, STRUCTURE AND FUNCTION, 3 HUMAN FACTOR IX,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
184	1edm	B	1210	1242	5.1e-07	0.32	0.76		FACTOR IX; CHAIN: B, C;	COAGULATION FACTOR COAGULATION FACTOR CRYSTAL STRUCTURE, EPIDERMAL GROWTH FACTOR, EGF, 2 CALCIUM-BINDING, EGF-LIKE DOMAIN, STRUCTURE AND FUNCTION, 3 HUMAN FACTOR IX, COAGULATION FACTOR
184	1fak	L	1210	1282	8.5e-10	-0.03	0.00		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
184	1fak	L	1210	1282	8.5e-10	-0.03	0.00		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
184	1pfx	L	1189	1242	5.2e-10	0.04	-0.11		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
184	1pfx	L	1189	1242	5.2e-10	0.04	-0.11		FACTOR IXA; CHAIN: C, L;; D-PHE- PRO-ARG; CHAIN: I;	GLYCOPROTEIN COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
184	1pfx	L	1210	1273	1e-08	0.15	0.11		FACTOR IXA; CHAIN: C, L;; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
184	1pfx	L	1210	1273	1e-08	0.15	0.11		FACTOR IXA; CHAIN: C, L;; D-PHE- PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
184	1qfk	L	1214	1282	3.4e-09	0.04	-0.13		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN:	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
184	1qfk	L	1214	1282	3.4e-09	0.04	-0.13		C; COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
184	1tpg		1189	1242	2.6e-10	0.44	0.07		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
184	1tpg		1189	1242	2.6e-10	0.44	0.07		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
184	1tpg		1197	1246	1.7e-07	-0.12	0.03		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
184	1tpg		1197	1246	1.7e-07	-0.12	0.03		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
184	1whe		1189	1245	3.9e-10	0.29	-0.14		COAGULATION FACTOR X; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN, HYDROLASE, SERINE PROTEASE, PLASMA, BLOOD 2 COAGULATION FACTOR
184	1whe		1189	1245	3.9e-10	0.29	-0.14		COAGULATION FACTOR X; CHAIN:	GLYCOPROTEIN GLYCOPROTEIN, HYDROLASE, SERINE PROTEASE,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									NULL;	PLASMA, BLOOD 2 COAGULATION FACTOR
184	9wga	A	1191	1293	5.1e-08	0.22	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
184	9wga	A	1191	1293	5.1e-08	0.22	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
185	1c7j	A	1	83	3.4e-29	-0.84	0.40		PARA-NITROBENZYL ESTERASE; CHAIN: A;	HYDROLASE PNB ESTERASE; ALPHA-BETA HYDROLASE, DIRECTED EVOLUTION, ORGANIC ACTIVITY, 2 PNB ESTERASE
185	1cle	A	1	83	1.5e-23	-0.66	0.33		CHOLESTEROL ESTERASE; 1CLE 4 CHAIN: A, B; 1CLE 5	LIPASE ESTERASE, SUBSTRATE/PRODUCT-BOUND 1CLE 9
185	1dx4	A	1	83	1.7e-24	-0.91	0.10		ACETYLCHOLINESTERASE; CHAIN: A;	HYDROLASE (SERINE ESTERASE) HYDROLASE (SERINE ESTERASE), HYDROLASE, SERINE ESTERASE, 2 SYNAPSE, MEMBRANE, NERVE, MUSCLE, SIGNAL, NEUROTRANSMITTER 3 DEGRADATION, GLYCOPROTEIN, GPI-ANCHOR, ALTERNATIVE SPLICING
185	1ea5	A	1	83	3.4e-30	-0.42	0.54		ACETYLCHOLINESTERASE; CHAIN: A;	CHOLINESTERASE SERINE HYDROLASE, NEUROTRANSMITTER CLEAVAGE,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
185	1f6w	A	1	83	5.1e-32	-0.93	0.25		BILE SALT ACTIVATED LIPASE; CHAIN: A;	CATALYTIC 2 TRIAD, ALPHA/BETA HYDROLASE HYDROLASE BILE SALT ACTIVATED LIPASE, ESTERASE, CATALYTIC DOMAIN
185	1lpp		1	83	8.5e-23	-0.93	0.16		HYDROLASE LIPASE (E.C.3.1.1.3) (TRIACYLGLYCERO L LIPASE) COMPLEXED WITH ILPP 3 HEXADECANESULF ONATE ILPP 4 ILPP 71	
185	1maa	A	2	83	1.7e-29	-0.76	0.75		ACETYLCHOLINEST ERASE; CHAIN: A, B, C, D;	HYDROLASE MACHE; HYDROLASE, SERINE ESTERASE, ACETYLCHOLINESTERASE, TETRAMER, 2 HYDROLASE FOLD, GLYCOSYLATED PROTEIN
185	1qe3	A	1	83	1.7e-29	-0.51	0.48		PARA- NITROBENZYL ESTERASE; CHAIN: A;	HYDROLASE PNB ESTERASE; ALPHA-BETA HYDROLASE DIRECTED EVOLUTION
185	1thg		1	83	1.5e-25	-0.65	0.19		HYDROLASE(CARB OXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) TRIACYLGLYCEROL HYDROLASE 1THG 3	
185	2bce		1	83	3.4e-32	-0.93	0.36		CHOLESTEROL ESTERASE; CHAIN: NULL;	HYDROLASE BILE SALT ACTIVATED LIPASE, BILE SALT STIMULATED HYDROLASE, SERINE ESTERASE, LIPASE
186	1mrt		132	165	0.0052	-0.83	0.77		METALLOTHIONEIN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI- BLAST	Verify Score	PMF Score	SeqFold Score	Compound	PDB annotation
									CD-7 METALLOTHIONEIN -2 (ALPHA DOMAIN) (NMRS) 1MRTA 2	

TABLE 6

SEQ ID NO:	Position of Signal Peptide	Maximum score	Mean score
94	1-26	0.988	0.911
95	1-17	0.977	0.921
96	1-32	0.969	0.847
97	1-32	0.969	0.847
98	1-16	0.896	0.833
99	1-19	0.914	0.625
100	1-20	0.888	0.583
101	1-22	0.932	0.756
103	1-18	0.972	0.936
104	1-17	0.979	0.961
105	1-24	0.961	0.807
106	1-29	0.977	0.852
107	1-45	0.971	0.702
108	1-24	0.969	0.898
109	1-34	0.988	0.805
110	1-17	0.984	0.923
114	1-18	0.975	0.958
120	1-17	0.977	0.921
124	1-31	0.985	0.926
126	1-42	0.988	0.594
127	1-19	0.960	0.851
136	1-26	0.981	0.865
137	1-18	0.975	0.958
142	1-17	0.977	0.921
150	1-16	0.896	0.833
156	1-19	0.914	0.625
162	1-16	0.939	0.838
164	1-28	0.961	0.857
167	1-22	0.968	0.875
169	1-25	0.971	0.893
170	1-16	0.948	0.836
172	1-19	0.960	0.851
174	1-30	0.972	0.658
175	1-31	0.965	0.894
176	1-22	0.979	0.697
182	1-15	0.926	0.631
185	1-20	0.952	0.660
186	1-42	0.994	0.973

TABLE 7

SEQ ID NO:	Chromosomal Location
1	22q11
2	5
3	20
4	20
5	20
7	17
10	17
11	19q13.3-q13.4
16	2p21
19	21
20	11q13
21	17
22	1p36.2
23	1p36.2
24	15
25	15
26	7
27	9q21-q22
28	17
31	1
32	13
36	11p15
37	7q22
38	17
40	11q23.3
41	10q25-q26
42	11q13
43	19p13.1
44	17
45	7q32
46	19
47	9q34
49	9q21-q22
50	20q13.3
51	2q35
52	9
54	9q34
55	9q34
56	17
57	14q32
58	20
60	5
61	16q24.3
62	16q24.3
64	4q34.1-q35.1
65	4q34.1-q35.1
66	9
67	15
68	11
69	14
70	10
71	2cen-q13
72	16
74	4p16.3

SEQ ID NO:	Chromosomal Location
75	13
76	1p36.2
77	4p16-p15
80	1
81	1p35-p31.3
82	1p35-p31.3
86	22q13.33
87	1q41
90	11p15
91	7q22
93	11p15.5

TABLE 8

SEQ ID NO: of Full-length Nucleotide Sequence	SEQ ID NO: of Full-length Peptide Sequence	SEQ ID NO: in Priority Application USSN 09/728,952
1	94	2
2	95	3
3	96	4
4	97	5
5	98	6
6	99	7
7	100	12
8	101	13
9	102	14
10	103	15
11	104	16
12	105	17
13	106	18
14	107	19
15	108	20
16	109	22
17	110	23
18	111	24
19	112	26
20	113	27
21	114	28
22	115	29
23	116	30
24	117	31
25	118	32
26	119	33
27	120	34
28	121	35
29	122	36
30	123	37
31	124	38
32	125	39
33	126	40
34	127	41
35	128	42
36	129	43
37	130	44
38	131	45
39	132	46
40	133	47
41	134	48
42	135	49
43	136	50
44	137	51
45	138	52
46	139	53
47	140	54
48	141	55
49	142	57
50	143	58
51	144	59

SEQ ID NO: of Full-length Nucleotide Sequence	SEQ ID NO: of Full-length Peptide Sequence	SEQ ID NO: in Priority Application USSN 09/728,952
52	145	60
53	146	61
54	147	62
55	148	63
56	149	64
57	150	65
58	151	66
59	152	67
60	153	68
61	154	69
62	155	70
63	156	71
64	157	72
65	158	73
66	159	74
67	160	75
68	161	76
69	162	77
70	163	78
71	164	79
72	165	80
73	166	81
74	167	82
75	168	83
76	169	84
77	170	85
78	171	86
79	172	87
80	173	88
81	174	89
82	175	90
83	176	91
84	177	92
85	178	93
86	179	94
87	180	95
88	181	96
89	182	97
90	183	98
91	184	99
92	185	100
93	186	101

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-93, a mature protein coding portion of SEQ ID NO: 1-93, an active domain coding portion of SEQ ID NO: 1-93, and complementary sequences thereof.
2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - (a) a polypeptide encoded by any one of the polynucleotides of claim 1;
 - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-93; and

(c) a polypeptide of any one of SEQ ID NO: 94-186.

11. A composition comprising the polypeptide of claim 10 and a carrier.

5 12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

10 b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

15 b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

20

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

25

16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

30 b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- 5 b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

- 10 a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the
- 15 polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

- a) culturing a host cell comprising a polynucleotide sequence selected from SEQ ID NO: 1-93, a mature protein coding portion of SEQ ID NO: 1-93, an active
- 20 domain coding portion of SEQ ID NO: 1-93, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-93, under conditions sufficient to express the polypeptide in said cell; and
- b) isolating the polypeptide from the cell culture or cells of step (a).

25 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO: 94-186, the mature protein portion thereof, or the active domain thereof.

30 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1-93.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
24. The collection of claim 23, wherein the array detects full-matches to any one of the
5 polynucleotides in the collection.
25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 10 26. The collection of claim 22, wherein the collection is provided in a computer-readable format.
27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20
15 and a pharmaceutically acceptable carrier.
28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

20

SEQUENCE LISTING

<110> Hyseq, Inc

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<140> NOT YET ASSIGNED

<141> 2001-11-30

<150> 09/728,952

<151> 2000-11-30

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<170> PatentIn version 3.0

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atg aag agg gcg tcc gct gga ggg agc cgg ctg ctg gca tgg gtg ctg      166
Met Lys Arg Ala Ser Ala Gly Gly Ser Arg Leu Leu Ala Trp Val Leu
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Trp Leu Gln Ala Trp Gln Val Ala Ala Pro Cys Pro Gly Ala Cys Val
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tgc tac aat gag ccc aag gtg acg aca agc tgc ccc cag cag ggc ctg      262
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His Gly Asn Arg Ile Ser His Val Pro Ala Ala Ser Phe Arg Ala Cys
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cgc aac ctc acc atc ctg tgg ctg cac tcg aat gtg ctg gcc cga att      406
Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Val Leu Ala Arg Ile
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gat gcg gct gcc ttc act ggc ctg gcc ctc ctg gag cag ctg gac ctc      454
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Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr
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ctg cag gac aac gcg ctg cag gca ctg cct gat gac acc ttc cgc gac      646
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Val Pro Glu Arg Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu
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ctg ccc act gag gcc ctg gcc ccc tgc gtg ccc tgc agt acc tga ggc      886
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acctcaaacg cctagctgcc aatgacctgc agggctgcgc tgtggccacc ggccttacca      1066

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Lys Gly Lys Trp Lys Asn Lys Glu Arg Ile Leu Ile Phe Ser Ser Arg	
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Gly Ile Asn Phe Arg Thr Arg His Leu Met Gln Asp Leu Arg Met Leu	
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Phe Val Ile Asn Glu Val Cys Glu Met Lys Asn Cys Asn Lys Cys Ile	
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Lys Ser Gln Pro Phe Val Asp His Val Phe Thr Phe Thr Ile Leu Asp	
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230 235 240	

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 Ser Pro Asn Met His Arg Arg Val Ile Arg Ser Ile Thr Ala Ala Lys
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 Tyr Arg Glu Lys Gln Gln Val Lys Asp Val Gln Lys Leu Arg Lys Lys
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 Glu Pro Lys Thr Leu Leu Pro His Asp Pro Thr Ala Asp Val Phe Val
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 Thr Pro Ala Glu Glu Lys Pro Ile Glu Ile Gln Trp Val Lys Pro Glu
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 Pro Lys Val Asp Leu Lys Ala Arg Lys Lys Arg Ile Tyr Lys Arg Gln
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 Leu Leu Leu Ala Leu Val Leu Val Pro Ser Asp Ala Ser Gly Gln Ser
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Thr	Asp	Gly	Met	Ile	Lys	Trp	Val	Lys	Ile	Ala	Leu	Ala	Ser	Phe	Tyr		
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Ser	Ser	Val	Ser	Arg	Gly	Thr	Ala	Pro	Ser	Asp	Asn	Arg	Val	Thr	Ser		
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Phe	Arg	Asp	Leu	Ile	His	Asp	Gln	Asp	Glu	Asp	Glu	Glu	Glu	Glu	Glu		
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ggc	cag	agg	ttt	tat	gct	ggg	ggc	tca	gag	aga	agt	gga	cag	cag	att		489
Gly	Gln	Arg	Phe	Tyr	Ala	Gly	Gly	Ser	Glu	Arg	Ser	Gly	Gln	Gln	Ile		
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Val	Gly	Pro	Pro	Arg	Lys	Lys	Ser	Pro	Asn	Glu	Leu	Val	Asp	Asp	Leu		
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Tyr	Arg	Leu	Gly	Ala	Ala	Pro	Glu	Glu	Glu	Ser	Ala	Tyr	Val	Ala	Gly		
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Pro	Ala	Glu	Leu	Arg	Arg	Leu	Ala	His	Gly	Gly	Gln	Val	Asn	Leu	Asp		
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Val Leu Ser Thr	Ser Ser Pro Ala Gln	Gln Ala Glu Asn	Glu Ala Lys	
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gcc agc tct tcc atc tta atc aac gaa tca gag cct acc aca aac atc				1065
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Gln Ile Arg Leu Ala Asp Gly Gly Arg	Leu Val Gln Lys	Phe Asn His		
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agc cac agg atc agc gac atc cga ctc ttc atc gtg gat gcc cgg cca				1161
Ser His Arg Ile	Ser Asp Ile Arg Leu Phe	Ile Val Asp Ala Arg	Pro	
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gcc atg gct gcc acc agc ttt atc ctc atg act act ttc ccg aac aaa				1209
Ala Met Ala Ala	Thr Ser Phe Ile Leu Met Thr Thr	Phe Pro Asn Lys		
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gag ctg gct gat gag agc cag acc ctg aag gaa gcc aac ctg ctc aat				1257
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ctt gca gac ggc ggg	agg ctg gtg cag aaa	ttt aac cac agc cac agg	1015
Leu Ala Asp Gly Gly	Arg Leu Val Gln Lys	Phe Asn His Ser His Arg	
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Ile Ser Asp Ile Arg	Leu Phe Ile Val Asp	Ala Arg Pro Ala Met Ala	
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gcc acc agc ttt atc	ctc atg act act ttc	cgg aac aaa gag ctg gct	1111
Ala Thr Ser Phe Ile	Leu Met Thr Thr Phe	Pro Asn Lys Glu Leu Ala	
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gat gag agc cag acc	ctg aag gaa gcc aac	ctg ctc aat gct gtc atc	1159
Asp Glu Ser Gln Thr	Leu Lys Glu Ala Asn	Leu Leu Asn Ala Val Ile	
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Glu Phe Val Ala Val	Thr Gly Ala Glu Glu	Asp Arg Ala Arg Phe Phe	
	15	20 25	
ctc gag tcg gcc ggc	tgg gac ttg cag atc	gcg cta gcg agc ttt tat	267
Leu Glu Ser Ala Gly	Trp Asp Leu Gln Ile	Ala Leu Ala Ser Phe Tyr	
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gag gac gga ggg gat gaa gac att gtg acg att tcg cag gca acc ccc Glu Asp Gly Gly Asp Glu Asp Ile Val Thr Ile Ser Gln Ala Thr Pro 45 50 55	315
agt tca gtg tcc aga ggc aca gcc ccc agt gat aat aga gtg aca tcc Ser Ser Val Ser Arg Gly Thr Ala Pro Ser Asp Asn Arg Val Thr Ser 60 65 70	363
ttc aga gac ctc att cat gac caa gat gaa gat gag gag gaa gag gaa Phe Arg Asp Leu Ile His Asp Gln Asp Glu Asp Glu Glu Glu Glu Glu 75 80 85 90	411
ggc cag agg agc agg ttt tat gct ggg ggc tca gag aga agt gga cag Gly Gln Arg Ser Arg Phe Tyr Ala Gly Gly Ser Glu Arg Ser Gly Gln 95 100 105	459
cag att gtt ggc cct ccc agg aag aaa agt ccc aac gag ctg gtg gat Gln Ile Val Gly Pro Pro Arg Lys Lys Ser Pro Asn Glu Leu Val Asp 110 115 120	507
gat ctc ttt aaa ggt gcc aaa gag cat gga gct gta gct gtg gag cga Asp Leu Phe Lys Gly Ala Lys Glu His Gly Ala Val Ala Val Glu Arg 125 130 135	555
gtg acc aag agc cct gga gag acc agt aaa ccg aga cca ttt gca gga Val Thr Lys Ser Pro Gly Glu Thr Ser Lys Pro Arg Pro Phe Ala Gly 140 145 150	603
ggt ggc tac cgc ctt ggg gcc agc acc aga gga aga gtc tgc cta tgt Gly Gly Tyr Arg Leu Gly Ala Ser Thr Arg Gly Arg Val Cys Leu Cys 155 160 165 170	651
ggc agg aga aaa gag gca gca ttc cag cca aga tgt tca tgt agt att Gly Arg Arg Lys Glu Ala Ala Phe Gln Pro Arg Cys Ser Cys Ser Ile 175 180 185	699
gaa act ctg gaa gag tgg att cag cct gga taa tggagaac tcagaagcta Glu Thr Leu Glu Glu Trp Ile Gln Pro Gly 190 195	750
ccaagaccga tccaatgccc agttttctgga gtctattcgc agaggggagg tgcagcagag	810
cttccgaggc tagcctcacg tggacagggtg aacttgata tggaggacca tcgggacgag	870
gactttgtga agcccaaagg agccttcaaa gccttcactg gcgagggtca gaaactgggc	930
agcactgccc ccaggtgtt gattaccagc tctccagccc aacaggcaga aaatgaagcc	990
aaagccagct cttccatctt aatcgacgaa tcagagccta ccacaaacat ccaaattcgg	1050
cttgacagcg gcgggaggct ggtgcagaaa ttttaaccaca gccacaggat cagcgacatc	1110
cgactcttca tcgtggatgc ccggccagcc atggctgcca ccagctttat cctcatgact	1170
actttcccga acaaagagct ggctgatgag agccagaccc tgaaggaagc caacctgctc	1230
aatgctgtca tcgtgcagcg gttaacataa	1260

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<210> 6
<211> 473
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (56)..(358)

<220>
<221> misc_feature
<222> (1)...(473)
<223> n = a,t,c or g

<400> 6
tctgccagct acccgcgctc tgagcccggg gccagattcc catggaagcg ccgcg atg      58
                                         Met
                                         1

ttc gcc ccc cgg ctg ctg gat ttg cag aag acg aaa tac gcg agg ttc      106
Phe Ala Pro Arg Leu Leu Asp Leu Gln Lys Thr Lys Tyr Ala Arg Phe
                    5                      10                      15

atg aac cac cga gtc cct gcc cac aag agg tac cag ccc aca gag tat      154
Met Asn His Arg Val Pro Ala His Lys Arg Tyr Gln Pro Thr Glu Tyr
                20                      25                      30

gaa cat gcg gcc aac tgt gcc acc cat gct ttc tgg atc atc ccc agc      202
Glu His Ala Ala Asn Cys Ala Thr His Ala Phe Trp Ile Ile Pro Ser
                35                      40                      45

atc ctg ggc agc tcc aac ctc tac ttc ctg tcg gac gat gac tgg gag      250
Ile Leu Gly Ser Ser Asn Leu Tyr Phe Leu Ser Asp Asp Asp Trp Glu
                50                      55                      60                      65

acc atc tct gcc tgg atc tac ggc ctc ggc ctc tgc ggc ctc ttc gtg      298
Thr Ile Ser Ala Trp Ile Tyr Gly Leu Gly Leu Cys Gly Leu Phe Val
                    70                      75                      80

gtg tcc act gtg ttt cac acc atc tcc tgg aag aag agc cac ctc aga      346
Val Ser Thr Val Phe His Thr Ile Ser Trp Lys Lys Ser His Leu Arg
                    85                      90                      95

tgg gga ttc tga ggg ccaaggggtc ttggctggac agaggagccc agccctgcta      401
Trp Gly Phe
                    100

acctgtaggc aggcacgata agtccagggc acggctctgn gggcactggc ccttccttgc      461

ttgcaggggc tg                                                         473

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<210> 7
<211> 2432
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS

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<222> (148) .. (1890)

<400> 7

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gccgcgaatt cggcaccgagc ctgtgggagg ctgtttttctg agggagctga gtgttttacag      60
ccactcagcc ctgctctgct cagctgaagc agaaaacaga gaccttttgc attactttgg      120
ttcaagagca agacaggagg cgactgc      atg aga cca tgg ctg aga cac cta      171
                                   Met Arg Pro Trp Leu Arg His Leu
                                   1                               5

gtc ctc cag gca ctg agg aac tcc agg gca ttc tgt ggg tct cat ggg      219
Val Leu Gln Ala Leu Arg Asn Ser Arg Ala Phe Cys Gly Ser His Gly
      10                               15                               20

aag cca gca cct cta cct gtt cct cag aag atc gtg gcc acc tgg gaa      267
Lys Pro Ala Pro Leu Pro Val Pro Gln Lys Ile Val Ala Thr Trp Glu
      25                               30                               35                               40

gcc atc agc ctg gga agg cag ctg gtg cct gag tac ttc aac ttc gcc      315
Ala Ile Ser Leu Gly Arg Gln Leu Val Pro Glu Tyr Phe Asn Phe Ala
                                   45                               50                               55

cat gat gtg ctg gat gtg tgg agt cgg ctg gaa gag gct gga cac cgc      363
His Asp Val Leu Asp Val Trp Ser Arg Leu Glu Glu Ala Gly His Arg
                                   60                               65                               70

ccc cca aat cct gcc ttc tgg tgg gtc aat ggc aca gga gca gag atc      411
Pro Pro Asn Pro Ala Phe Trp Trp Val Asn Gly Thr Gly Ala Glu Ile
                                   75                               80                               85

aag tgg agc ttt gag gag ctg ggg aag cag tcc agg aag gca gcc aat      459
Lys Trp Ser Phe Glu Glu Leu Gly Lys Gln Ser Arg Lys Ala Ala Asn
      90                               95                               100

gtg ctg ggg ggt gca tgc ggc ctg cag cct ggg gac aga atg atg ctg      507
Val Leu Gly Gly Ala Cys Gly Leu Gln Pro Gly Asp Arg Met Met Leu
      105                               110                               115                               120

gta ctc cca cgg ctc ccg gag tgg tgg ctg gtc agt gtg gct tgc atg      555
Val Leu Pro Arg Leu Pro Glu Trp Trp Leu Val Ser Val Ala Cys Met
                                   125                               130                               135

cgg aca ggg act gtg atg att ccg ggt gtg act cag ctg aca gag aag      603
Arg Thr Gly Thr Val Met Ile Pro Gly Val Thr Gln Leu Thr Glu Lys
                                   140                               145                               150

gac ctc aag tac cgg ctg cag gcg tcc agg gcc aag tcc att atc acc      651
Asp Leu Lys Tyr Arg Leu Gln Ala Ser Arg Ala Lys Ser Ile Ile Thr
                                   155                               160                               165

agt gac tcc cta gct cca agg gtg gat gcc atc agt gcc gaa tgc ccc      699
Ser Asp Ser Leu Ala Pro Arg Val Asp Ala Ile Ser Ala Glu Cys Pro
      170                               175                               180

tcc ctc cag acc aag ctg ctg gtg tca gac agc agt cgg cca ggc tgg      747
Ser Leu Gln Thr Lys Leu Leu Val Ser Asp Ser Ser Arg Pro Gly Trp
      185                               190                               195                               200

ttg aac ttc agg gaa ctc ctc cgg gag gct tct aca gag cac aac tgc      795
Leu Asn Phe Arg Glu Leu Leu Arg Glu Ala Ser Thr Glu His Asn Cys

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205								210				215				
atg	agg	aca	aag	agt	cga	gac	ccg	ctg	gcc	atc	tac	ttt	acc	aag	cgg	843
Met	Arg	Thr	Lys	Ser	Arg	Asp	Pro	Leu	Ala	Ile	Tyr	Phe	Thr	Lys	Arg	
			220					225					230			
gaa	cca	ccg	ggg	gcc	ccc	aag	atg	gtc	gag	cac	tcc	cag	agc	agc	tac	891
Glu	Pro	Pro	Gly	Ala	Pro	Lys	Met	Val	Glu	His	Ser	Gln	Ser	Ser	Tyr	
		235					240					245				
gga	ctg	ggt	ttt	gtg	gcc	agc	gga	aga	cgg	tgg	gtg	gcc	ttg	acc	gaa	939
Gly	Leu	Gly	Phe	Val	Ala	Ser	Gly	Arg	Arg	Trp	Val	Ala	Leu	Thr	Glu	
	250					255					260					
tct	gac	atc	ttc	tgg	aac	acg	act	gac	act	ggc	tgg	gtg	aag	gca	gcc	987
Ser	Asp	Ile	Phe	Trp	Asn	Thr	Thr	Asp	Thr	Gly	Trp	Val	Lys	Ala	Ala	
265					270					275					280	
tgg	act	ctc	ttc	tct	gcc	tgg	cct	aat	gga	tct	tgc	att	ttt	gtg	cat	1035
Trp	Thr	Leu	Phe	Ser	Ala	Trp	Pro	Asn	Gly	Ser	Cys	Ile	Phe	Val	His	
				285					290					295		
gag	ctg	ccc	cga	gtt	gat	gcc	aaa	gtt	atc	ctg	aat	act	ctc	tcc	aaa	1083
Glu	Leu	Pro	Arg	Val	Asp	Ala	Lys	Val	Ile	Leu	Asn	Thr	Leu	Ser	Lys	
			300					305						310		
ttc	ccg	ata	acc	acc	ctc	tgc	tgt	gtc	cca	acc	atc	ttt	cgg	ctg	ctt	1131
Phe	Pro	Ile	Thr	Thr	Leu	Cys	Cys	Val	Pro	Thr	Ile	Phe	Arg	Leu	Leu	
		315					320					325				
gtg	cag	gag	gat	ctg	acc	agg	tac	cag	ttt	cag	agc	ttg	agg	cac	tgt	1179
Val	Gln	Glu	Asp	Leu	Thr	Arg	Tyr	Gln	Phe	Gln	Ser	Leu	Arg	His	Cys	
	330					335					340					
ctg	acc	gga	gga	gag	gcc	ctc	aac	cct	gac	gtg	agg	gag	aag	tgg	aaa	1227
Leu	Thr	Gly	Gly	Glu	Ala	Leu	Asn	Pro	Asp	Val	Arg	Glu	Lys	Trp	Lys	
345					350					355					360	
cac	cag	act	ggt	gtg	gag	ctg	tac	gaa	ggc	tat	ggc	cag	tct	gaa	acg	1275
His	Gln	Thr	Gly	Val	Glu	Leu	Tyr	Glu	Gly	Tyr	Gly	Gln	Ser	Glu	Thr	
			365						370					375		
gtt	gtc	atc	tgt	gcc	aat	cca	aaa	ggc	atg	aaa	atc	aag	tct	gga	tcc	1323
Val	Val	Ile	Cys	Ala	Asn	Pro	Lys	Gly	Met	Lys	Ile	Lys	Ser	Gly	Ser	
			380					385					390			
atg	ggg	aag	gcg	tcc	cca	ccc	tac	gat	gtg	cag	att	gtg	gat	gat	gag	1371
Met	Gly	Lys	Ala	Ser	Pro	Pro	Tyr	Asp	Val	Gln	Ile	Val	Asp	Asp	Glu	
		395					400					405				
ggc	aac	gtc	ctg	cct	cct	gga	gaa	gag	ggg	aat	gtt	gcc	gtc	cgt	atc	1419
Gly	Asn	Val	Leu	Pro	Pro	Gly	Glu	Glu	Gly	Asn	Val	Ala	Val	Arg	Ile	
	410					415					420					
aga	ccc	act	cgg	ccc	ttc	tgt	ttc	ttc	aat	tgc	tat	ttg	gac	aat	cct	1467
Arg	Pro	Thr	Arg	Pro	Phe	Cys	Phe	Phe	Asn	Cys	Tyr	Leu	Asp	Asn	Pro	
425					430					435					440	
gag	aag	aca	gct	gca	tca	gaa	caa	ggg	gac	ttt	tac	atc	aca	ggg	gac	1515
Glu	Lys	Thr	Ala	Ala	Ser	Glu	Gln	Gly	Asp	Phe	Tyr	Ile	Thr	Gly	Asp	
				445					450					455		

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cga gct cgc atg gac aag gat ggc tac ttt tgg ttc atg gga aga aac      1563
Arg Ala Arg Met Asp Lys Asp Gly Tyr Phe Trp Phe Met Gly Arg Asn
          460                      465                      470

gac gat gtg atc aat tct tca agc tac cgg atc ggg cct gtt gaa gtg      1611
Asp Asp Val Ile Asn Ser Ser Ser Tyr Arg Ile Gly Pro Val Glu Val
          475                      480                      485

gaa agt gcc ctg gca gag cat cct gct gtc ctg gag tcg gct gtg gtc      1659
Glu Ser Ala Leu Ala Glu His Pro Ala Val Leu Glu Ser Ala Val Val
          490                      495                      500

agc agc cca gac ccc atc agg gga gag gtg gta aag gca ttt ata gtc      1707
Ser Ser Pro Asp Pro Ile Arg Gly Glu Val Val Lys Ala Phe Ile Val
          505                      510                      515                      520

ctt act cca gcc tac tcc tct cat gac cca gag gca cta acg cgg gaa      1755
Leu Thr Pro Ala Tyr Ser Ser His Asp Pro Glu Ala Leu Thr Arg Glu
          525                      530                      535

ctc cag gag cat gtg aaa agg gtg act gct cca tac aaa tac ccc agg      1803
Leu Gln Glu His Val Lys Arg Val Thr Ala Pro Tyr Lys Tyr Pro Arg
          540                      545                      550

aag gtg gcc ttt gtt tca gaa ctg cca aag acg gtt tct gga aag atc      1851
Lys Val Ala Phe Val Ser Glu Leu Pro Lys Thr Val Ser Gly Lys Ile
          555                      560                      565

caa agg agt aaa ttg cga agt cag gag tgg ggg aaa tga ggtgcacccc      1900
Gln Arg Ser Lys Leu Arg Ser Gln Glu Trp Gly Lys
          570                      575                      580

aggaaggccc cgtagacctc cgaagactcc acaagaaact aatggatcac tggtcagtcc      1960

ccatgggggag catcatctct tcgaccctaa agatgtcaaaa ggtgtgcagc ttccaaacgg      2020

catccccagg atcactgggc aatgctggaa agagcaaaag aatatcattg gccctgatca      2080

catagatgct gcgccgccta gcaaatgctt ggtggttcga cttctccctc tgtctggggg      2140

caggctcagc atctgccac tggtctcaact aagagctttc agatttcctt ccataggaca      2200

ggttaccata gacttggggc acttgtgggt actcattttc tgccagtggg aatgtaaagg      2260

cttcacctt tgtatgtaac catttgga aagtatgcag gaacataaaa taaaatatcc      2320

tttagctcag aaattctatc ttcgggagtc accacaaaag aaaaaaatca aaatgcagaa      2380

aatgtgtggt gcactaagat gatcacacag cattaaaact aaaaaaaaaa aa      2432

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<210> 8
 <211> 783
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (50) .. (379)

<400> 8

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cgccccccgc cgccgctgca caccggaccc agccgccgtg ccgcggggcc      atg gac      55
                               Met Asp
                               1

ctg ccc agg ggc ctg gtg gtg gcc tgg gcg ctc agc ctg tgg cca ggg      103
Leu Pro Arg Gly Leu Val Val Ala Trp Ala Leu Ser Leu Trp Pro Gly
                    5                      10                      15

ttc acg gac acc ttc aac atg gac acc agg aag ccc cgg gtc atc cct      151
Phe Thr Asp Thr Phe Asn Met Asp Thr Arg Lys Pro Arg Val Ile Pro
                20                      25                      30

ggc tcc agg acc gcc ttc ttt ggc tac aca gtg cag cag cac gac atc      199
Gly Ser Arg Thr Ala Phe Phe Gly Tyr Thr Val Gln Gln His Asp Ile
                35                      40                      45                      50

agt ggc aat aag tgg ctg gtc gtg ggc gcc cca ctg gaa acc aat ggc      247
Ser Gly Asn Lys Trp Leu Val Val Gly Ala Pro Leu Glu Thr Asn Gly
                    55                      60                      65

tac cag aag acg gga gac gtg tac aag tgt cca gtg atc cac ggg aac      295
Tyr Gln Lys Thr Gly Asp Val Tyr Lys Cys Pro Val Ile His Gly Asn
                    70                      75                      80

tgc acc aaa ctc aac ctg ggt aac gtg ggc tgg tgg tct ctt cac aat      343
Cys Thr Lys Leu Asn Leu Gly Asn Val Gly Trp Trp Ser Leu His Asn
                    85                      90                      95

gag gcc agc ggt tgt cta aca caa ggc agg ctc tga tgca cgcccatgtc      393
Glu Ala Ser Gly Cys Leu Thr Gln Gly Arg Leu
                100                      105

catggtcaca ctgactcctt cctgctactc catgagatga cccagctgat atcactgccc      453

ccactttaca catgaggaag ctgaggccag ggagaggagg caacttttcc acagtccacac      513

agcttgccag gggctcacca ggaatcaacc caggccctag ctgtcccaga ccattcctct      573

ttctgactca gccactgccc ttcaactcaa agttttctct cccaggagaa aaaaccaaac      633

caaagggggc ggccgtttta gaggatccag gtttacttcc cccggcatgc aacgcaataa      693

tcttttttat aggggcccc aaaattccat tcccgtgggc cggcggtttt tacaacctcc      753

ggggaagtgg gaaaacacct tgggggttcc      783

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<210> 9

<211> 1830

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (461) .. (931)

15

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ctggaaaagc tctcccatga gaagaacacg gtgctgggct ttcgggttca caggatgctg 1141
caggcggagt tcctgcagge cgccctggtc accatctacg actactacga gccttcccgg 1201
aggtgcagca ctttctacaa cctgcccaca gagcaatctt ccctgagaaa gatctgccac 1261
aaagacatct gcagatgtgc agagggacag tgcccatccc tgcagaagcc cagtggccaa 1321
ttgaggcagg aggagctcca gacaacagca tgtgaggcag gcgtggattt tgtgtacaag 1381
acaaagctgg aatctgtgga ggtctctgcc tccaaccctt acgtctatta caacacgcag 1441
ctcgaagaca tcattaagag tggtacggac cctgccacac ccctggccat gaagaaattc 1501
gtctcccatg ccacttgcca tgactccctg gggttgcaag aacaggaatc gtacctcatc 1561
atggggccaga cgtcagacct gtggagaatc aaatctgatt acagctatgt tctgggcaag 1621
gagacgttcc tcatcctttg gccagcagat ggagatgcca gcaagaaaga attgcggggac 1681
caactggagg aattttttga atatatgcgc acccacggct gccagtcctg agcctcttct 1741
gctttcaggg aggtgtcatc aggcagetct gggccactgg gtttaacccc aaataaagag 1801
cacaggatat gacacccaaa aaaaaaaaaa 1830

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```

<210> 10
<211> 885
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (242) .. (838)

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<400> 10
tttcgtgccg ggtgggttcct ctggagatta aatgtacttc acagaacctc agcgagcggg 60
ctccagttat attcctgtgt cttgtcggca cgcatttcac ttctaggact gggccgggggt 120
ctgcaggggt cagctgagcc catgagctcc cagagctaac ccctgaacac ccaggcggggc 180
aaagggctga tgtcggtagt ccccatcctg gaggggcagg ctctgcgcat ctgctcctgg 240
c      atg gcg ctg cgg cac ctc gcc ctc ctg gct ggc ctt ctc gtg gga 286
      Met Ala Leu Arg His Leu Ala Leu Leu Ala Gly Leu Leu Val Gly
        1             5             10             15

gtc gcc agc aag tcc atg gag aac acg gcc cag ctg ccc gag tgc tgt 334
Val Ala Ser Lys Ser Met Glu Asn Thr Ala Gln Leu Pro Glu Cys Cys
        20             25             30

gta gat gtg gtg ggc gtc aac gcc agc tgc cca ggc gca agt ctg tgt 382
Val Asp Val Val Gly Val Asn Ala Ser Cys Pro Gly Ala Ser Leu Cys
        35             40             45

```

ggt cca ggc tgt tac agg cgc tgg aac gcg gac ggg agc gcc agc tgc 430
 Gly Pro Gly Cys Tyr Arg Arg Trp Asn Ala Asp Gly Ser Ala Ser Cys
 50 55 60

gtc cgc tgt ggg aac gga acc ctc cca gcc tac aac ggc tcc gag tgt 478
 Val Arg Cys Gly Asn Gly Thr Leu Pro Ala Tyr Asn Gly Ser Glu Cys
 65 70 75

aga agc ttt gct ggc ccg ggt gcg cca ttc ccc atg aac aga agc tca 526
 Arg Ser Phe Ala Gly Pro Gly Ala Pro Phe Pro Met Asn Arg Ser Ser
 80 85 90 95

ggg acc ccc ggg cgg cca cat cct ggg gct ccg cgc gtg gcc gcc tcc 574
 Gly Thr Pro Gly Arg Pro His Pro Gly Ala Pro Arg Val Ala Ala Ser
 100 105 110

ctc ttc ctg ggc acg ttc ttc att agc tcc ggc ctc atc ctc tcc gta 622
 Leu Phe Leu Gly Thr Phe Phe Ile Ser Ser Gly Leu Ile Leu Ser Val
 115 120 125

gct ggg ttc ttc tac ctc aag cgc tcc agt aaa ctc ccc agg gcc tgc 670
 Ala Gly Phe Phe Tyr Leu Lys Arg Ser Ser Lys Leu Pro Arg Ala Cys
 130 135 140

tac aga aga aac aaa gct ccg gcc ctg cag cct ggc gaa gcc gct gca 718
 Tyr Arg Arg Asn Lys Ala Pro Ala Leu Gln Pro Gly Glu Ala Ala Ala
 145 150 155

atg atc ccc ccg cca cag tcc tca gta cgg aag ccg cgc tac gtc agg 766
 Met Ile Pro Pro Pro Gln Ser Ser Val Arg Lys Pro Arg Tyr Val Arg
 160 165 170 175

cgg gag cgg ccc ctg gac agg gcc acg gat ccc gct gcc ttc ccg ggg 814
 Arg Glu Arg Pro Leu Asp Arg Ala Thr Asp Pro Ala Ala Phe Pro Gly
 180 185 190

gag gcc cgt atc agc aat gtc tga cctggaggcc gagaccacgc cagcacttg 868
 Glu Ala Arg Ile Ser Asn Val
 195

gcggcaggga cccggag 885

<210> 11
 <211> 945
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (118)..(882)

<400> 11
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agaggatctg gcagacaaag agacaaggtg agaaggagac tttggaagtg acccacc 117
 atg ggg ctc agc atc ttt ttg ctc ctg tgt gtt ctt ggg ctc agc cag 165
 Met Gly Leu Ser Ile Phe Leu Leu Leu Cys Val Leu Gly Leu Ser Gln
 1 5 10 15

gca gcc aca ccg aag att ttc aat ggc act gag tgt ggg cgt aac tca	213
Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg Asn Ser	
20 25 30	
cag ccg tgg cag gtg ggg ctg ttt gag ggc acc agc ctg cgc tgc ggg	261
Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu Arg Cys Gly	
35 40 45	
ggc gtc ctt att gac cac agg tgg gtc ctc aca gcg gct cac tgc agc	309
Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala Ala His Cys Ser	
50 55 60	
ggc agc agg tac tgg gtg cgc ctg ggg gaa cac agc ctc agc cag ctc	357
Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His Ser Leu Ser Gln Leu	
65 70 75 80	
gac tgg acc gag cag atc cgg cac agc ggc ttc tct gtg acc cat ccc	405
Asp Trp Thr Glu Gln Ile Arg His Ser Gly Phe Ser Val Thr His Pro	
85 90 95	
ggc tac ctg gga gcc tcg acg agc cac gag cac gac ctc cgg ctg ctg	453
Gly Tyr Leu Gly Ala Ser Thr Ser His Glu His Asp Leu Arg Leu Leu	
100 105 110	
cgg ctg cgc ctg ccc gtc cgc gta acc agc agc gtt caa ccc ctg ccc	501
Arg Leu Arg Leu Pro Val Arg Val Thr Ser Ser Val Gln Pro Leu Pro	
115 120 125	
ctg ccc aat gac tgt gca acc gct ggc acc gag tgc cac gtc tca ggc	549
Leu Pro Asn Asp Cys Ala Thr Ala Gly Thr Glu Cys His Val Ser Gly	
130 135 140	
tgg ggc atc acc aac cac cca cgg aac cca ttc ccg gat ctg ctc cag	597
Trp Gly Ile Thr Asn His Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln	
145 150 155 160	
tgc ctc aac ctc tcc atc gtc tcc cat gcc acc tgc cat ggt gtg tat	645
Cys Leu Asn Leu Ser Ile Val Ser His Ala Thr Cys His Gly Val Tyr	
165 170 175	
ccc ggg aga atc acg agc aac atg gtg tgt gca ggc ggc gtc ccg ggg	693
Pro Gly Arg Ile Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly	
180 185 190	
cag gat gcc tgc cag ggt gat tct ggg ggc ccc ctg gtg tgt ggg gga	741
Gln Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly	
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Asn	Arg	Ile	Glu	Leu	Val	Arg	Ala	Ser	Trp	His	Glu	Leu	Ser	Ile	Ser	
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Val	Ser	Asp	Val	Ser	Leu	Ser	Asp	Glu	Gly	Gln	Tyr	Thr	Cys	Ser	Leu	
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Phe	Thr	Met	Pro	Val	Lys	Thr	Ser	Lys	Ala	Tyr	Leu	Thr	Val	Leu	Gly	
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Val	Pro	Glu	Lys	Pro	Gln	Ile	Ser	Gly	Phe	Ser	Ser	Pro	Val	Met	Glu	
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Ala	Asp	Ile	Arg	Trp	Phe	Lys	Asn	Asp	Lys	Glu	Ile	Lys	Asp	Val	Lys	
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Tyr	Leu	Lys	Glu	Glu	Asp	Ala	Asn	Arg	Lys	Thr	Phe	Thr	Val	Ser	Ser	
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Thr	Leu	Asp	Phe	Arg	Val	Asp	Arg	Ser	Asp	Asp	Gly	Val	Ala	Val	Ile	
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Cys	Arg	Val	Asp	His	Glu	Ser	Leu	Asn	Ala	Thr	Pro	Gln	Val	Ala	Met	
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Gln	Val	Leu	Glu	Ile	His	Tyr	Thr	Pro	Ser	Val	Lys	Ile	Ile	Pro	Ser	
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Glu	Leu	Pro	Asp	Pro	Asp	Arg	Met	Val	Val	Ser	Gly	Arg	Glu	Leu	Asn	
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Asp Pro Asn Ala Leu Ala Gly Gln Asn Gly Pro Asp His Ala Leu Ile			
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Gly Gly Ile Val Ala Val Val Val Phe Val Thr Leu Cys Ser Ile Phe			
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ctg ctt ggt cga tat ctg gca agg cat aaa gga acg tat tta aca aat			1758
Leu Leu Gly Arg Tyr Leu Ala Arg His Lys Gly Thr Tyr Leu Thr Asn			
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Glu Ala Lys Gly Ala Glu Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile			
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Asn Ala Glu Gly Ser Gln Val Asn Ala Glu Glu Lys Lys Glu Tyr Phe			
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Ile			
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Leu Leu Ala Trp Ser Ala Leu Leu Cys Met Ala Gly Gly Gln Gly Arg	
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Trp Asp Gly Ala Leu Glu Ala Ala Gly Pro Gly Arg Val Arg Arg Arg	
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Gly Ser Pro Gly Ile Leu Gln Gly Cys Val Val Pro Gly Met Leu Gly	
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Asp Pro Phe Gly Val Asp Trp Ala Val Leu Gly Pro Ala Glu Tyr Pro	
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Gly Gly Cys Pro His Gly Gln Gly Leu Thr Arg Pro Ile Ser Leu Ser	
85 90 95	
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Pro Lys Ala Glu Cys Val Arg Leu Pro Val Pro Cys Leu Leu Ser	
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Arg Leu Glu Asp Ile Pro Trp Gln Glu Pro Val Cys Arg Thr Arg Ala	
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Cys Gly Glu Gly Phe Cys Ser Gln Pro Asn Leu Cys Thr Cys Ala Asp	
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Val Ser Cys Met Asn Gly Gly Thr Cys Arg Gly Ala Ser Cys Leu Cys	
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Pro Cys Phe Gly Gln Val Gly Pro Glu Gly Cys Gln His Gln Leu Thr	
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Thr	Ile	Asp	Ile	Cys	Arg	His	Phe	Thr	Asn	Leu	Cys	Leu	Asn	Gly	Arg	
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Cys	Leu	Pro	Thr	Pro	Ser	Ser	Tyr	Arg	Cys	Glu	Cys	Asn	Val	Gly	Tyr	
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Thr	Gln	Asp	Val	Arg	Gly	Glu	Cys	Ile	Asp	Val	Asp	Glu	Cys	Thr	Ser	
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Ser	Pro	Cys	His	His	Gly	Asp	Cys	Val	Asn	Ile	Pro	Gly	Thr	Tyr	His	

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Cys	Arg	Cys	Tyr	Pro	Gly	Phe	Gln	Ala	Thr	Pro	Thr	Arg	Gln	Ala	Cys	
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Phe	Glu	Leu	Ser	Pro	Asp	Gly	Lys	Asn	Cys	Val	Ala	Ala	Ala	Pro	Gly	
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Ser	Ser	Asp	Trp	Ser	Arg	Trp	Glu	His	Ser	Pro	Ile	Trp	Ser	Pro	Leu	
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Leu	Pro	Glu	Met	Leu	Trp	Leu	Cys	Ser	Ser	Val	His	Thr	Pro	Thr	Leu	
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Pro	Gly	Arg	Pro	Glu	Pro	Leu	Gly	Arg	Ala	Val	Gly	Trp	Cys	Thr	Gly	
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Cys	Val	Asn	Gly	Val	Cys	Leu	Asn	Glu	Asp	Trp	Gln	Leu	Leu	Leu	Pro	
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cct gag gtt tgt gcc aat ggc gtg tgc gag aac ctt cgg ggc agc tac Pro Glu Val Cys Ala Asn Gly Val Cys Glu Asn Leu Arg Gly Ser Tyr 865 870 875 880	2640
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Cys Cys Ala Thr Leu Gly Ala Ala Trp Gly Ser Pro Cys Glu Arg Cys	
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Glu Ile Gly Ser Ile Leu Glu Ala Ser Gln Ala Pro Met Gly Lys	
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gcc ctc cat ggg gcg ggt ccc ccc ttg ggc tgg cat gag aaa atg act	3168
Ala Leu His Gly Ala Gly Pro Pro Leu Gly Trp His Glu Lys Met Thr	
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Pro Leu Phe Thr Leu Val Leu Pro Val Ala Asp Ser Thr Pro Glu Val	
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Thr Val Arg Asn Ser Arg Val Asp Glu Cys Leu Ser Ser Pro Cys Val	
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Pro Gly Ser Arg Leu Asp Pro Ser Gly Thr Phe Cys Leu Asp Ser Thr	
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Lys Gly Thr Cys Trp Leu Lys Ile Gln Glu Ser Arg Cys Glu Val Asn	
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Leu Gln Gly Ala Ser Leu Arg Ser Glu Cys Cys Ala Thr Leu Gly Ala	
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Ala Trp Gly Ser Pro Cys Glu Arg Cys Glu Ile Asp Pro Ala Cys Ala	
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cgg ggc ttt gcc cgg atg acg ggt gtc acc tgc aat gat gtg aac gag	3552
Arg Gly Phe Ala Arg Met Thr Gly Val Thr Cys Asn Asp Val Asn Glu	
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tgt gag tcc ttc ccg gga gtc tgt ccc aac ggg cgt tgc gtc aac act	3600
Cys Glu Ser Phe Pro Gly Val Cys Pro Asn Gly Arg Cys Val Asn Thr	
1185 1190 1195 1200	
gct ggg tct ttc cgc tgt gag tgt cca gag ggc ctg atg ctg gac gcc	3648
Ala Gly Ser Phe Arg Cys Glu Cys Pro Glu Gly Leu Met Leu Asp Ala	
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Ser Gly Arg Leu Cys Val Asp Val Arg Leu Glu Pro Cys Phe Leu Arg	
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Trp Asp Glu Asp Glu Cys Gly Val Thr Leu Pro Gly Lys Tyr Arg Met	
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Ala Cys Pro Asp Pro Glu Ser Leu Glu Phe Ala Ser Leu Cys Pro Arg	
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Gly Leu Gly Phe Ala Ser Arg Asp Phe Leu Ser Gly Arg Pro Phe Tyr	
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Lys Asp Val Asn Glu Cys Lys Val Phe Pro Gly Leu Cys Thr His Gly	
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acc tgc aga aac acg gtg ggc agc ttc cac tgc gcc tgt gcg ggg ggc	3984
Thr Cys Arg Asn Thr Val Gly Ser Phe His Cys Ala Cys Ala Gly Gly	
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Phe Ala Leu Asp Ala Gln Glu Arg Asn Cys Thr Asp Ile Asp Glu Cys	
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Arg Ile Ser Pro Asp Leu Cys Gly Gln Gly Thr Cys Val Asn Thr Pro	
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Gly Ser Phe Glu Cys Glu Cys Phe Pro Gly Tyr Glu Ser Gly Phe Met	
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Leu Cys Arg Gly Gly Thr Cys Thr Asn Thr Asp Gly Ser Tyr Lys Cys	
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Gln Cys Pro Pro Gly His Glu Leu Thr Ala Lys Gly Thr Ala Cys Glu	
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Asp Ile Asp Glu Cys Ser Leu Ser Asp Gly Leu Cys Pro His Gly Gln	
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tgt gtc aat gtc atc ggt gcc ttc cag tgc tcc tgc cat gcc ggc ttc	4368
Cys Val Asn Val Ile Gly Ala Phe Gln Cys Ser Cys His Ala Gly Phe	
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Gln Ser Thr Pro Asp Arg Gln Gly Cys Val Asp Ile Asn Glu Cys Arg	
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gtc cag aat ggt ggg tgt gac gtg cac tgt att aac act gag ggc agc	4464
Val Gln Asn Gly Gly Cys Asp Val His Cys Ile Asn Thr Glu Gly Ser	

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Tyr Arg Cys Ser Cys Gly Gln Gly Tyr Ser Leu Met Pro Asp Gly Arg			
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Ala Cys Ala Asp Val Asp Glu Cys Glu Glu Asn Pro Arg Val Cys Asp			
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Gln Gly His Cys Thr Asn Met Pro Gly Gly His Arg Cys Leu Cys Tyr			
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Asp Gly Phe Met Ala Thr Pro Asp Met Arg Thr Cys Val Asp Val Ala			
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Leu Leu Pro Pro Ala Leu Tyr Pro Gly Pro Gly His Leu Pro His Cys			
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Gly Thr Ser Asn Asn Cys Trp Leu Ser Leu Ala Ser Gly Ala Ile Trp		
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 Leu Ile Ala Val Thr Arg Val Ile Ser Gln Ile Ser Ala Asp Asn Tyr
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 Lys Ile His Gly Asp Pro Ser Ala Phe Lys Leu Thr Ala Lys Ala Val
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 Ala Val Leu Leu Pro Ile Leu Gly Thr Ser Trp Val Phe Gly Val Leu
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 Ala Val Asn Gly Cys Ala Val Val Phe Gln Tyr Met Phe Ala Thr Leu
 85 90 95 100

aac tcc ctg cag gga ctg ttc ata ttc ctc ttt cat tgt ctc ctg aat 390
 Asn Ser Leu Gln Gly Leu Phe Ile Phe Leu Phe His Cys Leu Leu Asn
 105 110 115

tca gag gtg aga gcc gcc ttc aag cac aaa acc aag gtc tgg tcg ctc 438
 Ser Glu Val Arg Ala Ala Phe Lys His Lys Thr Lys Val Trp Ser Leu
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acg agc agc tcc gcc cgc acc tcc aac gcg aag ccc ttc cac tcg gac 486
 Thr Ser Ser Ser Ala Arg Thr Ser Asn Ala Lys Pro Phe His Ser Asp
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 Trp Asp Lys Ser Ser His Ser Ala His Arg Val Asp Leu Ser Ala Val
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gcg	ctg	gag	ggc	gtg	ctg	ctg	gcc	gtg	ctg	ctg	gtg	ggg	ctg	cag	acc	103
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Ala	Thr	Gly	Arg	Leu	Leu	Ser	Gly	Gln	Pro	Val	Cys	Arg	Gly	Gly	Thr	
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Gln	Arg	Pro	Cys	Tyr	Lys	Val	Ile	Tyr	Phe	His	Asp	Thr	Ser	Arg	Arg	
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Leu	Asn	Phe	Glu	Glu	Ala	Lys	Glu	Ala	Cys	Arg	Arg	Asp	Gly	Gly	Gln	
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cta	gtc	agc	atc	gag	tct	gaa	gat	gaa	cag	aaa	ctg	ata	gaa	aag	ttc	295
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	70				75					80					85	
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Ile	Glu	Asn	Leu	Leu	Pro	Ser	Asp	Gly	Asp	Phe	Trp	Ile	Gly	Leu	Arg	
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Arg	Arg	Glu	Glu	Lys	Gln	Ser	Asn	Ser	Thr	Ala	Cys	Gln	Asp	Leu	Tyr	
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Ala	Trp	Thr	Asp	Gly	Ser	Ile	Ser	Gln	Phe	Arg	Asn	Trp	Tyr	Val	Asp	
		120					125					130				
gag	ccg	tcc	tgc	ggc	agc	gag	gtc	tgc	gtg	gtc	atg	tac	cat	cag	cca	487
Glu	Pro	Ser	Cys	Gly	Ser	Glu	Val	Cys	Val	Val	Met	Tyr	His	Gln	Pro	
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Ser	Ala	Pro	Ala	Gly	Ile	Gly	Gly	Pro	Tyr	Met	Phe	Gln	Trp	Asn	Asp	
	150				155					160					165	
gac	cgg	tgc	aac	atg	aag	aac	aat	ttc	att	tgc	aaa	tat	tct	gat	gag	583
Asp	Arg	Cys	Asn	Met	Lys	Asn	Asn	Phe	Ile	Cys	Lys	Tyr	Ser	Asp	Glu	
				170					175					180		

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Lys Pro Ala Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu	
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aca aca cct gta ctt cca gaa gaa aca cag gaa gaa gat gcc aaa aaa	679
Thr Thr Pro Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys	
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aca ttt aaa gaa agt aga gaa gct gcc ttg aat ctg gcc tac atc cta	727
Thr Phe Lys Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu	
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atc ccc agc att ccc ctt ctc ctc ctc ctt gtg gtc acc aca gtt gta	775
Ile Pro Ser Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val	
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Cys Trp Val Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro	
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Ser Thr Lys Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn	
265 270 275	
agc ccg gac cta gag gtc tac aat gtc ata aga aaa caa agc gaa gct	919
Ser Pro Asp Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala	
280 285 290	
gac tta gct gag acc cgg cca gac ctg aag aat att tca ttc cga gtg	967
Asp Leu Ala Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val	
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tgt tcg gga gaa gcc act ccc gat gac atg tct tgt gac tat gac aac	1015
Cys Ser Gly Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn	
310 315 320 325	
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Met Ala Val Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val	
330 335 340	
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Glu Ser Gly Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln	
345 350 355	
atg ggg agg agt aag gag tct gga tgg gtg gaa aat gaa ata tat ggt	1159
Met Gly Arg Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly	
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Tyr	
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 Leu Val Ser Leu Leu Gly Leu Leu Leu Leu Leu Ala Arg Ser Gly Thr
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cgg gcg ctg gtc tgc ctg ccc tgt gac gag tcc aag tgc gag gag ccc 144
 Arg Ala Leu Val Cys Leu Pro Cys Asp Glu Ser Lys Cys Glu Glu Pro
 35 40 45

agg aac tgc ccg ggg agc atc gtg cag ggc gtc tgc ggc tgc tgc tac 192
 Arg Asn Cys Pro Gly Ser Ile Val Gln Gly Val Cys Gly Cys Cys Tyr
 50 55 60

acg tgc gcc agc cag agg aac gag agc tgc ggc ggc acc ttc ggg att 240
 Thr Cys Ala Ser Gln Arg Asn Glu Ser Cys Gly Gly Thr Phe Gly Ile
 65 70 75 80

tac gga acc tgc gac cgg ggg ctg cgt tgt gtc atc cgc ccc ccg ctc 288
 Tyr Gly Thr Cys Asp Arg Gly Leu Arg Cys Val Ile Arg Pro Pro Leu
 85 90 95

aat ggc gac tcc ctc acc gag tac gaa gcg ggc gtt tgc gaa gat gag 336
 Asn Gly Asp Ser Leu Thr Glu Tyr Glu Ala Gly Val Cys Glu Asp Glu
 100 105 110

aac tgg act gat gac caa ctg ctt ggt ttt aaa cca tgc aat gaa aac 384
 Asn Trp Thr Asp Asp Gln Leu Leu Gly Phe Lys Pro Cys Asn Glu Asn
 115 120 125

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225 230 235 240	
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Ser Tyr Glu Thr Gln Val Arg Leu Thr Ala Asp Gly Cys Cys Pro Leu	
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Pro Pro Arg Cys Glu Cys Leu Ser Gly Leu Cys Gly Phe Pro Val Cys	
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Thr Ala Gln Cys Gly Glu Ile Asn Cys Glu Arg Tyr Tyr Val Pro Glu	
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His	Cys	Val	Ala	Thr	Val	Cys	Gly	Gln	Thr	Cys	Thr	Asn	Pro	Val	Lys	
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Val	Asp	Pro	Pro	Ala	Cys	Gly	Glu	Leu	Ser	Asn	Cys	Thr	Leu	Thr	Gly	
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Lys	Asp	Cys	Ile	Asn	Gly	Phe	Lys	Arg	Asp	His	Asn	Gly	Cys	Arg	Thr	
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Met Trp Leu Pro Pro Ala Leu Leu Leu Leu Ser Leu Ser Gly Cys Phe	
1 5 10 15	
tcc atc caa ggc cca gag tct gtg aga gcc cca gag cag ggg tcc ctg	216
Ser Ile Gln Gly Pro Glu Ser Val Arg Ala Pro Glu Gln Gly Ser Leu	
20 25 30	
acg gtt caa tgc cac tat aag caa gga tgg gag acc tac att aag tgg	264
Thr Val Gln Cys His Tyr Lys Gln Gly Trp Glu Thr Tyr Ile Lys Trp	
35 40 45	
tgg tgc cga ggg gtg cgc tgg gat aca tgc aag atc ctc att gaa acc	312

Trp	Cys	Arg	Gly	Val	Arg	Trp	Asp	Thr	Cys	Lys	Ile	Leu	Ile	Glu	Thr		
50						55					60						
aga	ggg	tcg	gag	caa	gga	gag	aag	agt	gac	cgt	gtg	tcc	atc	aag	gac	360	
Arg	Gly	Ser	Glu	Gln	Gly	Glu	Lys	Ser	Asp	Arg	Val	Ser	Ile	Lys	Asp		
65					70					75				80			
aat	cag	aaa	gac	cgc	acg	ttc	act	gtg	acc	atg	gag	ggg	ctc	agg	cga	408	
Asn	Gln	Lys	Asp	Arg	Thr	Phe	Thr	Val	Thr	Met	Glu	Gly	Leu	Arg	Arg		
			85					90					95				
gat	gac	gca	gat	gtt	tac	tgg	tgt	ggg	att	gaa	aga	aga	gga	cct	gac	456	
Asp	Asp	Ala	Asp	Val	Tyr	Trp	Cys	Gly	Ile	Glu	Arg	Arg	Gly	Pro	Asp		
			100					105					110				
ctt	ggg	act	caa	gtg	aaa	gtg	att	gtt	gac	cca	tag	ggag	cggcttcctc			506	
Leu	Gly	Thr	Gln	Val	Lys	Val	Ile	Val	Asp	Pro							
	115					120											
aacagcaagc	tcacctacca	acagcaatat	ggcagtggtg	atcggctccc	acaagaggaa											566	
ccactacatg	ctcctggtat	ttgtgaaggt	gccatctttg	ctcatcttgg	tcactgccat											626	
cctctggttg	aaggggtctc	agaggggtccc	tgaggagcca	ggggaacagc	ctatctacat											686	
gaacttctcc	gaacctctga	ctaa														710	

<210> 18
 <211> 688
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (108)..(470)

 <400> 18
 cggaattccc ggggtcgacga tttcgtggga ttttggtttc caggctgttt ctccatccaa 60
 ggcccagagt ccgtgagagc cccagagcag gggttcgtgc cggtgca atg agc tgt 116
 Met Ser Cys
 1
 atc ttg gga ttc tgt ttt cca ggc tgt ttc tcc atc caa ggc cca gag 164
 Ile Leu Gly Phe Cys Phe Pro Gly Cys Phe Ser Ile Gln Gly Pro Glu
 5 10 15
 tct gtg aga gcc cca gag cag ggg tcc ctg acg gtt caa tgc cac tat 212
 Ser Val Arg Ala Pro Glu Gln Gly Ser Leu Thr Val Gln Cys His Tyr
 20 25 30 35
 aag caa gga tgg gag acc tac att aag tgg tgg tgc cga ggg gtg cgc 260
 Lys Gln Gly Trp Glu Thr Tyr Ile Lys Trp Trp Cys Arg Gly Val Arg
 40 45 50
 tgg gat aca tgc aag atc ctc att gaa acc aga ggg tcg gag caa gga 308
 Trp Asp Thr Cys Lys Ile Leu Ile Glu Thr Arg Gly Ser Glu Gln Gly
 55 60 65

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gag aag agt gac cgt gtg tcc atc aag gac aat cag aaa gac cgc acg      356
Glu Lys Ser Asp Arg Val Ser Ile Lys Asp Asn Gln Lys Asp Arg Thr
      70                      75                      80

ttc act gtg acc atg gag ggg ctc agg cga gat gac gca gat gtt tac      404
Phe Thr Val Thr Met Glu Gly Leu Arg Arg Asp Asp Ala Asp Val Tyr
      85                      90                      95

tgg tgt ggg att gaa aga aga gga cct gac ctt ggg act caa gtg aaa      452
Trp Cys Gly Ile Glu Arg Arg Gly Pro Asp Leu Gly Thr Gln Val Lys
     100                      105                      110                      115

gtg att gtt gac cca tag ggagcg gcttctctcaa cagcaagctc acctaccaac      506
Val Ile Val Asp Pro
                      120

agcaatatgg cagtgttgat cggctccac aagaggaacc actacatgct cctgggtat    566
gtgaagggtgc ccatcttgct catcttggtc actgccatcc tctggttgaa ggggtctcag    626
agggtccctg aggagccagg ggaacagcct atctacatga acttctccga acctctgact    686
aa                                                                    688

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<210> 19
<211> 1700
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (232)..(1272)

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<220>
<221> misc_feature
<222> (1)...(1700)
<223> n = a,t,c or g

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<400> 19
tttcgtaaga ccacagaaac cctcctgtaa tggaacaagt tggctttggt actaattgca      60
acaaggcttt tgaaagcctt ctgtcatctt cctggggatc acctcttcag gtgtacagag      120
acagcatagg gaaaactagg tttnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      180
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnngg c atg gag      237
                               Met Glu
                               1

aga aaa ttt atg tcc ttg caa cca tcc atc tcc gta tca gaa atg gaa      285
Arg Lys Phe Met Ser Leu Gln Pro Ser Ile Ser Val Ser Glu Met Glu
      5                      10                      15

cca aat ggc acc ttc agc aat aac aac agc agg aac tgc aca att gaa      333
Pro Asn Gly Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys Thr Ile Glu
     20                      25                      30

```

aac ttc aag aga gaa ttt ttc cca att gta tat ctg ata ata ttt ttc	381
Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile Phe Phe	
35 40 45 50	
tgg gga gtc ttg gga aat ggg ttg tcc ata tat gtt ttc ctg cag cct	429
Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu Gln Pro	
55 60 65	
tat aag aag tcc aca tct gtg aac gtt ttc atg cta aat ctg gcc att	477
Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu Ala Ile	
70 75 80	
tca gat ctc ctg ttc ata agc acg ctt ccc ttc agg gct gac tat tat	525
Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp Tyr Tyr	
85 90 95	
ctt aga ggc tcc aat tgg ata ttt gga gac ctg gcc tgc agg att atg	573
Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg Ile Met	
100 105 110	
tct tat tcc ttg tat gtg aac atg tac agc agt att tat ttc ctg acc	621
Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe Leu Thr	
115 120 125 130	
gtg ctg agt gtt gtg cgt ttc ctg gca atg gtt cac ccc ttt cgg ctt	669
Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe Arg Leu	
135 140 145	
ctg cat gtc acc agc atc agg agt gcc tgg atc ctc tgt ggg atc ata	717
Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly Ile Ile	
150 155 160	
tgg atc ctt atc atg gct tcc tca ata atg ctc ctg gac agt ggc tct	765
Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser Gly Ser	
165 170 175	
gag cag aac ggc agt gtc aca tca tgc tta gag ctg aat ctc tat aaa	813
Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu Tyr Lys	
180 185 190	
att gct aag ctg cag acc atg aac tat att gcc ttg gtg gtg ggc tgc	861
Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val Gly Cys	
195 200 205 210	
ctg ctg cca ttt ttc aca ctc agc atc tgt tat ctg ctg atc att cgg	909
Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile Ile Arg	
215 220 225	
gtt ctg tta aaa gtg gag gtc cca gaa tcg ggg ctg cgg gtt tct cac	957
Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val Ser His	
230 235 240	
agg aag gca ctg acc acc atc atc atc acc ttg atc atc ttc ttc ttg	1005
Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe Phe Leu	
245 250 255	
tgt ttc ctg ccc tat cac aca ctg agg acc gtc cac ttg acg aca tgg	1053
Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr Thr Trp	
260 265 270	
aaa gtg ggt tta tgc aaa gac aga ctg cat aaa gct ttg gtt atc aca	1101

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<210> 20
<211> 1671
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (417) .. (1628)
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[illegible]

1	5	10	15	
tcg gtg gat ctg cag gga gac agc tcc tta cag gtg gag att tct gac Ser Val Asp Leu Gln Gly Asp Ser Ser Leu Gln Val Glu Ile Ser Asp	20	25	30	512
gca gtg agt gag cgg gac aag gtg aaa ttc act gtt caa aca aag agc Ala Val Ser Glu Arg Asp Lys Val Lys Phe Thr Val Gln Thr Lys Ser	35	40	45	560
tgc ctc cct cac ttc gcc cag acc gag ttc tca gtc gtg cgg cag cac Cys Leu Pro His Phe Ala Gln Thr Glu Phe Ser Val Val Arg Gln His	50	55	60	608
gag gag ttc atc tgg ctg cat gat gcc tac gtg gag aat gag gag tac Glu Glu Phe Ile Trp Leu His Asp Ala Tyr Val Glu Asn Glu Glu Tyr	65	70	75	656
gcc ggc ctc atc atc ccc cca gcc cct ccg agg cca gac ttt gag gct Ala Gly Leu Ile Ile Pro Pro Ala Pro Pro Arg Pro Asp Phe Glu Ala	85	90	95	704
tcg agg gaa aag cta cag aaa ttg ggc gag ggg gac agc tct gtc act Ser Arg Glu Lys Leu Gln Lys Leu Gly Glu Gly Asp Ser Ser Val Thr	100	105	110	752
cgg gaa gag ttt gcc aag atg aag cag gag ctg gaa gcg gag tac ctg Arg Glu Glu Phe Ala Lys Met Lys Gln Glu Leu Glu Ala Glu Tyr Leu	115	120	125	800
gcc atc ttt aag aag aca gtt gcg atg cac gaa gtc ttt ctg cag cgc Ala Ile Phe Lys Lys Thr Val Ala Met His Glu Val Phe Leu Gln Arg	130	135	140	848
ctg gcg gcc cac ccc acc ctg cgt cga gac cac aac ttc ttt gtg ttt Leu Ala Ala His Pro Thr Leu Arg Arg Asp His Asn Phe Phe Val Phe	145	150	155	896
ttg gaa tat gga cag gat ctg agt gtc cgg ggg aag aac agg aag gag Leu Glu Tyr Gly Gln Asp Leu Ser Val Arg Gly Lys Asn Arg Lys Glu	165	170	175	944
ctc ctc gga ggg ttt ctg agg aat att gtg aag tcc gcg gat gaa gcc Leu Leu Gly Gly Phe Leu Arg Asn Ile Val Lys Ser Ala Asp Glu Ala	180	185	190	992
ctc atc acg ggc atg tca ggg ctc aag gag gtg gat gac ttc ttt gag Leu Ile Thr Gly Met Ser Gly Leu Lys Glu Val Asp Asp Phe Phe Glu	195	200	205	1040
cat gag agg acc ttc ctg ttg gag tat cac acc cgt atc cga gat gcc His Glu Arg Thr Phe Leu Leu Glu Tyr His Thr Arg Ile Arg Asp Ala	210	215	220	1088
tgc ctg cgg gcc gac cgc gtc atg cgc gcc cac aag tgc ctg gca gac Cys Leu Arg Ala Asp Arg Val Met Arg Ala His Lys Cys Leu Ala Asp	225	230	235	1136
gat tat atc cct atc tca gct gcg ctg agc agt ctg gga aca cag gaa Asp Tyr Ile Pro Ile Ser Ala Ala Leu Ser Ser Leu Gly Thr Gln Glu	245	250	255	1184

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gtc aac cag cta agg acg agc ttc ctc aaa ttg gca gag ctc ttt gaa      1232
Val Asn Gln Leu Arg Thr Ser Phe Leu Lys Leu Ala Glu Leu Phe Glu
                260                265                270

cgg ctg agg aag ctg gag ggc cgg gtg gct tcc gat gag gac ctg aag      1280
Arg Leu Arg Lys Leu Glu Gly Arg Val Ala Ser Asp Glu Asp Leu Lys
                275                280                285

ctg tca gac atg ctg agg tac tac atg cgt gac tca cag gca gcc aag      1328
Leu Ser Asp Met Leu Arg Tyr Tyr Met Arg Asp Ser Gln Ala Ala Lys
                290                295                300

gac ctg ctg tac cgg cgg ctg cgg gca ctg gcc gac tac gag aat gcc      1376
Asp Leu Leu Tyr Arg Arg Leu Arg Ala Leu Ala Asp Tyr Glu Asn Ala
305                310                315                320

aac aag gcg ctg gac aag gcg cgc acc agg aac cgg gag gtg cgg ccc      1424
Asn Lys Ala Leu Asp Lys Ala Arg Thr Arg Asn Arg Glu Val Arg Pro
                325                330                335

gcc gag agc cac cag cag ctg tgc tgc caa cgc ttc gag cgc ctc tcc      1472
Ala Glu Ser His Gln Gln Leu Cys Cys Gln Arg Phe Glu Arg Leu Ser
                340                345                350

gac tcc gcc aag caa gag ctc atg gac ttc aag tcc cgc cgg gtc tcc      1520
Asp Ser Ala Lys Gln Glu Leu Met Asp Phe Lys Ser Arg Arg Val Ser
                355                360                365

tct ttt cga aag aat ctc att gag ctg gca gag ctg gag ctc aaa cac      1568
Ser Phe Arg Lys Asn Leu Ile Glu Leu Ala Glu Leu Glu Leu Lys His
370                375                380

gcc aag gcc agc acc ctg att ctc cgg aac acc ctt gtt gcc cta aag      1616
Ala Lys Ala Ser Thr Leu Ile Leu Arg Asn Thr Leu Val Ala Leu Lys
385                390                395                400

ggg gag cct tag agt agccagagct cagccagacc ctaatctggg atctccagtg      1671
Gly Glu Pro

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<210> 21
<211> 2753
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)..(2421)

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<400> 21
atg gcg gta cgc gcg ttg aag ctg ctg acc aca ctg ctg gct gtc gtg      48
Met Ala Val Arg Ala Leu Lys Leu Leu Thr Thr Leu Leu Ala Val Val
1                5                10                15

gcc gct gcc tcc caa gcc gag gtc gag tcc gag gca gga tgg ggc atg      96
Ala Ala Ala Ser Gln Ala Glu Val Glu Ser Glu Ala Gly Trp Gly Met

```

20	25	30	
gtg acg cct gat ctg ctc ttc gcc gag ggg acc gca gcc tac gcg cgc Val Thr Pro Asp Leu Leu Phe Ala Glu Gly Thr Ala Ala Tyr Ala Arg 35 40 45			144
ggg gac tgg ccc ggg gtg gtc ctg agc atg gaa cgg gcg ctg cgc tcc Gly Asp Trp Pro Gly Val Val Leu Ser Met Glu Arg Ala Leu Arg Ser 50 55 60			192
cgg gca gcc ctc cgc gcc ctt cgc ctg cgc tgc cgc acc cag tgt gcc Arg Ala Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Gln Cys Ala 65 70 75 80			240
gcc gac ttc ccg tgg gag ctg gac ccc gac tgg tcc ccc agc ccg gcc Ala Asp Phe Pro Trp Glu Leu Asp Pro Asp Trp Ser Pro Ser Pro Ala 85 90 95			288
cag gcc tcg ggc gcc gcc gcc ctg cgc gac ctg agc ttc ttc ggg ggc Gln Ala Ser Gly Ala Ala Ala Leu Arg Asp Leu Ser Phe Phe Gly Gly 100 105 110			336
ctt ctg cgt cgc gct gcc tgc ctg cgc cgc tgc ctc ggg ccg ccg gcc Leu Leu Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro Pro Ala 115 120 125			384
gcc cac tcg ctc agc gaa gag atg gag ctg gag ttc cgc aag cgg agc Ala His Ser Leu Ser Glu Glu Met Glu Leu Glu Phe Arg Lys Arg Ser 130 135 140			432
ccc tac aac tac ctg cag gtc gcc tac ttc aag gtg cag acc tgc ctg Pro Tyr Asn Tyr Leu Gln Val Ala Tyr Phe Lys Val Gln Thr Cys Leu 145 150 155 160			480
gaa cca ggc ggc cgg ggt cct tct ggg gag agg agt gtt gca ggg gac Glu Pro Gly Gly Arg Gly Pro Ser Gly Glu Arg Ser Val Ala Gly Asp 165 170 175			528
ctg agg agc ttg ggg gat cgg gga agt gtc cgc agg gag ggg aaa gtg Leu Arg Ser Leu Gly Asp Arg Gly Ser Val Arg Arg Glu Gly Lys Val 180 185 190			576
gcc tcc tgg ctg ggg agc tct cct cgg agc cgg gga gag ctg ctc cct Ala Ser Trp Leu Gly Ser Ser Pro Arg Ser Arg Gly Glu Leu Leu Pro 195 200 205			624
ggc agg aga cct tcc tcg ccc agt tcg cat ggg cag atg cta acc cca Gly Arg Arg Pro Ser Ser Pro Ser Ser His Gly Gln Met Leu Thr Pro 210 215 220			672
aag atc aac aag ttg gag aaa gct gtt gct gca gca cac acc ttc ttc Lys Ile Asn Lys Leu Glu Lys Ala Val Ala Ala Ala His Thr Phe Phe 225 230 235 240			720
gtg ggc aat cct gag cac atg gaa atg cag cag aac cta gac tat tac Val Gly Asn Pro Glu His Met Glu Met Gln Gln Asn Leu Asp Tyr Tyr 245 250 255			768
caa acc atg tct gga gtg aag gag gcc gac ttc aag gat ctt gag act Gln Thr Met Ser Gly Val Lys Glu Ala Asp Phe Lys Asp Leu Glu Thr 260 265 270			816

caa ccc cat atg caa gaa ttt cga ctg gga gtg cga ctc tac tca gag	864
Gln Pro His Met Gln Glu Phe Arg Leu Gly Val Arg Leu Tyr Ser Glu	
275 280 285	
gaa cag cca cag gaa gct gtg ccc cac cta gag gcg gcg ctg caa gaa	912
Glu Gln Pro Gln Glu Ala Val Pro His Leu Glu Ala Ala Leu Gln Glu	
290 295 300	
tac ttt gtg gcc tat gag gag tgc cgt gcc ctc tgc gaa ggg ccc tat	960
Tyr Phe Val Ala Tyr Glu Glu Cys Arg Ala Leu Cys Glu Gly Pro Tyr	
305 310 315 320	
gac tac gat ggc tac aac tac ctt gag tac aac gct gac ctc ttc cag	1008
Asp Tyr Asp Gly Tyr Asn Tyr Leu Glu Tyr Asn Ala Asp Leu Phe Gln	
325 330 335	
gcc atc aca gat cat tac atc cag gtc ctc aac tgt aag cag aac tgt	1056
Ala Ile Thr Asp His Tyr Ile Gln Val Leu Asn Cys Lys Gln Asn Cys	
340 345 350	
gtc acg gag ctt gct tcc cac cca agt cga gag aag ccc ttt gaa gac	1104
Val Thr Glu Leu Ala Ser His Pro Ser Arg Glu Lys Pro Phe Glu Asp	
355 360 365	
ttc ctc cca tcg cat tat aat tat ctg cag ttt gcc tac tat aac att	1152
Phe Leu Pro Ser His Tyr Asn Tyr Leu Gln Phe Ala Tyr Tyr Asn Ile	
370 375 380	
ggg aat tat aca cag gct gtt gaa tgt gcc aag acc tat ctt ctc ttc	1200
Gly Asn Tyr Thr Gln Ala Val Glu Cys Ala Lys Thr Tyr Leu Leu Phe	
385 390 395 400	
ttc ccc aat gac gag gtg atg aac caa aat ttg gcc tat tat gca gct	1248
Phe Pro Asn Asp Glu Val Met Asn Gln Asn Leu Ala Tyr Tyr Ala Ala	
405 410 415	
atg ctt gga gaa gaa cac acc aga tcc atc ggc ccc cgt gag agt gcc	1296
Met Leu Gly Glu Glu His Thr Arg Ser Ile Gly Pro Arg Glu Ser Ala	
420 425 430	
aag gag tac cga cag cga agc cta ctg gaa aaa gaa ctg ctt ttc ttc	1344
Lys Glu Tyr Arg Gln Arg Ser Leu Leu Glu Lys Glu Leu Phe Phe	
435 440 445	
gct tat gat gtt ttt gga att ccc ttt gtg gat ccg gat tca tgg act	1392
Ala Tyr Asp Val Phe Gly Ile Pro Phe Val Asp Pro Asp Ser Trp Thr	
450 455 460	
cca gaa gaa gtg att ccc aag aga ttg caa gag aaa cag aag tca gaa	1440
Pro Glu Glu Val Ile Pro Lys Arg Leu Gln Glu Lys Gln Lys Ser Glu	
465 470 475 480	
cgg gaa aca gcc gta cgc atc tcc cag gag att ggg aac ctt atg aag	1488
Arg Glu Thr Ala Val Arg Ile Ser Gln Glu Ile Gly Asn Leu Met Lys	
485 490 495	
gaa atc gag acc ctt gtg gaa gag aag acc aag gag tca ctg gat gtg	1536
Glu Ile Glu Thr Leu Val Glu Glu Lys Thr Lys Glu Ser Leu Asp Val	
500 505 510	

agc aga ctg acc cgg gaa ggt ggc ccc ctg ctg tat gaa ggc atc agt Ser Arg Leu Thr Arg Glu Gly Gly Pro Leu Leu Tyr Glu Gly Ile Ser 515 520 525	1584
ctc acc atg aac tcc aaa ctc ctg aat ggt tcc cag cgg gtg gtg atg Leu Thr Met Asn Ser Lys Leu Leu Asn Gly Ser Gln Arg Val Val Met 530 535 540	1632
gac ggc gta atc tct gac cac gag tgt cag gag ctg cag aga ctg acc Asp Gly Val Ile Ser Asp His Glu Cys Gln Glu Leu Gln Arg Leu Thr 545 550 555 560	1680
aat gtg gca gca acc tca gga gat ggc tac cgg ggt cag acc tcc cca Asn Val Ala Ala Thr Ser Gly Asp Gly Tyr Arg Gly Gln Thr Ser Pro 565 570 575	1728
cat act ccc aat gaa aag ttc tat ggt gtc act gtc ttc aaa gcc ctc His Thr Pro Asn Glu Lys Phe Tyr Gly Val Thr Val Phe Lys Ala Leu 580 585 590	1776
aag ctg ggg caa gaa ggc aaa gtt cct ctg cag agt gcc cac ctg tac Lys Leu Gly Gln Glu Gly Lys Val Pro Leu Gln Ser Ala His Leu Tyr 595 600 605	1824
tac aac gtg acg gag aag gtg cgg cgc atc atg gag tcc tac ttc cgc Tyr Asn Val Thr Glu Lys Val Arg Arg Ile Met Glu Ser Tyr Phe Arg 610 615 620	1872
ctg gat acg ccc ctc tac ttt tcc tac tct cat ctg gtg tgc cgc act Leu Asp Thr Pro Leu Tyr Phe Ser Tyr Ser His Leu Val Cys Arg Thr 625 630 635 640	1920
gcc atc gaa gag gtc cag gca gag agg aag gat gat agt cat cca gtc Ala Ile Glu Glu Val Gln Ala Glu Arg Lys Asp Asp Ser His Pro Val 645 650 655	1968
cac gtg gac aac tgc atc ctg aat gcc gag acc ctc gtg tgt gtc aaa His Val Asp Asn Cys Ile Leu Asn Ala Glu Thr Leu Val Cys Val Lys 660 665 670	2016
gag ccc cca gcc tac acc ttc cgc gac tac agc gcc atc ctt tac cta Glu Pro Pro Ala Tyr Thr Phe Arg Asp Tyr Ser Ala Ile Leu Tyr Leu 675 680 685	2064
aat ggg gac ttc gat ggc gga aac ttt tat ttc act gaa ctg gat gcc Asn Gly Asp Phe Asp Gly Gly Asn Phe Tyr Phe Thr Glu Leu Asp Ala 690 695 700	2112
aag acc gtg acg gca gag gtg cag cct cag tgt gga aga gcc gtg gga Lys Thr Val Thr Ala Glu Val Gln Pro Gln Cys Gly Arg Ala Val Gly 705 710 715 720	2160
ttc tct tca ggc act gaa aac cca cat gga gtg aag gct gtc acc agg Phe Ser Ser Gly Thr Glu Asn Pro His Gly Val Lys Ala Val Thr Arg 725 730 735	2208
ggg cag cgc tgt gcc atc gcc ctg tgg ttc acc ctg gac cct cga cac Gly Gln Arg Cys Ala Ile Ala Leu Trp Phe Thr Leu Asp Pro Arg His 740 745 750	2256
agc gag cgg gac agg gtg cag gca gat gac ctg gtg aag atg ctc ttc	2304

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Ser Glu Arg Asp Arg Val Gln Ala Asp Asp Leu Val Lys Met Leu Phe
      755                      760                      765

agc cca gaa gag atg gac ctc tcc cag gag cag ccc ctg gat gcc cag      2352
Ser Pro Glu Glu Met Asp Leu Ser Gln Glu Gln Pro Leu Asp Ala Gln
      770                      775                      780

cag ggc ccc ccc gaa cct gca caa gag tct ctc tca ggc agt gaa tcg      2400
Gln Gly Pro Pro Glu Pro Ala Gln Glu Ser Leu Ser Gly Ser Glu Ser
      785                      790                      795                      800

aag ccc aag gat gag cta tga ca gcgtccaggt cagacggatg ggtgactaga      2453
Lys Pro Lys Asp Glu Leu
                        805

cccatggaga ggaactcttc tgcactctga gctggccagc ccctcggggc tgcagagcag      2513

tgagcctaca tctgccactc agccgagggg accctgctca cagccttcta catggtgcta      2573

ctgctcttgg agtggacatg accagacacc gcacccctg gatctggctg agggctcagg      2633

acacaggccc agccaccccc aggggcctcc acaggccgct gcataacagc gatacagtac      2693

ttaagtgtct gtgtagacaa ccaaagaata aatgattcat ggtttttttt aaaaaaaaaa      2753

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<210> 22
 <211> 3000
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(2721)

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<400> 22
atg gcc ctg gag cag gcg ctg cag gcg gcg cgg cag ggc gag ctg gac      48
Met Ala Leu Glu Gln Ala Leu Gln Ala Ala Arg Gln Gly Glu Leu Asp
   1                      5                      10                      15

gtg ctg agg tcg ctg cac gcc gca ggc ctc ctg ggg ccc tcg ctg cgc      96
Val Leu Arg Ser Leu His Ala Ala Gly Leu Leu Gly Pro Ser Leu Arg
      20                      25                      30

gac ccg ctg gac gcg ctg ccc gtg cac cac gcg gcc cgc gct ggg aag      144
Asp Pro Leu Asp Ala Leu Pro Val His His Ala Ala Arg Ala Gly Lys
      35                      40                      45

ctg cac tgt ctg cgc ttc ctg gtg gag gaa gcc gcc ctc ccc gcc gcg      192
Leu His Cys Leu Arg Phe Leu Val Glu Glu Ala Ala Leu Pro Ala Ala
      50                      55                      60

gcc cgc gcc cgc aac ggc gcc aca ccg gcc cac gac gcc tcc gcc acc      240
Ala Arg Ala Arg Asn Gly Ala Thr Pro Ala His Asp Ala Ser Ala Thr
      65                      70                      75                      80

ggc cac ctc gcc tgc ctg cag tgg ctg ctg tcg cag ggc ggc tgc aga      288
Gly His Leu Ala Cys Leu Gln Trp Leu Leu Ser Gln Gly Gly Cys Arg
      85                      90                      95

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gtg cag gca ttc cct gag tcc ctg gga gtc agg gct gtg gcc ctg ggc	336
Val Gln Ala Phe Pro Glu Ser Leu Gly Val Arg Ala Val Ala Leu Gly	
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ctg gtg cca gtc tcc tgc cgt gac aac cag gac aaa gac aat tct ggt	384
Leu Val Pro Val Ser Cys Arg Asp Asn Gln Asp Lys Asp Asn Ser Gly	
115 120 125	
gcc aca gtc ttg cat ctg gct gcc cgc ttc ggc cac ccc gag gtg gtg	432
Ala Thr Val Leu His Leu Ala Ala Arg Phe Gly His Pro Glu Val Val	
130 135 140	
aac tgg ctc ttg cat cat ggc ggt ggg gac ccc acc gcg gcc aca gac	480
Asn Trp Leu Leu His His Gly Gly Gly Asp Pro Thr Ala Ala Thr Asp	
145 150 155 160	
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Met Gly Ala Leu Pro Ile His Tyr Ala Ala Ala Lys Gly Asp Phe Pro	
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tcc ctg agg ctt ctc gtc gag cac tac cct gag gga gtg aat gcc caa	576
Ser Leu Arg Leu Leu Val Glu His Tyr Pro Glu Gly Val Asn Ala Gln	
180 185 190	
acc aag aac ggt gcc acg ccc ctg tac ctg gcg tgc cag gag ggc cac	624
Thr Lys Asn Gly Ala Thr Pro Leu Tyr Leu Ala Cys Gln Glu Gly His	
195 200 205	
ctg gag gtg acc cag tac ctg gtg cag gaa tgc ggc gca gac ccg cac	672
Leu Glu Val Thr Gln Tyr Leu Val Gln Glu Cys Gly Ala Asp Pro His	
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Ala Arg Ala His Asp Gly Met Thr Pro Leu His Ala Ala Ala Gln Met	
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ggc cac agc cca gtc atc gtg tgg ttg gtg agc tgc acc gac gtg agc	768
Gly His Ser Pro Val Ile Val Trp Leu Val Ser Cys Thr Asp Val Ser	
245 250 255	
ctg tcc gag cag gac aaa gac ggc gcc acc gcc atg cac ttc gcg gcg	816
Leu Ser Glu Gln Asp Lys Asp Gly Ala Thr Ala Met His Phe Ala Ala	
260 265 270	
agc cgc ggc cac acc aag gtg ctc agc tgg ctg ctg ctg cac ggc ggc	864
Ser Arg Gly His Thr Lys Val Leu Ser Trp Leu Leu Leu His Gly Gly	
275 280 285	
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Glu Ile Ser Ala Asp Leu Trp Gly Gly Thr Pro Leu His Asp Ala Ala	
290 295 300	
gag aac ggg gag cta gag tgc tgc cag atc ctg gta gtg aac ggc gcg	960
Glu Asn Gly Glu Leu Glu Cys Cys Gln Ile Leu Val Val Asn Gly Ala	
305 310 315 320	
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Glu Leu Asp Val Arg Asp Arg Asp Gly Tyr Thr Ala Ala Asp Leu Ser	
325 330 335	

gac ttc aac ggc cac agc cac tgc acc cgc tac ctg cgc acg gtg gag	1056
Asp Phe Asn Gly His Ser His Cys Thr Arg Tyr Leu Arg Thr Val Glu	
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aac ctg cac agg ggg atg gtc ctg gct ctg ggg gct gca gaa cac agc	1104
Asn Leu His Arg Gly Met Val Leu Ala Leu Gly Ala Ala Glu His Ser	
355 360 365	
aag gcc cag agg cca gag gct gca ggg ggg cct gag gat gaa ctt ccc	1152
Lys Ala Gln Arg Pro Glu Ala Ala Gly Gly Pro Glu Asp Glu Leu Pro	
370 375 380	
ccc gcg aaa gag tct ctg gaa gag aat gaa tgg ccc agc agg ggt cag	1200
Pro Ala Lys Glu Ser Leu Glu Glu Asn Glu Trp Pro Ser Arg Gly Gln	
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ggc ttg gtg ccc tca gca ccc act gct gtt ggc cag agc gtg gag cac	1248
Gly Leu Val Pro Ser Ala Pro Thr Ala Val Gly Gln Ser Val Glu His	
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cgc gtg ctt tcc cgg gat cca tcc gca gag ctg gag gct aag cag ccg	1296
Arg Val Leu Ser Arg Asp Pro Ser Ala Glu Leu Glu Ala Lys Gln Pro	
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gat tca ggc atg tcc tca ccc aat acc acg gtg tcg gtc cag ccg ctg	1344
Asp Ser Gly Met Ser Ser Pro Asn Thr Thr Val Ser Val Gln Pro Leu	
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aac ttt gac ctc agc tcg cct acc agc acc ctc tcc aac tac gac tcc	1392
Asn Phe Asp Leu Ser Ser Pro Thr Ser Thr Leu Ser Asn Tyr Asp Ser	
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Cys Ser Ser Ser His Ser Ser Ile Lys Gly Gln His Pro Pro Cys Gly	
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Leu Ser Ser Ala Arg Ala Ala Asp Ile Gln Ser Tyr Met Asp Met Leu	
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Asn Pro Glu Leu Gly Leu Pro Arg Gly Thr Ile Gly Lys Pro Thr Pro	
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Pro Pro Pro Pro Pro Ser Phe Pro Pro Pro Pro Pro Pro Pro Gly Thr	
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Gln Leu Pro Pro Pro Pro Pro Gly Tyr Pro Ala Pro Lys Pro Pro Val	
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gga cca cag gca gct gac atc tac atg cag acc aag aac aaa ctc cgc	1680
Gly Pro Gln Ala Ala Asp Ile Tyr Met Gln Thr Lys Asn Lys Leu Arg	
545 550 555 560	
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His Val Glu Thr Glu Ala Leu Lys Lys Glu Leu Ser Ser Cys Asp Gly	
565 570 575	
cac gac ggg ctg cgg agg cag gac tcc agc cgc aag ccc cgc gcc ttc	1776

His	Asp	Gly	Leu	Arg	Arg	Gln	Asp	Ser	Ser	Arg	Lys	Pro	Arg	Ala	Phe	
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Ser	Lys	Gln	Pro	Ser	Thr	Gly	Asp	Tyr	Tyr	Arg	Gln	Leu	Gly	Arg	Cys	
		595					600					605				
ccc	ggc	gag	acg	ctg	gcc	gca	cgc	ccg	ggc	atg	gcg	cac	agc	gag	gag	1872
Pro	Gly	Glu	Thr	Leu	Ala	Ala	Arg	Pro	Gly	Met	Ala	His	Ser	Glu	Glu	
	610					615					620					
gcg	gcg	ctg	ctt	cct	ggg	aac	cat	gtt	cct	aac	ggc	tgc	gcc	gcg	gac	1920
Ala	Ala	Leu	Leu	Pro	Gly	Asn	His	Val	Pro	Asn	Gly	Cys	Ala	Ala	Asp	
	625				630					635					640	
ccc	aag	gcg	tcc	agg	gag	ctg	cca	ccg	ccg	ccc	cca	ccg	ccg	ccg	ccg	1968
Pro	Lys	Ala	Ser	Arg	Glu	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	
				645				650					655			
ccc	ctg	ccg	gag	gcc	gcg	agt	tcg	cca	ccg	ccg	gcc	ccg	cct	ctg	ccc	2016
Pro	Leu	Pro	Glu	Ala	Ala	Ser	Ser	Pro	Pro	Pro	Ala	Pro	Pro	Leu	Pro	
			660					665					670			
ctc	gag	agc	gct	ggc	cct	ggc	tgc	ggg	cag	cgc	cgc	tcc	tcc	tcg	tcc	2064
Leu	Glu	Ser	Ala	Gly	Pro	Gly	Cys	Gly	Gln	Arg	Arg	Ser	Ser	Ser	Ser	
		675					680					685				
acc	ggc	agc	acc	aag	tct	ttc	aac	atg	atg	tcc	ccg	acg	ggc	gac	aac	2112
Thr	Gly	Ser	Thr	Lys	Ser	Phe	Asn	Met	Met	Ser	Pro	Thr	Gly	Asp	Asn	
	690					695					700					
tcg	gag	cta	ctg	gct	gag	att	aag	gca	ggc	aag	agc	ctg	aag	ccg	acg	2160
Ser	Glu	Leu	Leu	Ala	Glu	Ile	Lys	Ala	Gly	Lys	Ser	Leu	Lys	Pro	Thr	
	705				710					715					720	
ccc	cag	agc	aag	ggg	ctg	acc	aca	gtg	ttc	tca	ggc	atc	ggg	cag	ccg	2208
Pro	Gln	Ser	Lys	Gly	Leu	Thr	Thr	Val	Phe	Ser	Gly	Ile	Gly	Gln	Pro	
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gcc	ttc	cag	ccc	gat	tcg	ccg	ctg	cct	tct	gtg	tca	cct	gca	ctg	tca	2256
Ala	Phe	Gln	Pro	Asp	Ser	Pro	Leu	Pro	Ser	Val	Ser	Pro	Ala	Leu	Ser	
			740					745					750			
cca	gtc	cgg	agc	ccc	aca	ccg	cca	gct	gcg	ggg	ttt	cag	ccg	ctg	ctc	2304
Pro	Val	Arg	Ser	Pro	Thr	Pro	Pro	Ala	Ala	Gly	Phe	Gln	Pro	Leu	Leu	
			755				760					765				
aat	gga	agc	ttg	gtt	ccc	gtg	ccg	ccc	act	act	cct	gcg	ccg	gga	gtg	2352
Asn	Gly	Ser	Leu	Val	Pro	Val	Pro	Pro	Thr	Thr	Pro	Ala	Pro	Gly	Val	
	770					775					780					
cag	ctg	gac	gtg	gag	gct	ctc	atc	ccc	acg	cac	gat	gag	cag	ggc	cgg	2400
Gln	Leu	Asp	Val	Glu	Ala	Leu	Ile	Pro	Thr	His	Asp	Glu	Gln	Gly	Arg	
	785				790					795					800	
ccc	atc	ccc	gag	tgg	aag	cgc	cag	gtg	atg	gtg	cgc	aag	atg	cag	ctg	2448
Pro	Ile	Pro	Glu	Trp	Lys	Arg	Gln	Val	Met	Val	Arg	Lys	Met	Gln	Leu	
				805					810					815		
aag	atg	cag	gag	gag	gag	gag	cag	agg	cgg	aag	gag	gag	gag	gag	gag	2496
Lys	Met	Gln	Glu	Glu	Glu	Glu	Gln	Arg	Arg	Lys	Glu	Glu	Glu	Glu	Glu	

820	825	830	
gcc cgg ctg gcc agc atg ccc gcc tgg agg cgg gac ctc ctg cgg aag			2544
Ala Arg Leu Ala Ser Met Pro Ala Trp Arg Arg Asp Leu Leu Arg Lys			
835	840	845	
aag ctg gaa gaa gag agg gag cag aag cgg aaa gag gag gag cga cag			2592
Lys Leu Glu Glu Glu Arg Glu Gln Lys Arg Lys Glu Glu Glu Arg Gln			
850	855	860	
aag cag gag gag ctg cgg cgg gag aag gaa cag tca gag aag ctg cgg			2640
Lys Gln Glu Glu Leu Arg Arg Glu Lys Glu Gln Ser Glu Lys Leu Arg			
865	870	875	880
acg ctg ggc tac gat gag agc aag ctg gcg ccc tgg cag cga cag gtc			2688
Thr Leu Gly Tyr Asp Glu Ser Lys Leu Ala Pro Trp Gln Arg Gln Val			
885	890	895	
atc ctg aag aag ggg gac atc gct aag tac tag aggccgca gactcctgtc			2739
Ile Leu Lys Lys Gly Asp Ile Ala Lys Tyr			
900	905		
cgccagcctcg cagctccgtg gggccctccg cccagcccc agccagccag gccctggtgg			2799
aaaggctggg agccgcacag ccctcccctc ctgcgctgga aaccctccct gacccccacc			2859
ctggcccccc gtatccccag cccttgga cactggagtg cacacgccgc cacggttgcc			2919
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gtg ctg agg tcg ctg cac gcc gca ggc ctc ctg ggg ccc tcg ctg cgc	96
Val Leu Arg Ser Leu His Ala Ala Gly Leu Leu Gly Pro Ser Leu Arg	
20 25 30	
gac ccg ctg gac gcg ctg ccc gtg cac cac gcg gcc cgc gct ggg aag	144
Asp Pro Leu Asp Ala Leu Pro Val His His Ala Ala Arg Ala Gly Lys	
35 40 45	
ctg cac tgt ctg cgc ttc ctg gtg gag gaa gcc gcc ctc ccc gcc gcg	192
Leu His Cys Leu Arg Phe Leu Val Glu Glu Ala Ala Leu Pro Ala Ala	
50 55 60	

gcc cgc gcc cgc aac ggc gcc aca ccg gcc cac gac gcc tcc gcc acc Ala Arg Ala Arg Asn Gly Ala Thr Pro Ala His Asp Ala Ser Ala Thr 65 70 75 80	240
ggc cac ctg gcc tgc ctg cag tgg ctg ctg tgc cag ggc ggc tgc aga Gly His Leu Ala Cys Leu Gln Trp Leu Ser Gln Gly Gly Cys Arg 85 90 95	288
gtg cag gca ttc cct gag tcc ctg gga gtc agg gct gtg gcc ctg ggc Val Gln Ala Phe Pro Glu Ser Leu Gly Val Arg Ala Val Ala Leu Gly 100 105 110	336
ctg gtg cca gtc tcc tgc cgt gac aac cag gac aaa gac aat tct ggt Leu Val Pro Val Ser Cys Arg Asp Asn Gln Asp Lys Asp Asn Ser Gly 115 120 125	384
gcc aca gtc ttg cat ctg gct gcc cgc ttc ggc cac ccc gag gtg gtg Ala Thr Val Leu His Leu Ala Ala Arg Phe Gly His Pro Glu Val Val 130 135 140	432
aac tgg ctg ttg cat cat ggc ggt ggg gac ccc acc gcg gcc aca gac Asn Trp Leu Leu His His Gly Gly Gly Asp Pro Thr Ala Ala Thr Asp 145 150 155 160	480
atg ggc gcc ctg cct atc cac tac gct gcc gcc aaa gga gac ttc ccc Met Gly Ala Leu Pro Ile His Tyr Ala Ala Ala Lys Gly Asp Phe Pro 165 170 175	528
tcc ctg agg ctt ctg gtc gag cac tac cct gag gga gtg aat gcc caa Ser Leu Arg Leu Leu Val Glu His Tyr Pro Glu Gly Val Asn Ala Gln 180 185 190	576
acc aag aac ggt gcc acg ccc ctg tac ctg gcg tgc cag gag ggc cac Thr Lys Asn Gly Ala Thr Pro Leu Tyr Leu Ala Cys Gln Glu Gly His 195 200 205	624
ctg gag gtg acc cag tac ctg gtg cag gaa tgc ggc gca gac ccg cac Leu Glu Val Thr Gln Tyr Leu Val Gln Glu Cys Gly Ala Asp Pro His 210 215 220	672
gcg cgc gcc cac gac ggc atg acc ccg ctg cac gcc gcg gcg cag atg Ala Arg Ala His Asp Gly Met Thr Pro Leu His Ala Ala Ala Gln Met 225 230 235 240	720
ggc cac agc cca gtc atc gtg tgg ttg gtg agc tgc acc gac gtg agc Gly His Ser Pro Val Ile Val Trp Leu Val Ser Cys Thr Asp Val Ser 245 250 255	768
ctg tcc gag cag gac aaa gac ggc gcc acc gcc atg cac ttc gcg gcg Leu Ser Glu Gln Asp Lys Asp Gly Ala Thr Ala Met His Phe Ala Ala 260 265 270	816
agc cgc ggc cac acc aag gtg ctg agc tgg ctg ctg ctg cac ggc ggc Ser Arg Gly His Thr Lys Val Leu Ser Trp Leu Leu Leu His Gly Gly 275 280 285	864
gag atc tgc gct gac ctg tgg ggc ggc acc ccg ctg cac gac gcc gcc Glu Ile Ser Ala Asp Leu Trp Gly Gly Thr Pro Leu His Asp Ala Ala 290 295 300	912
gag aac ggc gag cta gag tgc tgc cag atc ctg gta gtg aac ggc gcg	960

Glu	Asn	Gly	Glu	Leu	Glu	Cys	Cys	Gln	Ile	Leu	Val	Val	Asn	Gly	Ala		
305					310					315					320		
gag	ctg	gac	gtc	cgc	gac	cgc	gac	ggg	tac	acg	gcc	gcc	gac	ctg	tcg		1008
Glu	Leu	Asp	Val	Arg	Asp	Arg	Asp	Gly	Tyr	Thr	Ala	Ala	Asp	Leu	Ser		
				325					330					335			
gac	ttc	aac	ggc	cac	agc	cac	tgc	acc	cgc	tac	ctg	cgc	acg	gtg	gag		1056
Asp	Phe	Asn	Gly	His	Ser	His	Cys	Thr	Arg	Tyr	Leu	Arg	Thr	Val	Glu		
			340					345					350				
aac	ctg	agc	gtg	gag	cac	cgc	gtg	ctt	tcc	cgg	gat	cca	tcc	gca	gag		1104
Asn	Leu	Ser	Val	Glu	His	Arg	Val	Leu	Ser	Arg	Asp	Pro	Ser	Ala	Glu		
		355					360					365					
ctg	gag	gct	aag	cag	ccg	gat	tca	ggc	atg	tcc	tca	ccc	aat	acc	acg		1152
Leu	Glu	Ala	Lys	Gln	Pro	Asp	Ser	Gly	Met	Ser	Ser	Pro	Pro	Asn	Thr	Thr	
	370					375					380						
gtg	tcg	gtc	cag	ccg	ctg	aac	ttt	gac	ctc	agc	tcg	cct	acc	agc	acc		1200
Val	Ser	Val	Gln	Pro	Leu	Asn	Phe	Asp	Leu	Ser	Ser	Pro	Thr	Ser	Thr		
385					390					395					400		
ctc	tcc	aac	tac	gac	tcc	tgc	tcc	tcc	agc	cac	tcc	agc	atc	aag	ggc		1248
Leu	Ser	Asn	Tyr	Asp	Ser	Cys	Ser	Ser	Ser	His	Ser	Ser	Ile	Lys	Gly		
				405					410					415			
cag	cac	cct	cca	tgt	ggg	ctt	tcc	agc	gct	aga	gct	gca	gac	ata	cag		1296
Gln	His	Pro	Pro	Cys	Gly	Leu	Ser	Ser	Ala	Arg	Ala	Ala	Asp	Ile	Gln		
			420					425					430				
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Ser	Tyr	Met	Asp	Met	Leu	Asn	Pro	Glu	Leu	Gly	Leu	Pro	Arg	Gly	Thr		
		435					440					445					
att	ggg	aag	ccc	aca	ccc	cca	cca	ccc	cca	ccc	agc	ttc	ccc	ccg	cca		1392
Ile	Gly	Lys	Pro	Thr	Pro	Pro	Pro	Pro	Pro	Pro	Ser	Phe	Pro	Pro	Pro		
	450					455					460						
ccc	ccg	ccc	cca	ggc	acc	caa	ctg	ccc	cca	ccc	cca	cct	ggc	tac	cca		1440
Pro	Pro	Pro	Pro	Gly	Thr	Gln	Leu	Pro	Pro	Pro	Pro	Pro	Gly	Tyr	Pro		
465					470				475						480		
gct	ccc	aag	cct	cct	gta	gga	cca	cag	gca	gct	gac	atc	tac	atg	cag		1488
Ala	Pro	Lys	Pro	Pro	Val	Gly	Pro	Gln	Ala	Ala	Asp	Ile	Tyr	Met	Gln		
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Thr	Lys	Asn	Lys	Leu	Arg	His	Val	Glu	Thr	Glu	Ala	Leu	Lys	Lys	Glu		
			500					505					510				
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Leu	Ser	Ser	Cys	Asp	Gly	His	Asp	Gly	Leu	Arg	Arg	Gln	Asp	Ser	Ser		
		515					520					525					
cgc	aag	ccc	cgc	gcc	ttc	agc	aag	cag	ccc	agc	acg	ggg	gac	tac	tac		1632
Arg	Lys	Pro	Arg	Ala	Phe	Ser	Lys	Gln	Pro	Ser	Thr	Gly	Asp	Tyr	Tyr		
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cgg	cag	ctg	ggc	cgc	tgc	ccc	ggc	gag	acg	ctg	gcc	gca	cgc	ccg	ggc		1680
Arg	Gln	Leu	Gly	Arg	Cys	Pro	Gly	Glu	Thr	Leu	Ala	Ala	Arg	Pro	Gly		

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Met Ala His Ser Glu Glu Ala Ala Leu Leu Pro Gly Asn His Val Pro	565	570	575	
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Asn Gly Cys Ala Ala Asp Pro Lys Ala Ser Arg Glu Leu Pro Pro Pro	580	585	590	
ccc cca ccg ccg ccg ccg ccc ctg ccg gag gcc gcg agt tcg cca ccg				1824
Pro Pro Pro Pro Pro Pro Pro Leu Pro Glu Ala Ala Ser Ser Pro Pro	595	600	605	
ccg gcc ccg cct ctg ccc ctc gag agc gct ggc cct ggc tgc ggg cag				1872
Pro Ala Pro Pro Leu Pro Leu Glu Ser Ala Gly Pro Gly Cys Gly Gln	610	615	620	
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Arg Arg Ser Ser Ser Ser Thr Gly Ser Thr Lys Ser Phe Asn Met Met	625	630	635	640
tcc ccg acg ggc gac aac tcg gag cta ctg gct gag att aag gca ggc				1968
Ser Pro Thr Gly Asp Asn Ser Glu Leu Leu Ala Glu Ile Lys Ala Gly	645	650	655	
aag agc ctg aag ccg acg ccc cag agc aag ggc ctg acc aca gtg ttc				2016
Lys Ser Leu Lys Pro Thr Pro Gln Ser Lys Gly Leu Thr Thr Val Phe	660	665	670	
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Ser Gly Ile Gly Gln Pro Ala Phe Gln Pro Asp Ser Pro Leu Pro Ser	675	680	685	
gtg tca cct gca ctg tca cca gtc cgg agc ccc aca ccg cca gct gcg				2112
Val Ser Pro Ala Leu Ser Pro Val Arg Ser Pro Thr Pro Pro Ala Ala	690	695	700	
ggg ttt cag ccg ctg ctc aat gga agc ttg gtt ccc gtg ccg ccc act				2160
Gly Phe Gln Pro Leu Leu Asn Gly Ser Leu Val Pro Val Pro Pro Thr	705	710	715	720
act cct gcg ccg gga gtg cag ctg gac gtg gag gct ctc atc ccc acg				2208
Thr Pro Ala Pro Gly Val Gln Leu Asp Val Glu Ala Leu Ile Pro Thr	725	730	735	
cac gat gag cag ggc cgg ccc atc ccc gag tgg aag cgc cag gtg atg				2256
His Asp Glu Gln Gly Arg Pro Ile Pro Glu Trp Lys Arg Gln Val Met	740	745	750	
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Val Arg Lys Met Gln Leu Lys Met Gln Glu Glu Glu Glu Gln Arg Arg	755	760	765	
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Lys Glu Glu Glu Glu Glu Ala Arg Leu Ala Ser Met Pro Ala Trp Arg	770	775	780	
cgg gac ctc ctg cgg aag aag ctg gaa gaa gag agg gag cag aag cgg				2400
Arg Asp Leu Leu Arg Lys Lys Leu Glu Glu Glu Arg Glu Gln Lys Arg	785	790	795	800

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Lys Glu Glu Glu Arg Gln Lys Gln Glu Glu Leu Arg Arg Glu Lys Glu
                        805                        810                        815

cag tca gag aag ctg cgg acg ctg ggc tac gat gag agc aag ctg gcg      2496
Gln Ser Glu Lys Leu Arg Thr Leu Gly Tyr Asp Glu Ser Lys Leu Ala
                        820                        825                        830

ccc tgg cag cga cag gtc atc ctg aag aag ggg gac atc gct aag tac      2544
Pro Trp Gln Arg Gln Val Ile Leu Lys Lys Gly Asp Ile Ala Lys Tyr
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tgc ttc cct ctg cgc gcc gcg cgc ctc ttc acg cgt ttc gcc gag gcc      278
Cys Phe Pro Leu Arg Ala Ala Arg Leu Phe Thr Arg Phe Ala Glu Ala
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Gly Arg Ser Thr Leu Arg Leu Pro Ala His Asp Thr Pro Gly Ala Gly
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Ala Val Gln Leu Leu Leu Ser Asp Cys Pro Pro Asp Arg Leu Arg Arg
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Phe Leu Arg Thr Leu Arg Leu Lys Leu Ala Ala Ala Pro Gly Pro Gly
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Pro Ala Ser Ala Arg Ala Gln Leu Leu Gly Pro Arg Pro Arg Asp Phe
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Thr Arg Val Pro Asp Thr Thr Leu Val Lys Arg Pro Val Glu Pro Gln	
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Ala Gly Ala Glu Pro Ser Thr Glu Ala Pro Arg Trp Pro Leu Pro Val	
130 135 140	
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Lys Arg Leu Ser Leu Pro Ser Thr Lys Pro Gln Leu Ser Glu Glu Gln	
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Ala Ala Val Leu Arg Ala Ala Leu Lys Gly Gln Ser Ile Phe Phe Thr	
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Gly Ser Ala Gly Thr Gly Lys Ser Tyr Leu Leu Lys Arg Ile Leu Gly	
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Pro Pro Arg Phe Cys Phe Gln Ser Lys Ser Trp Lys Arg Gly Val Pro	
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Val Thr Leu Glu Leu Thr Lys Gly Gly Arg Gln Ala Asn Gln Thr Phe	
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Ile	Val	Ala	Thr	Arg	Leu	Cys	Thr	His	Gln	Asp	Asp	Val	Ala	Leu	Thr		
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Asn	Glu	Arg	Arg	Leu	Gln	Glu	Leu	Pro	Gly	Lys	Val	His	Arg	Phe	Glu		
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Asp	Glu	Ala	Ala	Ser	Asp	Gln	Glu	Asn	Met	Asp	Pro	Ile	Leu				

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Met Leu Arg Leu Gln Ala Pro Gly Pro Ala Gly Arg Pro Arg	
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Cys Phe Pro Leu Arg Ala Ala Arg Leu Phe Thr Arg Phe Ala Glu Ala	
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Ala Val Gln Leu Leu Leu Ser Asp Cys Pro Pro Asp Arg Leu Arg Arg	
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Val Thr Ile Ser Pro Val Gln Pro Glu Glu Arg Arg Leu Arg Ala Ala	
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Thr Arg Val Pro Asp Thr Thr Leu Val Lys Arg Pro Val Glu Pro Gln	
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Ala Gly Ala Glu Pro Ser Thr Glu Ala Pro Arg Trp Pro Leu Pro Val	
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Lys Arg Leu Ser Leu Pro Ser Thr Lys Pro Gln Leu Ser Glu Glu Gln	
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Gly Ser Ala Gly Thr Lys Ser Tyr Leu Leu Lys Arg Ile Leu Gly	
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Ala Cys His Ile Gly Gly Thr Thr Leu His Ala Phe Ala Gly Ile Gly	
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Ser Gly Gln Ala Pro Leu Ala Gln Cys Val Ala Leu Ala Gln Arg Pro	
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Arg Ala Val Arg Gln Gln Asn Lys Pro Phe Gly Gly Ile Gln Leu Ile	
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Ile Cys Gly Asp Phe Leu Gln Leu Pro Pro Val Thr Lys Gly Ser Gln	
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ccc cca cgg ttc tgc ttc cag tcc agc ccc aac agg tgt tca gat gag	1142

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Gly	Ile	Val	Ala	Thr	Arg	Leu	Cys	Thr	His	Gln	Asp	Asp	Val	Ala	Leu	
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Thr	Asn	Glu	Arg	Arg	Leu	Gln	Glu	Leu	Pro	Gly	Lys	Val	His	Arg	Phe	
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gag	gct	atg	gac	agc	aac	cct	gag	ctg	gcc	agt	acc	ctg	gat	gcc	cag	1334
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Leu	Val	Lys	Asn	Leu	Ser	Val	Ser	Arg	Gly	Leu	Val	Asn	Gly	Ala	Arg	
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Gly	Val	Val	Val	Gly	Phe	Glu	Ala	Glu	Gly	Arg	Gly	Leu	Pro	Gln	Val	
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Val	Gln	Ala	Thr	Gly	Gly	Gln	Leu	Leu	Ser	Arg	Gln	Gln	Leu	Pro	Leu	
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cag	ctg	gcc	tgg	gcg	atg	tcc	atc	cac	aag	agc	caa	ggc	cta	cgt	gtg	1622
Gln	Leu	Ala	Trp	Ala	Met	Ser	Ile	His	Lys	Ser	Gln	Gly	Leu	Arg	Val	
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ctg	gac	ttt	gac	ccc	atg	gcg	gtt	cgc	tgt	gac	ccc	cgt	gtg	ctg	cac	1670
Leu	Asp	Phe	Asp	Pro	Met	Ala	Val	Arg	Cys	Asp	Pro	Arg	Val	Leu	His	
		480				485					490					
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Phe	Tyr	Ala	Thr	Leu	Arg	Arg	Gly	Arg	Ser	Leu	Ser	Leu	Glu	Ser	Pro	
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gat	gat	gat	gag	gca	gcc	tca	gac	cag	gag	aac	atg	gac	cca	atc	ctc	1766
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Asn Tyr Phe Ala Ile Thr Ser Gly Ile Cys Thr Gly Pro Lys Ala Asp
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Ala Tyr Arg Ala Gln Ile Leu Arg Ile Gln Tyr Ala Trp Ala Asn Ser
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Glu Ile Ser Gln Val Cys Ala Thr Lys Leu Phe Lys Lys Tyr Ala Glu
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Lys Tyr Ser Ala Ile Ile Asp Ser Asp Asn Val Glu Ser Gly Leu Asn
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Asn Tyr Ala Glu Asn Ile Leu Thr Leu Ala Gly Ser Gln Gln Thr Asp
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agt gac aag tgg cag tct gga ttg tca ata aat aat gtt ttc aaa atg      336
Ser Asp Lys Trp Gln Ser Gly Leu Ser Ile Asn Asn Val Phe Lys Met
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agt agt gta cag aag atg atg caa gct ggc aaa aaa ttc aaa gac tct      384
Ser Ser Val Gln Lys Met Met Gln Ala Gly Lys Lys Phe Lys Asp Ser
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Leu Leu Glu Pro Ala Leu Ala Ser Val Val Ile His Lys Glu Ala Thr
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gac tca tta cct aac tca gct cat gat cga gac cgg acc caa gac ttc      528
Asp Ser Leu Pro Asn Ser Ala His Asp Arg Asp Arg Thr Gln Asp Phe
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ccg gag agc aat cgt ttg aaa ctc ctt cag aat gcc cag cca cct atg      576
Pro Glu Ser Asn Arg Leu Lys Leu Leu Gln Asn Ala Gln Pro Pro Met
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gtg act aac act gct agg act tgt cct aca ttc tca gca cct gta ggt      624

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Phe	Leu	Ser	Asn	Gln	Ser	Cys	Phe	Pro	Ala	Ala	Cys	Glu	Asn	Pro	Gln		
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Asn	Gly	Gly	Met	Gln	Cys	Lys	Pro	Tyr	Gly	Ala	Gly	Pro	Thr	Glu	Pro		
		355					360					365					
gca	cat	cca	gtt	gat	gag	cgt	ctg	aag	aac	ttg	gag	cca	aag	atg	att		1152
Ala	His	Pro	Val	Asp	Glu	Arg	Leu	Lys	Asn	Leu	Glu	Pro	Lys	Met	Ile		
	370					375					380						
gaa	ctt	att	atg	aat	gag	att	atg	gat	cat	gga	cct	cca	gta	aat	tgg		1200
Glu	Leu	Ile	Met	Asn	Glu	Ile	Met	Asp	His	Gly	Pro	Pro	Val	Asn	Trp		
	385				390					395					400		
gaa	gat	att	gca	gga	gta	gaa	ttt	gct	aaa	gcc	acc	ata	aag	gaa	ata		1248
Glu	Asp	Ile	Ala	Gly	Val	Glu	Phe	Ala	Lys	Ala	Thr	Ile	Lys	Glu	Ile		
				405					410					415			
gtt	gtg	tgg	ccc	atg	ttg	agg	cca	gac	atc	ttt	act	ggg	tta	agg	gga		1296
Val	Val	Trp	Pro	Met	Leu	Arg	Pro	Asp	Ile	Phe	Thr	Gly	Leu	Arg	Gly		
			420					425					430				
ccc	cct	aaa	gga	att	ttg	ctc	ttt	ggt	cct	cct	ggg	act	ggg	aaa	act		1344
Pro	Pro	Lys	Gly	Ile	Leu	Leu	Phe	Gly	Pro	Pro	Gly	Thr	Gly	Lys	Thr		

435	440	445	
cta att ggc aag tgc att gct agt cag tct ggg gca aca ttc ttt agc Leu Ile Gly Lys Cys Ile Ala Ser Gln Ser Gly Val Ala Thr Phe Phe Ser 450 455 460			1392
atc tct gct tca tcc tta act tct aaa tgg gta ggt gag ggg gag aaa Ile Ser Ala Ser Ser Leu Thr Ser Lys Trp Val Gly Glu Gly Glu Lys 465 470 475 480			1440
atg gtc cgt gca ttg ttt gct gtt gca agg tgt cag caa cca gct gtg Met Val Arg Ala Leu Phe Ala Val Ala Arg Cys Gln Gln Pro Ala Val 485 490 495			1488
ata ttt att gac gaa att gat tcc ttg tta tct caa cgg gga gat ggt Ile Phe Ile Asp Glu Ile Asp Ser Leu Leu Ser Gln Arg Gly Asp Gly 500 505 510			1536
gag cat gaa tct tct aga agg ata aaa aca gaa ttt tta gtt caa tta Glu His Glu Ser Ser Arg Arg Ile Lys Thr Glu Phe Leu Val Gln Leu 515 520 525			1584
gat gga gca aca aca tct tct gaa gat cgt atc cta gtg gtg gga gca Asp Gly Ala Thr Thr Ser Ser Glu Asp Arg Ile Leu Val Val Gly Ala 530 535 540			1632
aca aat cgg cca caa gaa att gat gag gct gcc cgg aga aga ttg gtg Thr Asn Arg Pro Gln Glu Ile Asp Glu Ala Ala Arg Arg Arg Leu Val 545 550 555 560			1680
aaa agg ctt tat att ccc ctc cca gaa gct tca gcc agg aaa cag ata Lys Arg Leu Tyr Ile Pro Leu Pro Glu Ala Ser Ala Arg Lys Gln Ile 565 570 575			1728
gta att aat cta atg tcc aaa gag cag tgt tgc ctc agt gaa gaa gaa Val Ile Asn Leu Met Ser Lys Glu Gln Cys Cys Leu Ser Glu Glu Glu 580 585 590			1776
att gaa cag att gta cag cag tct gat gcg ttt tca gga gca gac atg Ile Glu Gln Ile Val Gln Gln Ser Asp Ala Phe Ser Gly Ala Asp Met 595 600 605			1824
aca cag ctt tgc agg gag gct tct ctt ggt cct att cgc agt tta caa Thr Gln Leu Cys Arg Glu Ala Ser Leu Gly Pro Ile Arg Ser Leu Gln 610 615 620			1872
act gct gac att gct acc ata aca ccg gat caa gtt cga ccc ata gct Thr Ala Asp Ile Ala Thr Ile Thr Pro Asp Gln Val Arg Pro Ile Ala 625 630 635 640			1920
tac att gat ttt gaa aat gct ttt aga act gtg cga cct agt gtt tct Tyr Ile Asp Phe Glu Asn Ala Phe Arg Thr Val Arg Pro Ser Val Ser 645 650 655			1968
cca aaa gat tta gag ctt tat gaa aac tgg aac aaa act ttt ggt tgt Pro Lys Asp Leu Glu Leu Tyr Glu Asn Trp Asn Lys Thr Phe Gly Cys 660 665 670			2016
gga aag t Gly Lys			2023

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<210> 27
<211> 1486
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (187)..(1188)

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gaaagggtttt attccaaaag gagagggttg aagacatagc tcattctcctg ctgtgtatca      120
gccaaagaagg tgtgagggtgg tgttccttgg ggatccgctt gcatctactt ggggtggttt      180
tgaaac      atg aat ctt tgc ctc gtc ctg gct gcc ttt tgc ttg gga ata      228
              Met Asn Leu Ser Leu Val Leu Ala Ala Phe Cys Leu Gly Ile
                1             5             10

gcc tcc gct gtt cca aaa ttt gac caa aat ttg gat aca aag tgg tac      276
Ala Ser Ala Val Pro Lys Phe Asp Gln Asn Leu Asp Thr Lys Trp Tyr
   15             20             25             30

cag tgg aag gca aca cac aga aga tta tat ggc gcg aat gaa gaa gga      324
Gln Trp Lys Ala Thr His Arg Arg Leu Tyr Gly Ala Asn Glu Glu Gly
           35             40             45

tgg agg aga gca gtg tgg gaa aag aat atg aaa atg att gaa ctg cac      372
Trp Arg Arg Ala Val Trp Glu Lys Asn Met Lys Met Ile Glu Leu His
           50             55             60

aat ggg gaa tac agc caa ggg aaa cac agc ttc aca atg gcc atg aat      420
Asn Gly Glu Tyr Ser Gln Gly Lys His Ser Phe Thr Met Ala Met Asn
           65             70             75

gcc ttt gga gac atg acc aat gaa gaa ttc agg cag gtg atg aat ggt      468
Ala Phe Gly Asp Met Thr Asn Glu Glu Phe Arg Gln Val Met Asn Gly
           80             85             90

ttt caa tac cag aag cac agg aag ggg aaa cag ttc cag gaa cgc ctg      516
Phe Gln Tyr Gln Lys His Arg Lys Gly Lys Gln Phe Gln Glu Arg Leu
           95             100            105            110

ctt ctt gag atc ccc aca tct gtg gac tgg aga gag aaa ggc tac atg      564
Leu Leu Glu Ile Pro Thr Ser Val Asp Trp Arg Glu Lys Gly Tyr Met
           115            120            125

act cct gtg aag gat cag ggt cag tgt ggc tct tgt tgg gct ttt agt      612
Thr Pro Val Lys Asp Gln Gly Gln Cys Gly Ser Cys Trp Ala Phe Ser
           130            135            140

gca act ggt gct ctg gaa ggg cag atg ttc tgg aaa aca ggc aaa ctt      660
Ala Thr Gly Ala Leu Glu Gly Gln Met Phe Trp Lys Thr Gly Lys Leu
           145            150            155

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atc tca ctg aat gag cag aat ctg gta gac tgc tct ggg cct caa ggc      708
Ile Ser Leu Asn Glu Gln Asn Leu Val Asp Cys Ser Gly Pro Gln Gly
    160                               165                               170

aat gag ggc tgc aat ggt gac ttc atg gat aat ccc ttc cgg tat gtt      756
Asn Glu Gly Cys Asn Gly Asp Phe Met Asp Asn Pro Phe Arg Tyr Val
    175                               180                               185                               190

cag gag aac gga ggc ctg gac tct gag gaa tcc tat cca tat gag gca      804
Gln Glu Asn Gly Gly Leu Asp Ser Glu Glu Ser Tyr Pro Tyr Glu Ala
    195                               200                               205

aca gaa gaa tcc tgt aag tac aat ccc aag tat tct gtt gct aat gac      852
Thr Glu Glu Ser Cys Lys Tyr Asn Pro Lys Tyr Ser Val Ala Asn Asp
    210                               215                               220

acc ggc ttt gtg gac atc cct aag cag gag aag gcc ctg atg aag gca      900
Thr Gly Phe Val Asp Ile Pro Lys Gln Glu Lys Ala Leu Met Lys Ala
    225                               230                               235

gtt gca act gtg ggg ccc att tct gtt gct att gat gca ggt cat gag      948
Val Ala Thr Val Gly Pro Ile Ser Val Ala Ile Asp Ala Gly His Glu
    240                               245                               250

tcc ttc ctg ttc tat aaa gaa ggc att tat ttt gag cca gac tgt agc      996
Ser Phe Leu Phe Tyr Lys Glu Gly Ile Tyr Phe Glu Pro Asp Cys Ser
    255                               260                               265                               270

agt gaa gac atg gat cat ggt gtg ctg gtg gtt ggc tac gga ttt gaa     1044
Ser Glu Asp Met Asp His Gly Val Leu Val Val Gly Tyr Gly Phe Glu
    275                               280                               285

agc aca gaa tca gat aac aat aaa tat tgg ctg gtg aag aac agc tgg     1092
Ser Thr Glu Ser Asp Asn Asn Lys Tyr Trp Leu Val Lys Asn Ser Trp
    290                               295                               300

ggt gaa gaa tgg ggc atg ggt ggc tac gta aag atg gcc aaa gac cgg     1140
Gly Glu Glu Trp Gly Met Gly Gly Tyr Val Lys Met Ala Lys Asp Arg
    305                               310                               315

aga aac cat tgt gga att gcc tca gca gcc agc tac ccc act gtg tga     1188
Arg Asn His Cys Gly Ile Ala Ser Ala Ala Ser Tyr Pro Thr Val
    320                               325                               330

gctggtggac ggtgatgagg aaggacttga ctggggatgg cgcattgcatg ggaggaattc  1248

atcttcagtc taccagcccc cgctgtgtcg gatacacact cgaatcattg aagatccgag  1308

tgtgatttga attctgtgat attttcacac tggtaaattgt tacctctatt ttaattactg  1368

ctataaatag gtttatatta ttgattcact tactgacttt gcatttttcgt ttttaaaagg  1428

atgtataaat ttttacctgt ttaaataaaa ttttaatttca aatgtaaaaa aaaaaaaaa  1486

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<210> 28
<211> 3068
<212> DNA
<213> Homo sapiens

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<220>

<221> CDS

<222> (128) .. (2512)

<400> 28

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ttcgcgcacg cactctgggtg cttgcatata aataacccccg ggcccggccc cggccccccg      120
ccaagcc  atg ctg tgc ggc cgc tgg agg cgt tgc cgc cgc ccg ccc gag      169
          Met Leu Cys Gly Arg Trp Arg Arg Cys Arg Arg Pro Pro Glu
            1             5             10

gag ccc cca gtg gcc gcc cag gtc gca gcc caa gtc gcg gcg ccg gtc      217
Glu Pro Pro Val Ala Ala Gln Val Ala Ala Gln Val Ala Ala Pro Val
  15             20             25             30

gct ctc ccg tcc ccg ccg act ccc tcc gat ggc ggc acc aag agg ccc      265
Ala Leu Pro Ser Pro Pro Thr Pro Ser Asp Gly Gly Thr Lys Arg Pro
            35             40             45

ggg ctg cgg gcg ctg aag aag atg ggc ctg acg gag gac gag gac gtg      313
Gly Leu Arg Ala Leu Lys Lys Met Gly Leu Thr Glu Asp Glu Asp Val
            50             55             60

cgc gcc atg ctg cgg ggc tcc cgg ctc cgc aag atc cgc tcg cgc acg      361
Arg Ala Met Leu Arg Gly Ser Arg Leu Arg Lys Ile Arg Ser Arg Thr
            65             70             75

tgg cac aag gag cgg ctg tac cgg ctg cag gag gac ggc ctg agc gtg      409
Trp His Lys Glu Arg Leu Tyr Arg Leu Gln Glu Asp Gly Leu Ser Val
            80             85             90

tgg ttc cag cgg cgc atc ccg cgt gcg cca tcg cag cac atc ttc ttc      457
Trp Phe Gln Arg Arg Ile Pro Arg Ala Pro Ser Gln His Ile Phe Phe
            95             100             105             110

gtg cag cac atc gag gcg gtc cgc gag ggc cac cag tcc gag ggc ctg      505
Val Gln His Ile Glu Ala Val Arg Glu Gly His Gln Ser Glu Gly Leu
            115             120             125

cgg cgc ttc ggg ggt gcc ttc gcg cca gcg cgc tgc ctc acc atc gcc      553
Arg Arg Phe Gly Gly Ala Phe Ala Pro Ala Arg Cys Leu Thr Ile Ala
            130             135             140

ttc aag ggc cgc cgc aag aac ctg gac ctg gcg gcg ccc acg gct gag      601
Phe Lys Gly Arg Arg Lys Asn Leu Asp Leu Ala Ala Pro Thr Ala Glu
            145             150             155

gaa gcg cag cgc tgg gtg cgc ggt ctg acc aag ctc cgc gcg cgc ctg      649
Glu Ala Gln Arg Trp Val Arg Gly Leu Thr Lys Leu Arg Ala Arg Leu
            160             165             170

gac gcc atg agc cag cgc gag cgg cta gac cac tgg atc cac tcc tat      697
Asp Ala Met Ser Gln Arg Glu Arg Leu Asp His Trp Ile His Ser Tyr
            175             180             185             190

ctg cac cgg gct gac tcc aac cag gac agc aag atg agc ttc aag gag      745
Leu His Arg Ala Asp Ser Asn Gln Asp Ser Lys Met Ser Phe Lys Glu
            195             200             205

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atc aag agc ctg ctg aga atg gtc aac gtg gac atg aac gac atg tac	793
Ile Lys Ser Leu Leu Arg Met Val Asn Val Asp Met Asn Asp Met Tyr	
210 215 220	
gcc tac ctc ctc ttc aag gag tgt gac cac tcc aac aac gac cgt cta	841
Ala Tyr Leu Leu Phe Lys Glu Cys Asp His Ser Asn Asn Asp Arg Leu	
225 230 235	
gag ggg gct gag atc gag gag ttc ctg cgg cgg ctg ctg aag cgg ccg	889
Glu Gly Ala Glu Ile Glu Glu Phe Leu Arg Arg Leu Leu Lys Arg Pro	
240 245 250	
gag ctg gag gag atc ttc cat cag tac tcg ggc gag gac cgc gtg ctg	937
Glu Leu Glu Glu Ile Phe His Gln Tyr Ser Gly Glu Asp Arg Val Leu	
255 260 265 270	
agt gcc cct gag ctg ctg gag ttc ctg gag gac cag ggc gag gag ggc	985
Ser Ala Pro Glu Leu Leu Glu Phe Leu Glu Asp Gln Gly Glu Glu Gly	
275 280 285	
gcc aca ctg gcc cgc gcc cag cag ctc att cag acc tat gag ctc aac	1033
Ala Thr Leu Ala Arg Ala Gln Gln Leu Ile Gln Thr Tyr Glu Leu Asn	
290 295 300	
gag aca gcc aag cag cat gag ctg atg aca ctg gat ggc ttc atg atg	1081
Glu Thr Ala Lys Gln His Glu Leu Met Thr Leu Asp Gly Phe Met Met	
305 310 315	
tac ctg ttg tcg ccg gag ggg gct gcc ttg gac aac acc cac acg tgt	1129
Tyr Leu Leu Ser Pro Glu Gly Ala Ala Leu Asp Asn Thr His Thr Cys	
320 325 330	
gtg ttc cag gac atg aac cag ccc ctt gcc cac tac ttc atc tct tcc	1177
Val Phe Gln Asp Met Asn Gln Pro Leu Ala His Tyr Phe Ile Ser Ser	
335 340 345 350	
tcc cac aac acc tat ctg act gac tcc cag atc ggg ggg ccc agc agc	1225
Ser His Asn Thr Tyr Leu Thr Asp Ser Gln Ile Gly Gly Pro Ser Ser	
355 360 365	
acc gag gcc tat gtt agg tac tgt agc agg ggg gcc ttt gcc cag gga	1273
Thr Glu Ala Tyr Val Arg Tyr Cys Ser Arg Gly Ala Phe Ala Gln Gly	
370 375 380	
tgc cgc tgc gtg gag ctg gac tgc tgg gag ggg cca gga ggg gag ccc	1321
Cys Arg Cys Val Glu Leu Asp Cys Trp Glu Gly Pro Gly Gly Glu Pro	
385 390 395	
gtc atc tat cat ggc cat acc ctc acc tcc aag att ctc ttc cgg gac	1369
Val Ile Tyr His Gly His Thr Leu Thr Ser Lys Ile Leu Phe Arg Asp	
400 405 410	
gtg gtc caa gcc gtg cgc gac cat gcc ttc acg ctg tcc cct tac cct	1417
Val Val Gln Ala Val Arg Asp His Ala Phe Thr Leu Ser Pro Tyr Pro	
415 420 425 430	
gtc atc cta tcc ctg gag aac cac tgc ggg ctg gag cag cag gct gcc	1465
Val Ile Leu Ser Leu Glu Asn His Cys Gly Leu Glu Gln Gln Ala Ala	
435 440 445	

atg gcc cgc cac ctc tgc acc atc ctg ggg gac atg ctg gtg aca cag Met Ala Arg His Leu Cys Thr Ile Leu Gly Asp Met Leu Val Thr Gln 450 455 460	1513
gcg ctg gac tcc cca aat ccc gag gag ctg cca tcc cca gag cag ctg Ala Leu Asp Ser Pro Asn Pro Glu Glu Leu Pro Ser Pro Glu Gln Leu 465 470 475	1561
aag ggc cgg gtc ctg gtg aag gga aag aag ctg ccc gct gct cgg agc Lys Gly Arg Val Leu Val Lys Gly Lys Lys Leu Pro Ala Ala Arg Ser 480 485 490	1609
gag gat ggc cgg gct ctg tgc gat cgg gag gag gag gag gag gat gac Glu Asp Gly Arg Ala Leu Ser Asp Arg Glu Glu Glu Glu Glu Asp Asp 495 500 505 510	1657
gag gag gaa gaa gag gag gtg gag gct gca gcg cag agg cgg ctg gcc Glu Glu Glu Glu Glu Glu Val Glu Ala Ala Ala Gln Arg Arg Leu Ala 515 520 525	1705
aag cag atc tcc ccg gag ctg tgc gcc ctg gct gtg tac tgc cac gcc Lys Gln Ile Ser Pro Glu Leu Ser Ala Leu Ala Val Tyr Cys His Ala 530 535 540	1753
acc cgc ctg cgg acc ctg cac cct gcc ccc aac gcc cca caa ccc tgc Thr Arg Leu Arg Thr Leu His Pro Ala Pro Asn Ala Pro Gln Pro Cys 545 550 555	1801
cag gtc agc tcc ctc agc gag cgc aaa gcc aag aaa ctc att cgg gag Gln Val Ser Ser Leu Ser Glu Arg Lys Ala Lys Lys Leu Ile Arg Glu 560 565 570	1849
gca ggg aac agc ttt gtc agg cac aat gcc cgc cag ctg acc cgc gtg Ala Gly Asn Ser Phe Val Arg His Asn Ala Arg Gln Leu Thr Arg Val 575 580 585 590	1897
tac ccg ctg ggg ctg cgg atg aac tca gcc aac tac agt ccc cag gag Tyr Pro Leu Gly Leu Arg Met Asn Ser Ala Asn Tyr Ser Pro Gln Glu 595 600 605	1945
atg tgg aac tgc ggc tgt cag ctg gtg gcc ttg aac ttc cag acg cca Met Trp Asn Ser Gly Cys Gln Leu Val Ala Leu Asn Phe Gln Thr Pro 610 615 620	1993
ggc tac gag atg gac ctc aat gcc ggg cgc ttc cta gtc aat ggg cag Gly Tyr Glu Met Asp Leu Asn Ala Gly Arg Phe Leu Val Asn Gly Gln 625 630 635	2041
tgt ggc tac gtc cta aaa cct gcc tgc ctg cgg caa cct gac tgc acc Cys Gly Tyr Val Leu Lys Pro Ala Cys Leu Arg Gln Pro Asp Ser Thr 640 645 650	2089
ttt gac ccc gag tac cca gga cct ccc aga acc act ctc agc atc cag Phe Asp Pro Glu Tyr Pro Gly Pro Pro Arg Thr Thr Leu Ser Ile Gln 655 660 665 670	2137
gtg ctg act gca cag cag ctg ccc aag ctg aat gcc gag aag cca cac Val Leu Thr Ala Gln Gln Leu Pro Lys Leu Asn Ala Glu Lys Pro His 675 680 685	2185
tcc att gtg gac ccc ctg gtg cgc att gag atc cat ggg gtg ccc gca	2233

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Ser Ile Val Asp Pro Leu Val Arg Ile Glu Ile His Gly Val Pro Ala
      690                      695                      700

gac tgt gcc cgg cag gag act gac tac gtg ctc aac aat ggc ttc aac      2281
Asp Cys Ala Arg Gln Glu Thr Asp Tyr Val Leu Asn Asn Gly Phe Asn
      705                      710                      715

ccc cgc tgg ggg cag acc ctg cag ttc cag ctg cgg gct ccg gag ctg      2329
Pro Arg Trp Gly Gln Thr Leu Gln Phe Gln Leu Arg Ala Pro Glu Leu
      720                      725                      730

gca ctg gtc cgg ttt gtg gtg gaa gat tat gac gcc acc tcc ccc aat      2377
Ala Leu Val Arg Phe Val Val Glu Asp Tyr Asp Ala Thr Ser Pro Asn
      735                      740                      745

gac ttt gtg ggc cag ttt aca ctg cct ctt agc agc cta aag caa ggg      2425
Asp Phe Val Gly Gln Phe Thr Leu Pro Leu Ser Ser Leu Lys Gln Gly
      755                      760                      765

tac cgc cac ata cac ctg ctt tcc aag gac ggg gcc tca ctg tca cca      2473
Tyr Arg His Ile His Leu Leu Ser Lys Asp Gly Ala Ser Leu Ser Pro
      770                      775                      780

gcc acg ctc ttc atc caa atc cgc atc cag cgc tcc tga gggccacct      2522
Ala Thr Leu Phe Ile Gln Ile Arg Ile Gln Arg Ser
      785                      790

cactgcctt ggggttctgc gagtgccagt ccacatcccc tgcagagccc tctcctcctc      2582

tggagtcagg tgggtgggagt accagccccc cagcccaccc acttggccca ctcagcccat      2642

tcaccaggcg ctggtctcac ctgggtgctg agggctgcct gggcccctcc tgaagaacag      2702

aaaggtgttc atgtgacttc agtgagctcc aaccctgggg ccctgagatg gccccagctc      2762

ctcttgtcct cagcccaccc ctcatgtga cttatgagga gcaagcctgt tgctgccagg      2822

agacttgggg agcaggacac ttgtgggccc tcagttcccc tctgtcctcc cgtgggccat      2882

cccagcctcc ttccccaga ggagcgcagt cactccactt ggccccgacc ccgagcttag      2942

cccctaagcc ctcttttacc ccaggccttc ctggactcct ccctccagct ccggaacctg      3002

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tggcag      3068

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<210> 29
 <211> 1413
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (229) .. (1089)

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tttacagcaa tcatcacctt ttgcagagga ggtgagctca ccaggactca tctgccattt	180
cagacctttt gctgctacct gccagggtggc cccactgct gacgagag atg gtg gat	237
Met Val Asp	
1	
ctc tca gtc tcc ccg gac tcc ttg aag cca gta tgc ctg acc agc agt	285
Leu Ser Val Ser Pro Asp Ser Leu Lys Pro Val Ser Leu Thr Ser Ser	
5 10 15	
ctt gtc ttc ctc atg cac ctc ctc ctc ctt cag cct ggg gag ccg agc	333
Leu Val Phe Leu Met His Leu Leu Leu Leu Gln Pro Gly Glu Pro Ser	
20 25 30 35	
tca gag gtc aag gtg cta ggc cct gag tat ccc atc ctg gcc ctc gtc	381
Ser Glu Val Lys Val Leu Gly Pro Glu Tyr Pro Ile Leu Ala Leu Val	
40 45 50	
ggg gag gag gtg gag ttc ccg tgc cac cta tgg cca cag ctg gat gcc	429
Gly Glu Glu Val Glu Phe Pro Cys His Leu Trp Pro Gln Leu Asp Ala	
55 60 65	
cag caa atg gag atc cgc tgg ttc cgg agt cag acc ttc aat gtg gta	477
Gln Gln Met Glu Ile Arg Trp Phe Arg Ser Gln Thr Phe Asn Val Val	
70 75 80	
cac ctg tac cag gag cag cag gag ctc cct ggc agg cag atg ccg gcg	525
His Leu Tyr Gln Glu Gln Gln Glu Leu Pro Gly Arg Gln Met Pro Ala	
85 90 95	
ttc cgg aac agg acc aag ttg gtc aag gac gac atc gcc tat ggc agc	573
Phe Arg Asn Arg Thr Lys Leu Val Lys Asp Asp Ile Ala Tyr Gly Ser	
100 105 110 115	
gtg gtc ctg cag ctt cac agc atc atc ccc tct gac aag ggc aca tat	621
Val Val Leu Gln Leu His Ser Ile Ile Pro Ser Asp Lys Gly Thr Tyr	
120 125 130	
ggc tgc cgc ttc cac tcc gac aac ttc tct ggc gaa gct ctc tgg gaa	669
Gly Cys Arg Phe His Ser Asp Asn Phe Ser Gly Glu Ala Leu Trp Glu	
135 140 145	
ctg gag gta gca ggg ctg ggc tca gac cct cac ctc tcc ctt gag ggc	717
Leu Glu Val Ala Gly Leu Gly Ser Asp Pro His Leu Ser Leu Glu Gly	
150 155 160	
ttc aag gaa gga ggc att cag ctg agg ctc aga tcc agt ggc tgg tac	765
Phe Lys Glu Gly Gly Ile Gln Leu Arg Leu Arg Ser Ser Gly Trp Tyr	
165 170 175	
ccc aag cct aag gtt cag tgg aga gac cac cag gga cag tgc ctg cct	813
Pro Lys Pro Lys Val Gln Trp Arg Asp His Gln Gly Gln Cys Leu Pro	
180 185 190 195	
cca gag ttt gaa gcc atc gtc tgg gat gcc cag gac ctg ttc agt ctg	861
Pro Glu Phe Glu Ala Ile Val Trp Asp Ala Gln Asp Leu Phe Ser Leu	
200 205 210	

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gaa aca tct gtg gtt gtc cga gcg gga gcc ctc agc aat gtg tcc gtc      909
Glu Thr Ser Val Val Val Arg Ala Gly Ala Leu Ser Asn Val Ser Val
                215                      220                      225

tcc atc cag aat ctc ctc ttg agc cag aag aaa gag ttg gtg gtc cag      957
Ser Ile Gln Asn Leu Leu Leu Ser Gln Lys Lys Glu Leu Val Val Gln
                230                      235                      240

ata gca ggt cag tgg ctg tta gct cac acc cat ctt cct agt cct cat      1005
Ile Ala Gly Gln Trp Leu Leu Ala His Thr His Leu Pro Ser Pro His
                245                      250                      255

gtg tac ata cac att ggc cca aag gca gtc tat aaa gag aca atg gta      1053
Val Tyr Ile His Ile Gly Pro Lys Ala Val Tyr Lys Glu Thr Met Val
                260                      265                      270                      275

ctg cgc ctg tct gca tat agg gtg tgt tgg cct tga cacc tgaaaattca      1103
Leu Arg Leu Ser Ala Tyr Arg Val Cys Trp Pro
                280                      285

gcaccttggga tattaggaac acactaagaa cgctactgag aacccaaaca gtcagtgaga      1163

gaggccccag agagccccgcc tttctgtgcc taaggccata cactaaaacc catcaactct      1223

gctcatcaga ggcacatgag gagccaatag attcgtaatg ctgtctctca aacagtatgt      1283

attgagtttc cacaacgtga ccccgatccc taccctcagg tcccatgcc agtgggggat      1343

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gtcgacagca                                                                1413

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<210> 30
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<213> Homo sapiens

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<222> (254) .. (1909)

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acttgaaagg aaccagggga aaagtgtcca ggtgtgagca tgagcgggta gaggtgtgcc      180

cttgtttgct tcaggctgtc tgcttttcgc cctgactgt tttttctgtt tctggccatg      240

gaggaagaga aag      atg aca agc cca cag gct gac ttc tgc ctg ggc acc      289
                Met Thr Ser Pro Gln Ala Asp Phe Cys Leu Gly Thr
                  1                5                10

gcc ctg cac tct tgg gga ctg tgg ttc acg gag gaa ggt tca ccg tcc      337
Ala Leu His Ser Trp Gly Leu Trp Phe Thr Glu Glu Gly Ser Pro Ser
                15                20                25

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acc atg ctg acg ggg att gca gtt gga gcc ctc ctg gcc ctg gcc ttg Thr Met Leu Thr Gly Ile Ala Val Gly Ala Leu Leu Ala Leu Ala Leu 30 35 40	385
gtt ggt gtc ctc atc ctt ttc atg ttc aga agg ctt aga caa ttt cga Val Gly Val Leu Ile Leu Phe Met Phe Arg Arg Leu Arg Gln Phe Arg 45 50 55 60	433
caa gca cag ccc act cct cag tac cgg ttc cgg aag aga gac aaa gtg Gln Ala Gln Pro Thr Pro Gln Tyr Arg Phe Arg Lys Arg Asp Lys Val 65 70 75	481
atg ttt tac ggc cgg aag atc atg agg aag gtg acc aca ctc ccc aac Met Phe Tyr Gly Arg Lys Ile Met Arg Lys Val Thr Thr Leu Pro Asn 80 85 90	529
acc ctt gtg gag aac act gcc ctg ccc cgg cag cgg gcc agg aag agg Thr Leu Val Glu Asn Thr Ala Leu Pro Arg Gln Arg Ala Arg Lys Arg 95 100 105	577
acc aag gtg ctg tct ttg gcc aag agg att ctg cgt ttc aag aag gaa Thr Lys Val Leu Ser Leu Ala Lys Arg Ile Leu Arg Phe Lys Lys Glu 110 115 120	625
tac ccg gcc ctg cag ccc aag gag ccc ccg ccc tcc ctg ctg gag gcc Tyr Pro Ala Leu Gln Pro Lys Glu Pro Pro Pro Ser Leu Leu Glu Ala 125 130 135 140	673
gac ctc acg gag ttt gac gtg aag aat tct cac ctg cca tcg gaa gtt Asp Leu Thr Glu Phe Asp Val Lys Asn Ser His Leu Pro Ser Glu Val 145 150 155	721
ctg tac atg ctg aaa aac gtt cgg gtc ctg ggc cac ttt gag aag ccg Leu Tyr Met Leu Lys Asn Val Arg Val Leu Gly His Phe Glu Lys Pro 160 165 170	769
ctg ttc ctg gag ctt tgc aaa cac atc gtc ttt gtg cag ctg cag gaa Leu Phe Leu Glu Leu Cys Lys His Ile Val Phe Val Gln Leu Gln Glu 175 180 185	817
ggg gag cac gtc ttc cag ccc agg gag ccg gac ccc agc atc tgt gtg Gly Glu His Val Phe Gln Pro Arg Glu Pro Asp Pro Ser Ile Cys Val 190 195 200	865
gtg cag gac ggg cgg ctg gag gtc tgc atc cag gac act gac ggc acc Val Gln Asp Gly Arg Leu Glu Val Cys Ile Gln Asp Thr Asp Gly Thr 205 210 215 220	913
gag gtg gtg gtg aaa gag gtt ctg gcg gga gac agc gtc cac agc ctg Glu Val Val Val Lys Glu Val Leu Ala Gly Asp Ser Val His Ser Leu 225 230 235	961
ctc agc atc ctg gac atc atc acc ggc cat gct gca cct tac aaa acg Leu Ser Ile Leu Asp Ile Ile Thr Gly His Ala Ala Pro Tyr Lys Thr 240 245 250	1009
gtc tcc gtc cgc gcg gcc atc ccg tcc acc atc ctc cgg ctt cca gct Val Ser Val Arg Ala Ala Ile Pro Ser Thr Ile Leu Arg Leu Pro Ala 255 260 265	1057
gcg gct ttt cat gga gtt ttt gag aaa tat ccg gaa act ctg gtg agg	1105

Ala	Ala	Phe	His	Gly	Val	Phe	Glu	Lys	Tyr	Pro	Glu	Thr	Leu	Val	Arg	
270						275					280					
gtg	gtg	cag	atc	atc	atg	gtg	cgg	ctg	cag	agg	gtg	acc	ttt	ctg	gct	1153
Val	Val	Gln	Ile	Ile	Met	Val	Arg	Leu	Gln	Arg	Val	Thr	Phe	Leu	Ala	
285					290					295					300	
ctg	cac	aac	tac	ctc	ggc	ctg	acc	aca	gag	ctc	ttc	aac	gct	gag	agc	1201
Leu	His	Asn	Tyr	Leu	Gly	Leu	Thr	Thr	Glu	Leu	Phe	Asn	Ala	Glu	Ser	
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cag	gcc	atc	cct	ctc	gtg	tct	gta	gcc	agt	gtg	gct	gcc	ggg	aag	gcc	1249
Gln	Ala	Ile	Pro	Leu	Val	Ser	Val	Ala	Ser	Val	Ala	Ala	Gly	Lys	Ala	
			320					325					330			
aag	aag	cag	gtg	ttc	tat	ggc	gaa	gaa	gag	cgg	ctt	aaa	aag	cca	ccg	1297
Lys	Lys	Gln	Val	Phe	Tyr	Gly	Glu	Glu	Glu	Arg	Leu	Lys	Lys	Pro	Pro	
		335					340					345				
cgg	ctc	cag	gag	tcc	tgt	gac	tca	ggg	act	gtc	ctg	cac	caa	gga	ggg	1345
Arg	Leu	Gln	Glu	Ser	Cys	Asp	Ser	Gly	Thr	Val	Leu	His	Gln	Gly	Gly	
		350				355					360					
caa	tgt	cca	gcc	cca	gag	tcc	ggg	gga	tcc	tgc	tcc	cac	tgc	ctc	agg	1393
Gln	Cys	Pro	Ala	Pro	Glu	Ser	Gly	Gly	Ser	Cys	Ser	His	Cys	Leu	Arg	
365					370					375					380	
tca	ccc	cag	gtc	atc	ttg	cac	atg	cct	gag	gcc	acc	aca	cac	atc	ccc	1441
Ser	Pro	Gln	Val	Ile	Leu	His	Met	Pro	Glu	Ala	Thr	Thr	His	Ile	Pro	
				385					390					395		
ggg	tca	cct	cac	acg	gcc	cag	gtc	acc	cta	caa	gtc	cca	caa	gtc	acc	1489
Gly	Ser	Pro	His	Thr	Ala	Gln	Val	Thr	Leu	Gln	Val	Pro	Gln	Val	Thr	
			400					405				410				
tca	cat	gcc	ccc	cag	gtc	tac	tca	cac	gca	ccc	cag	gtc	ccc	tca	cgt	1537
Ser	His	Ala	Pro	Gln	Val	Tyr	Ser	His	Ala	Pro	Gln	Val	Pro	Ser	Arg	
		415					420				425					
gcc	tca	ggg	ccc	ctc	aca	cgt	gcc	cca	ggg	cac	ctc	aca	tgc	ccc	cca	1585
Ala	Ser	Gly	Pro	Leu	Thr	Arg	Ala	Pro	Gly	His	Leu	Thr	Cys	Pro	Pro	
	430					435					440					
ggg	ctc	atc	aga	tgg	ccc	ccc	agg	tct	cct	cac	gtg	tcc	cca	tct	cct	1633
Gly	Leu	Ile	Arg	Trp	Pro	Pro	Arg	Ser	Pro	His	Val	Ser	Pro	Ser	Pro	
445					450					455					460	
cac	atg	cgg	gct	gga	tgt	cct	cag	acc	tcc	cca	ggg	ctc	atc	agg	tgt	1681
His	Met	Arg	Ala	Gly	Cys	Pro	Gln	Thr	Ser	Pro	Gly	Leu	Ile	Arg	Cys	
				465					470					475		
gcc	cat	ctc	ctc	aca	tgt	ggg	ctg	gat	gtc	ctc	aaa	cct	cca	acg	gtc	1729
Ala	His	Leu	Leu	Thr	Cys	Gly	Leu	Asp	Val	Leu	Lys	Pro	Pro	Thr	Val	
			480					485					490			
tca	tta	cgt	gtg	ccc	gtc	tcc	tca	cat	gag	gcc	cgg	atg	tcc	tca	gac	1777
Ser	Leu	Arg	Val	Pro	Val	Ser	Ser	His	Glu	Ala	Arg	Met	Ser	Ser	Asp	
		495					500					505				
agg	ccc	agg	acc	ctt	cac	cct	cca	ttc	ttc	agt	tgt	tcc	cag	aat	tct	1825
Arg	Pro	Arg	Thr	Leu	His	Pro	Pro	Phe	Phe	Ser	Cys	Ser	Gln	Asn	Ser	

510	515	520	
cca ctg ggc cag gtg cct ggt ggg gag tgg gcc tcc cgc gat ggg ctc			1873
Pro Leu Gly Gln Val Pro Gly Gly Glu Trp Ala Ser Arg Asp Gly Leu			
525	530	535	540
tca ccc gct gtt ctg agt gct aac cgg ggg gcc tga atct gaggaggaag			1923
Ser Pro Ala Val Leu Ser Ala Asn Arg Gly Ala			
	545	550	
cggtcgggtg cggcgtgcac tgcattgagtc accccaacgac gatctgtgtg atggagttaa			1983
cagccaccct acagatgagg tgcgcgcttg gttatttata gcccatcatg ttcccaaaag			2043
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 <213> Homo sapiens

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 <222> (531)..(1517)

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ggcaggggaa tcgctgaaat gacctagaag ggcctcttaa actttctggt tggaccgagc	180
agaggaggga gagagagggtg tgtctcttgt gaggtgggtg aacgtctttt tattccctcc	240
caatccacca acttccgccc aagccaggat ctgtcacaac tcgagagggtg gaaattccgg	300
tttccctggc ctagagctcc cagtgtctggc tttggcatga tgggcacctg gagggccgca	360
ctcccgttcc agccaggctg agccttctgt cccctgcctc tggggcctgg gaacccccct	420
tcttctttct cctgaatggc acccccgcgc tagaatccag acaccgagtt tcccactgtg	480
gctgggttcaa gggatatgtga gagctccctg gtgacagtct gtggctgagc atg gcc	536
	Met Ala
	1
ctc cca gcc ctg ggc ctg gac ccc tgg agc ctc ctg ggc ctt ttc ctc	584
Leu Pro Ala Leu Gly Leu Asp Pro Trp Ser Leu Leu Gly Leu Phe Leu	
5 10 15	
ttc caa ctg ctt cag ctg ctg ctg ccg acg acg acc gcg ggg gga ggc	632
Phe Gln Leu Leu Gln Leu Leu Leu Pro Thr Thr Thr Ala Gly Gly Gly	
20 25 30	
ggg cag ggg ccc atg ccc agg gtc aga tac tat gca ggg gat gaa cgt	680
Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr Ala Gly Asp Glu Arg	
35 40 45 50	

agg gca ctt agc ttc ttc cac cag aag ggc ctc cag gat ttt gac act	728
Arg Ala Leu Ser Phe Phe His Gln Lys Gly Leu Gln Asp Phe Asp Thr	
55 60 65	
ctg ctc ctg agt ggt gat gga aat act ctc tac gtg ggg gct cga gaa	776
Leu Leu Leu Ser Gly Asp Gly Asn Thr Leu Tyr Val Gly Ala Arg Glu	
70 75 80	
gcc att ctg gcc ttg gat atc cag gat cca ggg gtc ccc agg cta aag	824
Ala Ile Leu Ala Leu Asp Ile Gln Asp Pro Gly Val Pro Arg Leu Lys	
85 90 95	
aac atg ata ccg tgg cca gcc agt gac aga aaa aag agt gaa tgt gcc	872
Asn Met Ile Pro Trp Pro Ala Ser Asp Arg Lys Lys Ser Glu Cys Ala	
100 105 110	
ttt aag aag aag agc aat gag aca cag tgt ttc aac ttc atc cgt gtc	920
Phe Lys Lys Lys Ser Asn Glu Thr Gln Cys Phe Asn Phe Ile Arg Val	
115 120 125 130	
ctg gtt tct tac aat gtc acc cat ctc tac acc tgc ggc acc ttc gcc	968
Leu Val Ser Tyr Asn Val Thr His Leu Tyr Thr Cys Gly Thr Phe Ala	
135 140 145	
ttc agc cct gct tgt acc ttc att gaa ctt caa gat tcc tac ctg ttg	1016
Phe Ser Pro Ala Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr Leu Leu	
150 155 160	
ccc atc tcg gag gac aag gtc atg gag gga aaa ggc caa agc ccc ttt	1064
Pro Ile Ser Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser Pro Phe	
165 170 175	
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Asp Pro Ala His Lys His Thr Ala Val Leu Val Asp Gly Met Leu Tyr	
180 185 190	
tct ggt act atg aac aac ttc ctg ggc agt gag ccc atc ctg atg cgc	1160
Ser Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu Met Arg	
195 200 205 210	
aca ctg gga tcc cag cct gtc ctc aag acc gac aac ttc ctc cgc tgg	1208
Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu Arg Trp	
215 220 225	
ctg cat cat gac gcc tcc ttt gtg gca gcc atc cct tcg acc cag gtc	1256
Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr Gln Val	
230 235 240	
gtc tac ttc ttc ttc gag gag aca gcc agc gag ttt gac ttc ttt gag	1304
Val Tyr Phe Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp Phe Phe Glu	
245 250 255	
agg ctc cac aca tcg cgg gtg gct aga gtc tgc aag aat gac gtg ggc	1352
Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys Asn Asp Val Gly	
260 265 270	
ggc gaa aag ctg ctg cag aag aag tgg acc acc ttc ctg aag gcc cag	1400
Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr Phe Leu Lys Ala Gln	
275 280 285 290	
ctg ctc tgc acc cag ccg ggg cag ctg ccc ttc aac gtc atc cgc cac	1448

Leu Leu Cys Thr Gln Pro Gly Gln Leu Pro Phe Asn Val Ile Arg His
 295 300 305
 gcg gtc ctg ctc ccc gcc gat tct ccc aca gct ccc cac atc tac gca 1496
 Ala Val Leu Leu Pro Ala Asp Ser Pro Thr Ala Pro His Ile Tyr Ala
 310 315 320
 gtc ttc acc tcc cag tgg tga gc agcagggctg gaccatgggg gctggacacg 1549
 Val Phe Thr Ser Gln Trp
 325
 ggacttgacg ccagtggaggc cccagctcgt gagcggaggc aggaattgac atgagccagc 1609
 acctactcag cactttcaca taggaaggca ttaaactcgt cccccctctc aggaaaaaaa 1669
 aaaaaa 1674

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 <212> DNA
 <213> Homo sapiens

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 <222> (487) .. (648)

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 ccttcttccc ctcacatgtg gggactttta attccatgta tattaggctg catgaagctt 180
 cccacaacc tactgatgct cttttcatta gaaacatttc ttactctgcg tttcattttg 240
 gatagtttct attcctatgt tttcaaacc accaataaaa gattctgcaa catctgacct 300
 gccattaatc ccgtccagtg tatttttcat ctctgtatt gtagttttca tctctacaat 360
 ccagcttgag cctttgggta tatcttccat gttgctcctg cactgtttga acatgcagaa 420
 tggctagtgg ggcagtgagc tgaggagaag ggacagaggg gaagctcggc tgttgggtct 480
 acgggt atg atg gag acc atg cag ctg aaa gta aac cgt cac ccc ttc 528
 Met Met Glu Thr Met Gln Leu Lys Val Asn Arg His Pro Phe
 1 5 10
 tgc ttc agt gtg aaa ggc cag gtg aag atg ctg cag ctg atg agg ctg 576
 Cys Phe Ser Val Lys Gly Gln Val Lys Met Leu Gln Leu Met Arg Leu
 15 20 25 30
 ggc ctt agg gtg cgg ggg gtg gtg gaa tct gct tgt ggg cgg gag atg 624
 Gly Leu Arg Val Arg Gly Val Val Glu Ser Ala Cys Gly Arg Glu Met
 35 40 45
 tgg cta tgt ggc tat aaa gga tga agatgaacgc cctgtttgct tttcagcctc 678
 Trp Leu Cys Gly Tyr Lys Gly
 50


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ctc atg gtc ctg gtg gcc ttt gcc att ggc ttc tgt ggg cca gtg ggg      950
Leu Met Val Leu Val Ala Phe Ala Ile Gly Phe Cys Gly Pro Val Gly
    75                      80                      85

atc atc ctg tcc tgc tat atg aag atc acc tgg aag ctg tgc agc aca      998
Ile Ile Leu Ser Cys Tyr Met Lys Ile Thr Trp Lys Leu Cys Ser Thr
    90                      95                      100                      105

gct ggg aga acc cag tga ccagcg ggaaaggaca ccaccggcgg ggcagcccgg      1052
Ala Gly Arg Thr Gln
                      110

gaggacccag tgaccagcag gaaaggacgc caccggcggg gcagcccagg aggacccagt      1112

gaccagcggg aaaggacacc accagcagga cagcccgaga ggaccagtg accagcggga      1172

aaggatgcc aaggcgggac agcccgggag gaccagtgga ccagcaggaa aggacgccac      1232

tggcgaggct gcctgcttac gctgctgatg ctggtggcgg tgggtggtctg cttcagcccc      1292

taccacctca acatcaagca gttcatggcg agagggatgc tccacctgcc atcctgtgcc      1352

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atctactgac taatggattc tccaattggt aagcctatgt tacaggacaa aggccgtcgc      180

tttgtaaaag cttgaagtgc agtttgctgc tgagtacaga agacctttgc aaacagagag      240

gggagatttt ctctgtaagg ttgcaaacia gagcaggtcc tggaagataa gattccccgc      300

c   atg tta tcc tcc gtg gtg ttt tgg gga cta att gcc ctc att ggc      346
Met Leu Ser Ser Val Val Phe Trp Gly Leu Ile Ala Leu Ile Gly
    1                      5                      10                      15

act tcc agg ggc tca tac ccc ttc agt cac tca atg aag cct cac cta      394
Thr Ser Arg Gly Ser Tyr Pro Phe Ser His Ser Met Lys Pro His Leu
    20                      25                      30

cat cca cgc ctg tac cac ggc tgc tat ggg gac atc atg acc atg aag      442

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His	Pro	Arg	Leu	Tyr	His	Gly	Cys	Tyr	Gly	Asp	Ile	Met	Thr	Met	Lys		
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acc	tct	ggg	gcc	act	tgt	gat	gca	aac	agt	gtg	atg	aac	tgc	ggg	atc		490
Thr	Ser	Gly	Ala	Thr	Cys	Asp	Ala	Asn	Ser	Val	Met	Asn	Cys	Gly	Ile		
		50					55					60					
cgt	ggg	tct	gaa	atg	ttt	gct	gag	atg	gat	ttg	agg	gcc	ata	aaa	cct		538
Arg	Gly	Ser	Glu	Met	Phe	Ala	Glu	Met	Asp	Leu	Arg	Ala	Ile	Lys	Pro		
		65				70				75							
tac	cag	act	ctg	atc	aaa	gaa	gtc	ggg	cag	aga	cat	tgc	gtg	gac	cct		586
Tyr	Gln	Thr	Leu	Ile	Lys	Glu	Val	Gly	Gln	Arg	His	Cys	Val	Asp	Pro		
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gct	gtc	atc	gca	gcc	atc	atc	tcc	agg	gaa	agc	cat	ggc	gga	tct	gtc		634
Ala	Val	Ile	Ala	Ala	Ile	Ile	Ser	Arg	Glu	Ser	His	Gly	Gly	Ser	Val		
				100				105						110			
ctg	caa	gac	ggc	tgg	gac	cac	agg	gga	ctt	aaa	ttt	ggc	ttg	atg	cag		682
Leu	Gln	Asp	Gly	Trp	Asp	His	Arg	Gly	Leu	Lys	Phe	Gly	Leu	Met	Gln		
			115				120						125				
ctt	gat	aaa	caa	acg	tac	cac	cct	gtc	ggg	gcc	tgg	gat	agc	aaa	gag		730
Leu	Asp	Lys	Gln	Thr	Tyr	His	Pro	Val	Gly	Ala	Trp	Asp	Ser	Lys	Glu		
		130					135					140					
cac	ctt	tca	cag	gct	act	ggg	att	cta	aca	gag	aga	att	aag	gca	atc		778
His	Leu	Ser	Gln	Ala	Thr	Gly	Ile	Leu	Thr	Glu	Arg	Ile	Lys	Ala	Ile		
		145				150					155						
cag	aaa	aaa	ttc	ccc	acg	tgg	agt	gtt	gct	cag	cac	ctc	aaa	ggg	ggg		826
Gln	Lys	Lys	Phe	Pro	Thr	Trp	Ser	Val	Ala	Gln	His	Leu	Lys	Gly	Gly		
	160				165				170					175			
ctc	tca	gct	ttt	aag	tca	gga	att	gaa	gcg	att	gcc	acc	cca	tcg	gac		874
Leu	Ser	Ala	Phe	Lys	Ser	Gly	Ile	Glu	Ala	Ile	Ala	Thr	Pro	Ser	Asp		
				180				185						190			
ata	gac	aat	gac	ttc	gtc	aat	gat	atc	att	gct	cga	gct	aag	ttc	tat		922
Ile	Asp	Asn	Asp	Phe	Val	Asn	Asp	Ile	Ile	Ala	Arg	Ala	Lys	Phe	Tyr		
		195					200						205				
aaa	aga	caa	agc	ttc	tag	gcaaag	ctctgtgggt	gggccaggtt	ggcagagtgc								976
Lys	Arg	Gln	Ser	Phe													
		210															
tcagatggcc	gcctttgaga	gttttacgtg	aatgtgttgt	atacaacact	ggcacagaaa												1036
tgattaaaaat	catgaaagaa	aattcatttc	ccaattttct	gaatgaaaat	aatcattgaa												1096
aaaaggaaaag	aaaaataaaa	gaaatccatc	cagttcacaa	tatggttcct	aggaaacgga												1156
catagacata	tatataacta	ctttgcagta	aatgtgaata	tcattggcaaa	tggtccctag												1216
gtattccagc	caggcttcat	tttagcctgt	gattccaatg	cccacctact	ccctgtctac												1276
cagaattgct	aacaagttaa	gtaagcctta	cccgagcctt	tgtctttttt	ccagtatctg												1336
cccagagccc	tcaagctttg	cttatgagaa	gttc														1370

<400> 35

77

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gat acc acc tca ttc cca tta tca gta tat cct cca ggg tca aca gtg	890
Asp Thr Thr Ser Phe Pro Leu Ser Val Tyr Pro Pro Gly Ser Thr Val	
160 165 170	
acg tac cgt tgc cag tcc ttc tat aaa ctc cag ggc tct gta act gta	938
Thr Tyr Arg Cys Gln Ser Phe Tyr Lys Leu Gln Gly Ser Val Thr Val	
175 180 185	
aca tgc aga aat aaa cag tgg tca gaa cca cca aga tgc cta gat cca	986
Thr Cys Arg Asn Lys Gln Trp Ser Glu Pro Pro Arg Cys Leu Asp Pro	
190 195 200	
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Cys Val Val Ser Glu Glu Asn Met Asn Lys Asn Asn Ile Gln Leu Lys	
205 210 215 220	
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Trp Arg Asn Asp Gly Lys Leu Tyr Ala Lys Thr Gly Asp Ala Val Glu	
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Phe Gln Cys Lys Phe Pro His Lys Ala Met Ile Ser Ser Pro Pro Phe	
240 245 250	
cga gca atc tgt cag gaa ggg aaa ttt gaa tat cct ata tgt gaa tga	1178
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tcccc atg ggg ccg gac gag gcc aca cca ccc gac ctg gtg ctt cct	347
Met Gly Pro Asp Glu Ala Thr Pro Pro Asp Leu Val Leu Pro	
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gcc tgg cgt ctg cgc cac gga gca ttc agg acg ctg gtg acc agg gag Ala Trp Arg Leu Arg His Gly Ala Phe Arg Thr Leu Val Thr Arg Glu 15 20 25 30	395
cca gga gcc ccc agg atg ggt gcc ccg agc gcg tgc cgg acg ctg gtg Pro Gly Ala Pro Arg Met Gly Ala Pro Ser Ala Cys Arg Thr Leu Val 35 40 45	443
ttg gct ctg gcg gcc atg ctc gtg gtg ccg cag gca gag acc cag ggc Leu Ala Leu Ala Ala Met Leu Val Val Pro Gln Ala Glu Thr Gln Gly 50 55 60	491
cct gtg gag ccg agc tgg gag aat gca ggg cac acc atg gat ggc ggt Pro Val Glu Pro Ser Trp Glu Asn Ala Gly His Thr Met Asp Gly Gly 65 70 75	539
gcc ccg acg tcc tcg ccc acc cgg cgc gtg agc ttt gtt cca ccc gtc Ala Pro Thr Ser Ser Pro Thr Arg Arg Val Ser Phe Val Pro Pro Val 80 85 90	587
act gtc ttc ccc agc ctg agc ccc ctg aac ccg gcg cac aat ggg cgg Thr Val Phe Pro Ser Leu Ser Pro Leu Asn Pro Ala His Asn Gly Arg 95 100 105 110	635
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gtc ttc cgc ttc cct ggc ctt tgc aac tac gtg ttc tct gag cac tgc Val Phe Arg Phe Pro Gly Leu Cys Asn Tyr Val Phe Ser Glu His Cys 130 135 140	731
cgc gcc gcc tac gag gac ttc aac gtc cag cta cgc cga ggc cta gtg Arg Ala Ala Tyr Glu Asp Phe Asn Val Gln Leu Arg Arg Gly Leu Val 145 150 155	779
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gag ctg cct tac agc cgc act ggc ctc ctg gtg gag cag agc ggg gac Glu Leu Pro Tyr Ser Arg Thr Gly Leu Leu Val Glu Gln Ser Gly Asp 195 200 205	923
tac atc aag gtc agc atc cgg ctg gtg ctg aca ttc ctg tgg aac gga Tyr Ile Lys Val Ser Ile Arg Leu Val Leu Thr Phe Leu Trp Asn Gly 210 215 220	971
gag gac agt gcc ctg ctg gag ctg gat ccc aaa tac gcc aac cag acc Glu Asp Ser Ala Leu Leu Glu Leu Asp Pro Lys Tyr Ala Asn Gln Thr 225 230 235	1019
tgt ggc ctg tgt ggg gac ttc aac ggc ctc ccg gcc ttc aac gag ttc Cys Gly Leu Cys Gly Asp Phe Asn Gly Leu Pro Ala Phe Asn Glu Phe 240 245 250	1067
tat gcc cac agt gag tgc cac ctg gac gcc agg ctg acc ccg ctc cag	1115

Tyr	Ala	His	Ser	Glu	Cys	His	Leu	Asp	Ala	Arg	Leu	Thr	Pro	Leu	Gln		
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ttt	ggg	aac	ctg	cag	aag	ttg	gat	ggg	ccc	acg	gag	cag	tgc	ccg	gac		1163
Phe	Gly	Asn	Leu	Gln	Lys	Leu	Asp	Gly	Pro	Thr	Glu	Gln	Cys	Pro	Asp		
				275				280					285				
ccg	ctg	ccc	ttg	ccg	gcc	ggc	aac	tgc	acg	gac	gag	gag	ggc	atc	tgc		1211
Pro	Leu	Pro	Leu	Pro	Ala	Gly	Asn	Cys	Thr	Asp	Glu	Glu	Gly	Ile	Cys		
			290					295					300				
cac	cgc	acc	ctg	ctg	ggg	ccg	gcc	ttt	gcg	gag	tgc	cac	gca	ctg	gtg		1259
His	Arg	Thr	Leu	Leu	Gly	Pro	Ala	Phe	Ala	Glu	Cys	His	Ala	Leu	Val		
		305					310					315					
gac	agc	act	gcg	tac	ctg	gcc	gcc	tgc	gcc	cag	gac	ctg	tgc	cgc	tgc		1307
Asp	Ser	Thr	Ala	Tyr	Leu	Ala	Ala	Cys	Ala	Gln	Asp	Leu	Cys	Arg	Cys		
	320				325					330							
ccc	acc	tgc	ccg	tgt	gcc	acc	ttt	gtg	gaa	tac	tca	cgc	cag	tgc	gcc		1355
Pro	Thr	Cys	Pro	Cys	Ala	Thr	Phe	Val	Glu	Tyr	Ser	Arg	Gln	Cys	Ala		
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cac	gcg	ggg	ggc	cag	ccg	cgg	aac	tgg	agg	tgc	cct	gag	ctc	tgc	ccc		1403
His	Ala	Gly	Gly	Gln	Pro	Arg	Asn	Trp	Arg	Cys	Pro	Glu	Leu	Cys	Pro		
			355					360						365			
cgg	acc	tgc	ccc	ctc	aac	atg	cag	cac	cag	gag	tgt	ggc	tca	ccc	tgc		1451
Arg	Thr	Cys	Pro	Leu	Asn	Met	Gln	His	Gln	Glu	Cys	Gly	Ser	Pro	Cys		
			370				375					380					
acg	gac	acc	tgc	tcc	aac	ccc	cag	cgc	gcg	cag	ctc	tgt	gag	gac	cac		1499
Thr	Asp	Thr	Cys	Ser	Asn	Pro	Gln	Arg	Ala	Gln	Leu	Cys	Glu	Asp	His		
		385				390						395					
tgt	gtg	gac	ggc	tgc	ttc	tgc	ccc	cca	ggc	acg	gtg	ctg	gat	gac	atc		1547
Cys	Val	Asp	Gly	Cys	Phe	Cys	Pro	Pro	Gly	Thr	Val	Leu	Asp	Asp	Ile		
	400					405					410						
acg	cac	tct	ggc	tgc	ctg	ccc	ctc	ggg	cag	tgc	ccc	tgc	acc	cac	ggc		1595
Thr	His	Ser	Gly	Cys	Leu	Pro	Leu	Gly	Gln	Cys	Pro	Cys	Thr	His	Gly		
415				420					425					430			
ggc	cgc	acc	tac	agc	ccg	ggc	acc	tcc	ttc	aac	acc	acc	tgc	agc	tcc		1643
Gly	Arg	Thr	Tyr	Ser	Pro	Gly	Thr	Ser	Phe	Asn	Thr	Thr	Cys	Ser	Ser		
			435					440					445				
tgc	acc	tgc	tcc	ggg	ggg	cta	tgg	cag	tgc	cag	gac	ctg	ccg	tgc	cct		1691
Cys	Thr	Cys	Ser	Gly	Gly	Leu	Trp	Gln	Cys	Gln	Asp	Leu	Pro	Cys	Pro		
			450				455					460					
ggc	acc	tgc	tct	gtg	cag	ggc	ggg	gcc	cac	atc	tcc	acc	tat	gat	gag		1739
Gly	Thr	Cys	Ser	Val	Gln	Gly	Gly	Ala	His	Ile	Ser	Thr	Tyr	Asp	Glu		
		465				470					475						
aaa	ctc	tac	gac	ctg	cat	ggc	gac	tgc	agc	tac	gtt	ctg	tcc	aag	aaa		1787
Lys	Leu	Tyr	Asp	Leu	His	Gly	Asp	Cys	Ser	Tyr	Val	Leu	Ser	Lys	Lys		
	480					485					490						
tgt	gcc	gac	agc	agc	ttc	acc	gtg	ctg	gct	gag	ctg	cgg	aag	tgc	ggc		1835
Cys	Ala	Asp	Ser	Ser	Phe	Thr	Val	Leu	Ala	Glu	Leu	Arg	Lys	Cys	Gly		

495	500	505	510	
ctg acg gac aac gag aac tgc ctg aaa gcg gtg acg ctc agc ctg gac Leu Thr Asp Asn Glu Asn Cys Leu Lys Ala Val Thr Leu Ser Leu Asp	515	520	525	1883
ggc ggg gac acg gcc atc cgg gtc caa gcg gac ggc ggc gtg ttc ctc Gly Gly Asp Thr Ala Ile Arg Val Gln Ala Asp Gly Gly Val Phe Leu	530	535	540	1931
aac tcc atc tac acg cag ctg ccc ctg tcg gca gcc aac atc acc ctg Asn Ser Ile Tyr Thr Gln Leu Pro Leu Ser Ala Ala Asn Ile Thr Leu	545	550	555	1979
ttc aca ccc tcg agc ttc ttc atc gtg gtg cag aca ggc ctg ggg ctg Phe Thr Pro Ser Ser Phe Phe Ile Val Val Gln Thr Gly Leu Gly Leu	560	565	570	2027
cag ctg ctg gtg cag ctg gtg cca ctc atg cag gtg ttt gtc agg ctg Gln Leu Leu Val Gln Leu Val Pro Leu Met Gln Val Phe Val Arg Leu	575	580	585	2075
gac ccc gcc cac cag ggc cag atg tgc ggc ctg tgt ggg aac ttc aac Asp Pro Ala His Gln Gly Gln Met Cys Gly Leu Cys Gly Asn Phe Asn	595	600	605	2123
cag aac cag gct gac gac ttc acg gcc ctc agc ggg gtg gtg gag gcc Gln Asn Gln Ala Asp Asp Phe Thr Ala Leu Ser Gly Val Val Glu Ala	610	615	620	2171
acg ggc gca gcc ttc gcc aac acc tgg aag gcc cag gct gcc tgt gcc Thr Gly Ala Ala Phe Ala Asn Thr Trp Lys Ala Gln Ala Ala Cys Ala	625	630	635	2219
aat gcc agg aac agc ttt gag gac ccc tgc tcc ctc agt gtg gag aat Asn Ala Arg Asn Ser Phe Glu Asp Pro Cys Ser Leu Ser Val Glu Asn	640	645	650	2267
gag aac tac gcc cgg cac tgg tgc tcg cgc ctg acc gat ccc aac agt Glu Asn Tyr Ala Arg His Trp Cys Ser Arg Leu Thr Asp Pro Asn Ser	655	660	665	2315
gcc ttc tcg cgc tgc cac tcc atc atc aac ccc aag ccc ttc cac tcg Ala Phe Ser Arg Cys His Ser Ile Ile Asn Pro Lys Pro Phe His Ser	675	680	685	2363
aac tgc atg ttc gac acc tgc aac tgt gag cgg agc gag gac tgc ctg Asn Cys Met Phe Asp Thr Cys Asn Cys Glu Arg Ser Glu Asp Cys Leu	690	695	700	2411
tgc gcc gcg ctg tcc tcc tat gtg cac gcc tgt gcc gcc aag ggc gta Cys Ala Ala Leu Ser Ser Tyr Val His Ala Cys Ala Ala Lys Gly Val	705	710	715	2459
cag ctc agc gac tgg agg gac ggc gtc tgc acc aag tac atg cag aac Gln Leu Ser Asp Trp Arg Asp Gly Val Cys Thr Lys Tyr Met Gln Asn	720	725	730	2507
tgc ccc aag tcc cag cgc tac gcc tac gtg gtg gat gcc tgc cag ccc Cys Pro Lys Ser Gln Arg Tyr Ala Tyr Val Val Asp Ala Cys Gln Pro	735	740	745	2555
			750	

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gcg ggc gcc tgt gtg ccc gcc cag aag tgc ccc tgc tac gct cac ggc Ala Gly Ala Cys Val Pro Ala Gln Lys Cys Pro Cys Tyr Ala His Gly 785 790 795	2699
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tgc ccc tgt gtg cac aac gag gcc acc tac aag cct gga gag acc atc Cys Pro Cys Val His Asn Glu Ala Thr Tyr Lys Pro Gly Glu Thr Ile 895 900 905 910	3035
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Pro Gly Leu Glu Gly Cys Tyr Pro Lys Cys Pro Pro Ser Gln Pro Phe
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Lys Asp Gly Asn Tyr Tyr Asp Val Gly Ala Arg Val Pro Thr Ala Glu
1265 1270 1275

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1295 1300 1305 1310

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Gln Asp Val Ile Tyr Asn Thr Thr Asp Gly Leu Gly Ala Cys Leu Ile
1315 1320 1325

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1330 1335 1340

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Gln Asn Thr Glu Thr Ser Ser Leu Val Ser Met Thr Ser Ala Thr Ile
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Pro Ser Val Arg Pro Thr Phe Thr Ser Thr His Asn Thr Leu Thr Ser
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Ser Leu Leu Thr Thr Phe Pro Gly Thr Tyr Ser Phe Ser Ser Ser Met	
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tct gcc agc agt gat ggg acc act cac aca gaa act atc acc tca ctt	240
Ser Ala Ser Ser Asp Gly Thr Thr His Thr Glu Thr Ile Thr Ser Leu	
65 70 75	
cca gcc agc acc agt aca ctc cac acc aca gct gaa tcc acc aca gca	288
Pro Ala Ser Thr Ser Thr Leu His Thr Thr Ala Glu Ser Thr Thr Ala	
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His Thr Thr Thr Thr Ser Phe Thr Thr Ser Thr Thr Met Glu Ser Pro	
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Ser Ser Ser Val Ala Thr Thr Ser Thr Gly Gln Thr Thr Phe Ser Ser	
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Ser Thr Ala Thr Phe Thr Glu Thr Thr Thr Leu Thr Pro Thr Thr Asp	
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Thr Ser Ser Ile Thr Pro Thr Asn Thr Val Thr Ser Met Thr Thr Met	
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Thr Ser Trp Pro Thr Ala Thr Asn Thr Leu Ser Ser Leu Thr Thr Asn	
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att tta tct tct aca cct gtc ccg agc aca gag agg acc acc agt cat	624
Ile Leu Ser Ser Thr Pro Val Pro Ser Thr Glu Arg Thr Thr Ser His	
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Ser Thr Ser Thr Val Thr Glu Ser Thr Thr Glu Ile Thr Tyr Ser Thr	
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Thr Met Thr Glu Thr Ser Ser Ser Ala Thr Ser Leu Pro Leu Thr Ser	
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Pro Leu Val Ser Thr Thr Glu Thr Ala Lys Thr Pro Thr Thr Ile Leu	
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Val Thr Thr Thr Thr	Lys Thr Thr Ser His Ser Thr Thr Ser Phe Thr	
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Ser Val Pro Thr Thr Leu Gly Thr Met Val Thr Ser Thr Ser Arg Ile	320 325 330	
cca tct act gtg agt acg agt atc cct acc tca caa cca aaa acc gtc		1056
Pro Ser Thr Val Ser Thr Ser Ile Pro Thr Ser Gln Pro Lys Thr Val	335 340 345	
aat tcc tca tct ggg ggc atc act ggt tca tta cct atg atg aca gac		1104
Asn Ser Ser Ser Gly Gly Ile Thr Gly Ser Leu Pro Met Met Thr Asp	350 355 360	
ctt acc tca ggg tac acc gtc tcc agt atg tct gca att ccc aca act		1152
Leu Thr Ser Gly Tyr Thr Val Ser Ser Met Ser Ala Ile Pro Thr Thr	365 370 375 380	
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Val Ile Pro Thr Ser Leu Thr Val Gln Asn Thr Glu Thr Ser Ile Phe	385 390 395	
gtc agc atg acc tct gcc acc act ccc agt ggg aga cca act ttc aca		1248
Val Ser Met Thr Ser Ala Thr Thr Pro Ser Gly Arg Pro Thr Phe Thr	400 405 410	
agt act gtg aac act ccc aca agg tcc ctc ctg aca agc ttt cca acg		1296
Ser Thr Val Asn Thr Pro Thr Arg Ser Leu Leu Thr Ser Phe Pro Thr	415 420 425	
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Thr His Leu Phe Ser Ser Ser Met Ser Glu Ser Ser Ala Gly Thr Thr	430 435 440	
cac aca gag agt atc tcc tca cct cca gcc acc acc agt aca ctc cac		1392
His Thr Glu Ser Ile Ser Ser Pro Pro Ala Thr Thr Ser Thr Leu His	445 450 455 460	
aca aca gct gaa tcc acc ccg tcg tgc act acc acc acg tca ttc atc		1440
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<210> 41
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<213> Homo sapiens

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<223> n = a,t,c or g

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                                   Met Met Gly Gln
                                   1

gac aaa ata caa ggc cac tct gta atc agt gaa gaa tct gat gga aag 161
Asp Lys Ile Gln Gly His Ser Val Ile Ser Glu Glu Ser Asp Gly Lys
 5              10              15              20

ctt att gaa gac agc ctg att cag ctg aga tgt cac ttt aca tgg aag 209
Leu Ile Glu Asp Ser Leu Ile Gln Leu Arg Cys His Phe Thr Trp Lys

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	25	30	35	
ttg tta att gaa gcc cct gaa att cct gat tta gaa aac agg atc tgg				257
Leu Leu Ile Glu Ala Pro Glu Ile Pro Asp Leu Glu Asn Arg Ile Trp	40	45	50	
gaa gag att cag ttc ctg gac acc aaa tac aat gtg gga ata cac aac				305
Glu Glu Ile Gln Phe Leu Asp Thr Lys Tyr Asn Val Gly Ile His Asn	55	60	65	
cta cta gcc tat gtg aaa cac ctg aaa ggc cag aat gag gaa gcc ctg				353
Leu Leu Ala Tyr Val Lys His Leu Lys Gly Gln Asn Glu Glu Ala Leu	70	75	80	
gtc agc ttg aaa aag gct gaa gac tta att cag aaa gaa cat gcc aac				401
Val Ser Leu Lys Lys Ala Glu Asp Leu Ile Gln Lys Glu His Ala Asn	85	90	95	100
caa gca gat att aga agt ctg gtg acc tgg ggc aac ttt gcc tgg gtg				449
Gln Ala Asp Ile Arg Ser Leu Val Thr Trp Gly Asn Phe Ala Trp Val	105	110	115	
tat tac cac atg ggc aga ttg gca gaa gcc cag act tac ctg gac aag				497
Tyr Tyr His Met Gly Arg Leu Ala Glu Ala Gln Thr Tyr Leu Asp Lys	120	125	130	
gtg gag aac act tgc aag aag ttt gca aat cct tcc cgc tat aga atg				545
Val Glu Asn Thr Cys Lys Lys Phe Ala Asn Pro Ser Arg Tyr Arg Met	135	140	145	
gag tgt cca gag gtg gac tgt gag gaa gga tgg gcc ttg gcg aag tgt				593
Glu Cys Pro Glu Val Asp Cys Glu Glu Gly Trp Ala Leu Ala Lys Cys	150	155	160	
gga gga aag aat tat gaa cgg gcc aag acc tgc ttt gaa aag gct ctg				641
Gly Gly Lys Asn Tyr Glu Arg Ala Lys Thr Cys Phe Glu Lys Ala Leu	165	170	175	180
gaa ggg aac cct gaa aac cct gaa ttc aat act ggg tac gca atc acc				689
Glu Gly Asn Pro Glu Asn Pro Glu Phe Asn Thr Gly Tyr Ala Ile Thr	185	190	195	
gtc tat cgc ctg gat aaa ttt aac aca gca tca ggg agg aat aag gca				737
Val Tyr Arg Leu Asp Lys Phe Asn Thr Ala Ser Gly Arg Asn Lys Ala	200	205	210	
ttt tct ctg cac gtc cta aaa cga gct gtc agg cta aat cca gat gat				785
Phe Ser Leu His Val Leu Lys Arg Ala Val Arg Leu Asn Pro Asp Asp	215	220	225	
gta tat att agg gtt ctc ctt gcc ctg aag ctt cag gat gaa gga cag				833
Val Tyr Ile Arg Val Leu Leu Ala Leu Lys Leu Gln Asp Glu Gly Gln	230	235	240	
gaa gct gaa gga gaa aag tac att gaa gaa gct ctg acc agt ata tct				881
Glu Ala Glu Gly Glu Lys Tyr Ile Glu Glu Ala Leu Thr Ser Ile Ser	245	250	255	260
tca cag gcc tat gtc ttt caa tat gca gcc aag ttt tat cga aga aaa				929
Ser Gln Ala Tyr Val Phe Gln Tyr Ala Ala Lys Phe Tyr Arg Arg Lys	265	270	275	

ggg tct gtg gat aaa gct ctt gag ctc tta aaa atg gcc ttg gag aca Gly Ser Val Asp Lys Ala Leu Glu Leu Leu Lys Met Ala Leu Glu Thr 280 285 290	977
aca ccc act tct gcc ttc ctg cat cac caa atg ggg ctt tgc tac agg Thr Pro Thr Ser Ala Phe Leu His His Gln Met Gly Leu Cys Tyr Arg 295 300 305	1025
gca caa atg atc caa atc aag gaa gct aca aac tgg cag cct aga ggg Ala Gln Met Ile Gln Ile Lys Glu Ala Thr Asn Trp Gln Pro Arg Gly 310 315 320	1073
caa gat agg gaa act gtg gac aga ttg gtt caa ttg gct ata tgc aaa Gln Asp Arg Glu Thr Val Asp Arg Leu Val Gln Leu Ala Ile Cys Lys 325 330 335 340	1121
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gac ctg gct gaa acg tat gca gaa ata ggc cac cac aga aag gct gag Asp Leu Ala Glu Thr Tyr Ala Glu Ile Gly His His Arg Lys Ala Glu 360 365 370	1217
gaa cat ttt cag aaa ggg tta cgc atg aag atc ttt gaa gat cag cta Glu His Phe Gln Lys Gly Leu Arg Met Lys Ile Phe Glu Asp Gln Leu 375 380 385	1265
aag caa gag att cat tac cac tac ggc cgt ttc caa gaa cat cat ggg Lys Gln Glu Ile His Tyr His Tyr Gly Arg Phe Gln Glu His His Gly 390 395 400	1313
aaa tct caa gat aaa gca att acc cat tat tta aaa ggt ttg aaa ata Lys Ser Gln Asp Lys Ala Ile Thr His Tyr Leu Lys Gly Leu Lys Ile 405 410 415 420	1361
gaa aaa atg tcc cat tcc agg gaa aaa ctt ctc aat gct tta gag aaa Glu Lys Met Ser His Ser Arg Glu Lys Leu Leu Asn Ala Leu Glu Lys 425 430 435	1409
ttg gct aaa aga tgt att cac cag aat gta cgg gtt gtg gaa agt gtc Leu Ala Lys Arg Cys Ile His Gln Asn Val Arg Val Val Glu Ser Val 440 445 450	1457
agc ctc ctt ggg ctt atc cac aaa ttg aaa gga gaa gta agt gat gct Ser Leu Leu Gly Leu Ile His Lys Leu Lys Gly Glu Val Ser Asp Ala 455 460 465	1505
ttg ctg tgc tat gag agg gct ctg agg ctg gct gct gac ctg aac cct Leu Leu Cys Tyr Glu Arg Ala Leu Arg Leu Ala Ala Asp Leu Asn Pro 470 475 480	1553
ata ttt taa catagag gtcaccatta tccatttaat ggtcttataa ctaaatagaa Ile Phe 485	1609
tgactatgaa attaaataat gcaaacttaa agctgttgga aatttacctt attttgagcc	1669
ttgagaggaa tgtggctgtg tggcctgagt tatgtagcat gcaactgcaa cttctgcttt	1729

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<210> 42
<211> 1671
<212> DNA
<213> Homo sapiens

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<220>
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<222> (417) .. (1628)

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ctatcacggg cccactctcc gtgccgctg tcccttaaaa gctggggcct gggacaggaa 180
cgacagacaa tgcagccaat ggcgtcacgc gcggtgcccc gctaccaaat cgaaaggcgt 240
ggctgagggg aacgcggtgg gaaccgcccc cgactccagg cgactccttg gccgggcggg 300
ggagagcgtc cccgtcagct gagagcatcc tcaactcggtc agttcctcgg gcgagttacg 360

gggacgacct gcgggagcac gcgggcagtg gccggacgct gaagcccagg agagcg 416
atg gag acg tat gcg gag gtt ggg aag gag ggc aag cct tcc tgt gca 464
Met Glu Thr Tyr Ala Glu Val Gly Lys Glu Gly Lys Pro Ser Cys Ala
  1             5             10            15

tcg gtg gat ctg cag gga gac agc tcc tta cag gtg gag att tct gac 512
Ser Val Asp Leu Gln Gly Asp Ser Ser Leu Gln Val Glu Ile Ser Asp
      20             25             30

gca gtg agt gag cgg gac aag gtg aaa ttc act gtt caa aca aag agc 560
Ala Val Ser Glu Arg Asp Lys Val Lys Phe Thr Val Gln Thr Lys Ser
      35             40             45

tgc ctc cct cac ttc gcc cag acc gag ttc tca gtc gtg cgg cag cac 608
Cys Leu Pro His Phe Ala Gln Thr Glu Phe Ser Val Val Arg Gln His
      50             55             60

gag gag ttc atc tgg ctg cat gat gcc tac gtg gag aat gag gag tac 656

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Glu 65	Glu	Phe	Ile	Trp	Leu 70	His	Asp	Ala	Tyr	Val 75	Glu	Asn	Glu	Glu	Tyr 80	
gcc	ggc	ctc	atc	atc	ccc	cca	gcc	cct	ccg	agg	cca	gac	ttt	gag	gct	704
Ala	Gly	Leu	Ile	Ile	Pro	Pro	Ala	Pro	Pro	Arg	Pro	Asp	Phe	Glu	Ala	
				85					90					95		
tcg	agg	gaa	aag	cta	cag	aaa	ttg	ggc	gag	ggg	gac	agc	tct	gtc	act	752
Ser	Arg	Glu	Lys	Leu	Gln	Lys	Leu	Gly	Glu	Gly	Asp	Ser	Ser	Val	Thr	
			100					105					110			
cgg	gaa	gag	ttt	gcc	aag	atg	aag	cag	gag	ctg	gaa	gcg	gag	tac	ctg	800
Arg	Glu	Glu	Phe	Ala	Lys	Met	Lys	Gln	Glu	Leu	Glu	Ala	Glu	Tyr	Leu	
			115				120					125				
gcc	atc	ttt	aag	aag	aca	gtt	gcg	atg	cac	gaa	gtc	ttt	ctg	cag	cgc	848
Ala	Ile	Phe	Lys	Lys	Thr	Val	Ala	Met	His	Glu	Val	Phe	Leu	Gln	Arg	
			130			135					140					
ctg	gcg	gcc	cac	ccc	acc	ctg	cgt	cga	gac	cac	aac	ttc	ttt	gtg	ttt	896
Leu	Ala	Ala	His	Pro	Thr	Leu	Arg	Arg	Asp	His	Asn	Phe	Phe	Val	Phe	
					150					155					160	
ttg	gaa	tat	gga	cag	gat	ctg	agt	gtc	cgg	ggg	aag	aac	agg	aag	gag	944
Leu	Glu	Tyr	Gly	Gln	Asp	Leu	Ser	Val	Arg	Gly	Lys	Asn	Arg	Lys	Glu	
				165					170					175		
ctc	ctc	gga	ggg	ttt	ctg	agg	aat	att	gtg	aag	tcc	gcg	gat	gaa	gcc	992
Leu	Leu	Gly	Gly	Phe	Leu	Arg	Asn	Ile	Val	Lys	Ser	Ala	Asp	Glu	Ala	
			180					185					190			
ctc	atc	acg	ggc	atg	tca	ggg	ctc	aag	gag	gtg	gat	gac	ttc	ttt	gag	1040
Leu	Ile	Thr	Gly	Met	Ser	Gly	Leu	Lys	Glu	Val	Asp	Asp	Phe	Phe	Glu	
			195				200					205				
cat	gag	agg	acc	ttc	ctg	ttg	gag	tat	cac	acc	cgt	atc	cga	gat	gcc	1088
His	Glu	Arg	Thr	Phe	Leu	Leu	Glu	Tyr	His	Thr	Arg	Ile	Arg	Asp	Ala	
			210			215					220					
tgc	ctg	cgg	gcc	gac	cgc	gtc	atg	cgc	gcc	cac	aag	tgc	ctg	gca	gac	1136
Cys	Leu	Arg	Ala	Asp	Arg	Val	Met	Arg	Ala	His	Lys	Cys	Leu	Ala	Asp	
					230					235					240	
gat	tat	atc	cct	atc	tca	gct	gcg	ctg	agc	agt	ctg	gga	aca	cag	gaa	1184
Asp	Tyr	Ile	Pro	Ile	Ser	Ala	Ala	Leu	Ser	Ser	Leu	Gly	Thr	Gln	Glu	
				245					250					255		
gtc	aac	cag	cta	agg	acg	agc	ttc	ctc	aaa	ttg	gca	gag	ctc	ttt	gaa	1232
Val	Asn	Gln	Leu	Arg	Thr	Ser	Phe	Leu	Lys	Leu	Ala	Glu	Leu	Phe	Glu	
			260					265					270			
cgg	ctg	agg	aag	ctg	gag	ggc	cgg	gtg	gct	tcc	gat	gag	gac	ctg	aag	1280
Arg	Leu	Arg	Lys	Leu	Glu	Gly	Arg	Val	Ala	Ser	Asp	Glu	Asp	Leu	Lys	
			275				280					285				
ctg	tca	gac	atg	ctg	agg	tac	tac	atg	cgt	gac	tca	cag	gca	gcc	aag	1328
Leu	Ser	Asp	Met	Leu	Arg	Tyr	Tyr	Met	Arg	Asp	Ser	Gln	Ala	Ala	Lys	
			290			295					300					
gac	ctg	ctg	tac	cgg	cgg	ctg	cgg	gca	ctg	gcc	gac	tac	gag	aat	gcc	1376
Asp	Leu	Leu	Tyr	Arg	Arg	Leu	Arg	Ala	Leu	Ala	Asp	Tyr	Glu	Asn	Ala	

305	310	315	320	
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Asn Lys Ala Leu Asp Lys Ala Arg Thr Arg Asn Arg Glu Val Arg Pro	325	330	335	
gcc gag agc cac cag cag ctg tgc tgc caa cgc ttc gag cgc ctc tcc				1472
Ala Glu Ser His Gln Gln Leu Cys Cys Gln Arg Phe Glu Arg Leu Ser	340	345	350	
gac tcc gcc aag caa gag ctc atg gac ttc aag tcc cgc cgg gtc tcc				1520
Asp Ser Ala Lys Gln Glu Leu Met Asp Phe Lys Ser Arg Arg Val Ser	355	360	365	
tct ttt cga aag aat ctc att gag ctg gca gag ctg gag ctc aaa cac				1568
Ser Phe Arg Lys Asn Leu Ile Glu Leu Ala Glu Leu Glu Leu Lys His	370	375	380	
gcc aag gcc agc acc ctg att ctc cgg aac acc ctt gtt gcc cta aag				1616
Ala Lys Ala Ser Thr Leu Ile Leu Arg Asn Thr Leu Val Ala Leu Lys	385	390	395	400
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Gly Glu Pro				

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 <213> Homo sapiens

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aaaggcgctt atttcccagg cagccgctgc agtcgccaca cttttgcccc tgctgcg	177
atg acc ctg tcg cca ctt ctg ctg ttc ctg cca ccg ctg ctg ctg ctg	225
Met Thr Leu Ser Pro Leu Leu Leu Phe Leu Pro Pro Leu Leu Leu Leu	
1 5 10 15	
ctg gac gtc ccc acg gcg gcg gtg cag gcg tcc cct ctg caa gcg tta	273
Leu Asp Val Pro Thr Ala Ala Val Gln Ala Ser Pro Leu Gln Ala Leu	
20 25 30	
gac ttc ttt ggg aat ggg cca cca gtt aac tac aag aca ggc aat cta	321
Asp Phe Phe Gly Asn Gly Pro Pro Val Asn Tyr Lys Thr Gly Asn Leu	
35 40 45	
tac ctg cgg ggg ccc ctg aag aag tcc aat gca ccg ctt gtc aat gtg	369
Tyr Leu Arg Gly Pro Leu Lys Lys Ser Asn Ala Pro Leu Val Asn Val	
50 55 60	

acc ctc tac tat gaa gca ctg tgc ggt ggc tgc cga gcc ttc ctg atc	417
Thr Leu Tyr Tyr Glu Ala Leu Cys Gly Gly Cys Arg Ala Phe Leu Ile	
65 70 75 80	
cgg gag ctc ttc cca aca tgg ctg ttg gtc atg gag atc ctc aat gtc	465
Arg Glu Leu Phe Pro Thr Trp Leu Leu Val Met Glu Ile Leu Asn Val	
85 90 95	
acg ctg gtg ccc tac gga aac gca cag gaa caa aat gtc agt ggc agg	513
Thr Leu Val Pro Tyr Gly Asn Ala Gln Glu Gln Asn Val Ser Gly Arg	
100 105 110	
tgg gag ttc aag tgc cag cat gga gaa gag gag tgc aaa ttc aac aag	561
Trp Glu Phe Lys Cys Gln His Gly Glu Glu Glu Cys Lys Phe Asn Lys	
115 120 125	
gtg gag gcc tgc gtg ttg gat gaa ctt gac atg gag cta gcc ttc ctg	609
Val Glu Ala Cys Val Leu Asp Glu Leu Asp Met Glu Leu Ala Phe Leu	
130 135 140	
acc att gtc tgc atg gaa gag ttt gag gac atg gag aga agt ctg cca	657
Thr Ile Val Cys Met Glu Glu Phe Glu Asp Met Glu Arg Ser Leu Pro	
145 150 155 160	
cta tgc ctg cag ctc tac gcc cca ggg ctg tgc cca gac act atc atg	705
Leu Cys Leu Gln Leu Tyr Ala Pro Gly Leu Ser Pro Asp Thr Ile Met	
165 170 175	
gag tgt gca atg ggg gac cgc ggc atg cag ctc atg cac gcc aac gcc	753
Glu Cys Ala Met Gly Asp Arg Gly Met Gln Leu Met His Ala Asn Ala	
180 185 190	
cag cgg aca gat gct ctc cag cca cca cac gag tat gtg ccc tgg gtc	801
Gln Arg Thr Asp Ala Leu Gln Pro Pro His Glu Tyr Val Pro Trp Val	
195 200 205	
acc gtc aat ggg aaa ccc ctt gga aga tca gac cca gct cct tac cct	849
Thr Val Asn Gly Lys Pro Leu Gly Arg Ser Asp Pro Ala Pro Tyr Pro	
210 215 220	
tgt ctg cca gtt gta cca ggg caa gaa gcc gga tgt ctg ccc ttc ctc	897
Cys Leu Pro Val Val Pro Gly Gln Glu Ala Gly Cys Leu Pro Phe Leu	
225 230 235 240	
aac cag ctc cct cag gag tgt ttg ctt caa gtg atg gcc ggt gag ctg	945
Asn Gln Leu Pro Gln Glu Cys Leu Leu Gln Val Met Ala Gly Glu Leu	
245 250 255	
cgg aga gct cat gga agg cga gtg gga acc cgg ctg cct gcc ttt ttt	993
Arg Arg Ala His Gly Arg Arg Val Gly Thr Arg Leu Pro Ala Phe Phe	
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Phe	

<210> 44

<211> 2753
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (2421)

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gcc gct gcc tcc caa gcc gag gtc gag tcc gag gca gga tgg ggc atg 96
 Ala Ala Ala Ser Gln Ala Glu Val Glu Ser Glu Ala Gly Trp Gly Met
 20 25 30

gtg acg cct gat ctg ctc ttc gcc gag ggg acc gca gcc tac gcg cgc 144
 Val Thr Pro Asp Leu Leu Phe Ala Glu Gly Thr Ala Ala Tyr Ala Arg
 35 40 45

ggg gac tgg ccc ggg gtg gtc ctg agc atg gaa cgg gcg ctg cgc tcc 192
 Gly Asp Trp Pro Gly Val Val Leu Ser Met Glu Arg Ala Leu Arg Ser
 50 55 60

cgg gca gcc ctc cgc gcc ctt cgc ctg cgc tgc cgc acc cag tgt gcc 240
 Arg Ala Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Gln Cys Ala
 65 70 75 80

gcc gac ttc ccg tgg gag ctg gac ccc gac tgg tcc ccc agc ccg gcc 288
 Ala Asp Phe Pro Trp Glu Leu Asp Pro Asp Trp Ser Pro Ser Pro Ala
 85 90 95

cag gcc tcg ggc gcc gcc gcc ctg cgc gac ctg agc ttc ttc ggg ggc 336
 Gln Ala Ser Gly Ala Ala Ala Leu Arg Asp Leu Ser Phe Phe Gly Gly
 100 105 110

ctt ctg cgt cgc gct gcc tgc ctg cgc cgc tgc ctc ggg ccg ccg gcc 384
 Leu Leu Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro Pro Ala
 115 120 125

gcc cac tcg ctc agc gaa gag atg gag ctg gag ttc cgc aag cgg agc 432
 Ala His Ser Leu Ser Glu Glu Met Glu Leu Glu Phe Arg Lys Arg Ser
 130 135 140

ccc tac aac tac ctg cag gtc gcc tac ttc aag gtg cag acc tgc ctg 480
 Pro Tyr Asn Tyr Leu Gln Val Ala Tyr Phe Lys Val Gln Thr Cys Leu
 145 150 155 160

gaa cca ggc ggc cgg ggt cct tct ggg gag agg agt gtt gca ggg gac 528
 Glu Pro Gly Gly Arg Gly Pro Ser Gly Glu Arg Ser Val Ala Gly Asp
 165 170 175

ctg agg agc ttg ggg gat cgg gga agt gtc cgc agg gag ggg aaa gtg 576
 Leu Arg Ser Leu Gly Asp Arg Gly Ser Val Arg Arg Glu Gly Lys Val
 180 185 190

gcc tcc tgg ctg ggg agc tct cct cgg agc cgg gga gag ctg ctc cct 624
 Ala Ser Trp Leu Gly Ser Ser Pro Arg Ser Arg Gly Glu Leu Leu Pro
 195 200 205

ggc agg aga cct tcc tcg ccc agt tcg cat ggg cag atg cta acc cca Gly Arg Arg Pro Ser Ser Pro Ser Ser His Gly Gln Met Leu Thr Pro 210 215 220	672
aag atc aac aag ttg gag aaa gct gtt gct gca gca cac acc ttc ttc Lys Ile Asn Lys Leu Glu Lys Ala Val Ala Ala His Thr Phe Phe 225 230 235 240	720
gtg ggc aat cct gag cac atg gaa atg cag cag aac cta gac tat tac Val Gly Asn Pro Glu His Met Glu Met Gln Gln Asn Leu Asp Tyr Tyr 245 250 255	768
caa acc atg tct gga gtg aag gag gcc gac ttc aag gat ctt gag act Gln Thr Met Ser Gly Val Lys Glu Ala Asp Phe Lys Asp Leu Glu Thr 260 265 270	816
caa ccc cat atg caa gaa ttt cga ctg gga gtg cga ctc tac tca gag Gln Pro His Met Gln Glu Phe Arg Leu Gly Val Arg Leu Tyr Ser Glu 275 280 285	864
gaa cag cca cag gaa gct gtg ccc cac cta gag gcg gcg ctg caa gaa Glu Gln Pro Gln Glu Ala Val Pro His Leu Glu Ala Ala Leu Gln Glu 290 295 300	912
tac ttt gtg gcc tat gag gag tgc cgt gcc ctc tgc gaa ggg ccc tat Tyr Phe Val Ala Tyr Glu Glu Cys Arg Ala Leu Cys Glu Gly Pro Tyr 305 310 315 320	960
gac tac gat ggc tac aac tac ctt gag tac aac gct gac ctc ttc cag Asp Tyr Asp Gly Tyr Asn Tyr Leu Glu Tyr Asn Ala Asp Leu Phe Gln 325 330 335	1008
gcc atc aca gat cat tac atc cag gtc ctc aac tgt aag cag aac tgt Ala Ile Thr Asp His Tyr Ile Gln Val Leu Asn Cys Lys Gln Asn Cys 340 345 350	1056
gtc acg gag ctt gct tcc cac cca agt cga gag aag ccc ttt gaa gac Val Thr Glu Leu Ala Ser His Pro Ser Arg Glu Lys Pro Phe Glu Asp 355 360 365	1104
ttc ctc cca tcg cat tat aat tat ctg cag ttt gcc tac tat aac att Phe Leu Pro Ser His Tyr Asn Tyr Leu Gln Phe Ala Tyr Tyr Asn Ile 370 375 380	1152
ggg aat tat aca cag gct gtt gaa tgt gcc aag acc tat ctt ctc ttc Gly Asn Tyr Thr Gln Ala Val Glu Cys Ala Lys Thr Tyr Leu Leu Phe 385 390 395 400	1200
ttc ccc aat gac gag gtg atg aac caa aat ttg gcc tat tat gca gct Phe Pro Asn Asp Glu Val Met Asn Gln Asn Leu Ala Tyr Tyr Ala Ala 405 410 415	1248
atg ctt gga gaa gaa cac acc aga tcc atc ggc ccc cgt gag agt gcc Met Leu Gly Glu Glu His Thr Arg Ser Ile Gly Pro Arg Glu Ser Ala 420 425 430	1296
aag gag tac cga cag cga agc cta ctg gaa aaa gaa ctg ctt ttc ttc Lys Glu Tyr Arg Gln Arg Ser Leu Leu Glu Lys Glu Leu Leu Phe Phe 435 440 445	1344
gct tat gat gtt ttt gga att ccc ttt gtg gat ccg gat tca tgg act	1392

Ala	Tyr	Asp	Val	Phe	Gly	Ile	Pro	Phe	Val	Asp	Pro	Asp	Ser	Trp	Thr		
450						455					460						
cca	gaa	gaa	gtg	att	ccc	aag	aga	ttg	caa	gag	aaa	cag	aag	tca	gaa	1440	
Pro	Glu	Glu	Val	Ile	Pro	Lys	Arg	Leu	Gln	Glu	Lys	Gln	Lys	Ser	Glu		
465					470					475					480		
cgg	gaa	aca	gcc	gta	cgc	atc	tcc	cag	gag	att	ggg	aac	ctt	atg	aag	1488	
Arg	Glu	Thr	Ala	Val	Arg	Ile	Ser	Gln	Glu	Ile	Gly	Asn	Leu	Met	Lys		
				485					490					495			
gaa	atc	gag	acc	ctt	gtg	gaa	gag	aag	acc	aag	gag	tca	ctg	gat	gtg	1536	
Glu	Ile	Glu	Thr	Leu	Val	Glu	Glu	Lys	Thr	Lys	Glu	Ser	Leu	Asp	Val		
			500					505					510				
agc	aga	ctg	acc	cgg	gaa	ggg	ggc	ccc	ctg	ctg	tat	gaa	ggc	atc	agt	1584	
Ser	Arg	Leu	Thr	Arg	Glu	Gly	Gly	Pro	Leu	Leu	Tyr	Glu	Gly	Ile	Ser		
		515					520					525					
ctc	acc	atg	aac	tcc	aaa	ctc	ctg	aat	ggg	tcc	cag	cgg	gtg	gtg	atg	1632	
Leu	Thr	Met	Asn	Ser	Lys	Leu	Leu	Asn	Gly	Ser	Gln	Arg	Val	Val	Met		
		530				535					540						
gac	ggc	gta	atc	tct	gac	cac	gag	tgt	cag	gag	ctg	cag	aga	ctg	acc	1680	
Asp	Gly	Val	Ile	Ser	Asp	His	Glu	Cys	Gln	Glu	Leu	Gln	Arg	Leu	Thr		
545					550					555					560		
aat	gtg	gca	gca	acc	tca	gga	gat	ggc	tac	cgg	ggg	cag	acc	tcc	cca	1728	
Asn	Val	Ala	Ala	Thr	Ser	Gly	Asp	Gly	Tyr	Arg	Gly	Gln	Thr	Ser	Pro		
				565					570					575			
cat	act	ccc	aat	gaa	aag	ttc	tat	ggg	gtc	act	gtc	ttc	aaa	gcc	ctc	1776	
His	Thr	Pro	Asn	Glu	Lys	Phe	Tyr	Gly	Val	Thr	Val	Phe	Lys	Ala	Leu		
			580					585					590				
aag	ctg	ggg	caa	gaa	ggc	aaa	gtt	cct	ctg	cag	agt	gcc	cac	ctg	tac	1824	
Lys	Leu	Gly	Gln	Glu	Gly	Lys	Val	Pro	Leu	Gln	Ser	Ala	His	Leu	Tyr		
		595					600					605					
tac	aac	gtg	acg	gag	aag	gtg	cgg	cgc	atc	atg	gag	tcc	tac	ttc	cgc	1872	
Tyr	Asn	Val	Thr	Glu	Lys	Val	Arg	Arg	Ile	Met	Glu	Ser	Tyr	Phe	Arg		
		610				615					620						
ctg	gat	acg	ccc	ctc	tac	ttt	tcc	tac	tct	cat	ctg	gtg	tgc	cgc	act	1920	
Leu	Asp	Thr	Pro	Leu	Tyr	Phe	Ser	Tyr	Ser	His	Leu	Val	Cys	Arg	Thr		
					630					635					640		
gcc	atc	gaa	gag	gtc	cag	gca	gag	agg	aag	gat	gat	agt	cat	cca	gtc	1968	
Ala	Ile	Glu	Glu	Val	Gln	Ala	Glu	Arg	Lys	Asp	Asp	Ser	His	Pro	Val		
				645					650					655			
cac	gtg	gac	aac	tgc	atc	ctg	aat	gcc	gag	acc	ctc	gtg	tgt	gtc	aaa	2016	
His	Val	Asp	Asn	Cys	Ile	Leu	Asn	Ala	Glu	Thr	Leu	Val	Cys	Val	Lys		
			660					665					670				
gag	ccc	cca	gcc	tac	acc	ttc	cgc	gac	tac	agc	gcc	atc	ctt	tac	cta	2064	
Glu	Pro	Pro	Ala	Tyr	Thr	Phe	Arg	Asp	Tyr	Ser	Ala	Ile	Leu	Tyr	Leu		
		675					680					685					
aat	ggg	gac	ttc	gat	ggc	gga	aac	ttt	tat	ttc	act	gaa	ctg	gat	gcc	2112	
Asn	Gly	Asp	Phe	Asp	Gly	Gly	Asn	Phe	Tyr	Phe	Thr	Glu	Leu	Asp	Ala		

690	695	700	
aag acc gtg acg gca gag gtg cag cct cag tgt gga aga gcc gtg gga Lys Thr Val Thr Ala Glu Val Gln Pro Gln Cys Gly Arg Ala Val Gly 705 710 715 720			2160
ttc tct tca ggc act gaa aac cca cat gga gtg aag gct gtc acc agg Phe Ser Ser Gly Thr Glu Asn Pro His Gly Val Lys Ala Val Thr Arg 725 730 735			2208
ggg cag cgc tgt gcc atc gcc ctg tgg ttc acc ctg gac cct cga cac Gly Gln Arg Cys Ala Ile Ala Leu Trp Phe Thr Leu Asp Pro Arg His 740 745 750			2256
agc gag cgg gac agg gtg cag gca gat gac ctg gtg aag atg ctc ttc Ser Glu Arg Asp Arg Val Gln Ala Asp Asp Leu Val Lys Met Leu Phe 755 760 765			2304
agc cca gaa gag atg gac ctc tcc cag gag cag ccc ctg gat gcc cag Ser Pro Glu Glu Met Asp Leu Ser Gln Glu Gln Pro Leu Asp Ala Gln 770 775 780			2352
cag ggc ccc ccc gaa cct gca caa gag tct ctc tca ggc agt gaa tcg Gln Gly Pro Pro Glu Pro Ala Gln Glu Ser Leu Ser Gly Ser Glu Ser 785 790 795 800			2400
aag ccc aag gat gag cta tga ca gcgtccaggt cagacggatg ggtgactaga Lys Pro Lys Asp Glu Leu 805			2453
cccatggaga ggaactcttc tgcactctga gctggccagc ccctcggggc tgcagagcag			2513
tgagcctaca tctgccactc agccgagggg accctgctca cagccttcta catggtgcta			2573
ctgctcttgg agtggacatg accagacacc gcacccctg gatctggctg agggctcagg			2633
acacaggccc agccaccccc aggggcctcc acaggccgct gcataacagc gatacagtac			2693
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<211> 1476

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<213> Homo sapiens

<220>

<221> CDS

<222> (633)..(1367)

<400> 45

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gtgtcaaagg gtcagctcaa taggggtgat tcaggggtgtg ctccatgatg gtcaaaagcg	120
ccagccacgt ctcttggct gtggggatga tctgggaggc tggcagcagg aagccatagc	180
gccagtgctc ccggagctcg aaggtgaagg agtacttgat gccctggctg taggtccagt	240

caatagtgct tccactggct tgataaattg ccttgatgat gctgccatag ttgaacttgg	300
tcccgtagag agaggccagg gctgtcacag cagccttggga aagctgatcc agctcaccct	360
ggtcagggac tggttctgtt ttgtagccat agggatacat gaggagctgg gagtagctgt	420
ggatggagat gaaggccttg atgttcccat ggtccttcac aaagtctaca atggacttga	480
cctccacttc ggaattggca aacttgccgt ggtaagtctc cgagcagggg ttactgctgg	540
ctccggacaa cccaaagcca gcgtcccagt tcctgttggg gtccacgcca atacagaggg	600
agcctgctgt gtgggaccga gtcttgccgc ac atg cga ttc gtg ctg tgc gtg	653
Met Arg Phe Val Leu Cys Val	
1 5	
aag gca aag cca tca ggg ttg gtg acg atc tcc agg aag atc act caa	701
Lys Ala Lys Pro Ser Gly Leu Val Thr Ile Ser Arg Lys Ile Thr Gln	
10 15 20	
gac tac ggg cag gat gca gct ttc acc gcc att ctc gac acc ttg gac	749
Asp Tyr Gly Gln Asp Ala Ala Phe Thr Ala Ile Leu Asp Thr Leu Asp	
25 30 35	
atc ttc ctg gag atc gtc acc aac cct gat ggc ttt gcc ttc acg cac	797
Ile Phe Leu Glu Ile Val Thr Asn Pro Asp Gly Phe Ala Phe Thr His	
40 45 50 55	
agc acg aat cgc atg tgg cgc aag act cgg tcc cac aca gca ggc tcc	845
Ser Thr Asn Arg Met Trp Arg Lys Thr Arg Ser His Thr Ala Gly Ser	
60 65 70	
ctc tgt att ggc gtg gac ccc aac agg aac tgg gac gct ggc ttt ggg	893
Leu Cys Ile Gly Val Asp Pro Asn Arg Asn Trp Asp Ala Gly Phe Gly	
75 80 85	
ttg tcc gga gcc agc agt aac ccc tgc tgc gag act tac cac ggc aag	941
Leu Ser Gly Ala Ser Ser Asn Pro Cys Ser Glu Thr Tyr His Gly Lys	
90 95 100	
ttt gcc aat tcc gaa gtg gag gtc aag tcc att gta gac ttt gtg aag	989
Phe Ala Asn Ser Glu Val Glu Val Lys Ser Ile Val Asp Phe Val Lys	
105 110 115	
gac cat ggg aac atc aag gcc ttc atc tcc atc cac agc tac tcc cag	1037
Asp His Gly Asn Ile Lys Ala Phe Ile Ser Ile His Ser Tyr Ser Gln	
120 125 130 135	
ctc ctc atg tat ccc tat ggc tac aaa aca gaa cca gtc cct gac cag	1085
Leu Leu Met Tyr Pro Tyr Gly Tyr Lys Thr Glu Pro Val Pro Asp Gln	
140 145 150	
gat gag ctg gat cag ctt tcc aag gct gct gtg aca gcc ctg gcc tct	1133
Asp Glu Leu Asp Gln Leu Ser Lys Ala Ala Val Thr Ala Leu Ala Ser	
155 160 165	
ctc tac ggg acc aag ttc aac tat ggc agc atc atc aag gca att tat	1181
Leu Tyr Gly Thr Lys Phe Asn Tyr Gly Ser Ile Ile Lys Ala Ile Tyr	
170 175 180	
caa gcc agt gga agc act att gac tgg acc tac agc cag ggc atc aag	1229

Gln Ala Ser Gly Ser Thr Ile Asp Trp Thr Tyr Ser Gln Gly Ile Lys
 185 190 195

tac tcc ttc acc ttc gag ctc cgg gac act ggg cgc tat ggc ttc ctg 1277
 Tyr Ser Phe Thr Phe Glu Leu Arg Asp Thr Gly Arg Tyr Gly Phe Leu
 200 205 210 215

ctg cca gcc tcc cag atc atc ccc aca gcc aag gag acg tgg ctg gcg 1325
 Leu Pro Ala Ser Gln Ile Ile Pro Thr Ala Lys Glu Thr Trp Leu Ala
 220 225 230

ctt ctg acc atc atg gag cac acc ctg aat cac ccc tac tga gctgacc 1374
 Leu Leu Thr Ile Met Glu His Thr Leu Asn His Pro Tyr
 235 240

ctttgacacc cttcttgtcc tcctctctgg ccccatccag gcaaccaaataaagtttgag 1434

tgtaccagga acagaatcct ggggcttgca aaaaaaaaaa aa 1476

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 <211> 1769
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (137)..(1753)

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gccgtcgccc aggatgggct gggaatgaag cgatgtagcc ttttaagaga tttgctctga 120

cccatctgaa gtccat atg gct ctg tat gat gaa gac ctc ctg aaa aat 169
 Met Ala Leu Tyr Asp Glu Asp Leu Leu Lys Asn
 1 5 10

cct ttc tat ctg gct ctg caa aag tgc cgc cct gac ttg tgc agc aaa 217
 Pro Phe Tyr Leu Ala Leu Gln Lys Cys Arg Pro Asp Leu Cys Ser Lys
 15 20 25

gtg gcc caa atc cat ggc att gtc tta gta ccc tgc aaa gga agc ctg 265
 Val Ala Gln Ile His Gly Ile Val Leu Val Pro Cys Lys Gly Ser Leu
 30 35 40

tgc agc agc atc cag tct act tgt cag ttt gag tcc tac att ttg ata 313
 Ser Ser Ser Ile Gln Ser Thr Cys Gln Phe Glu Ser Tyr Ile Leu Ile
 45 50 55

cct gtg gaa gag cat ttt cag acc tta aat gga aag gat gtc ttt att 361
 Pro Val Glu Glu His Phe Gln Thr Leu Asn Gly Lys Asp Val Phe Ile
 60 65 70 75

caa ggg aac agg att aaa tta gga gct ggt ttt gcc tgt ctt ctc tca 409
 Gln Gly Asn Arg Ile Lys Leu Gly Ala Gly Phe Ala Cys Leu Leu Ser
 80 85 90

gtg ccc att ctc ttt gaa gaa act ttc tac aat gaa aaa gaa gag agt 457

Val	Pro	Ile	Leu	Phe	Glu	Glu	Thr	Phe	Tyr	Asn	Glu	Lys	Glu	Glu	Ser		
			95					100					105				
ttc	agc	atc	ctg	tgt	ata	gcc	cat	cct	ttg	gaa	aag	aga	gag	agt	tca		505
Phe	Ser	Ile	Leu	Cys	Ile	Ala	His	Pro	Leu	Glu	Lys	Arg	Glu	Ser	Ser		
		110					115					120					
gaa	gag	cct	ttg	gca	ccc	tca	gat	ccc	ttt	tcc	ctg	aaa	acc	att	gaa		553
Glu	Glu	Pro	Leu	Ala	Pro	Ser	Asp	Pro	Phe	Ser	Leu	Lys	Thr	Ile	Glu		
		125				130					135						
gat	gtg	aga	gag	ttc	ttg	gga	aga	cac	tcc	gag	cga	ttt	gac	agg	aac		601
Asp	Val	Arg	Glu	Phe	Leu	Gly	Arg	His	Ser	Glu	Arg	Phe	Asp	Arg	Asn		
140					145					150					155		
atc	gcc	tct	ttc	cat	cga	aca	ttc	cga	gaa	tgc	gag	aga	aag	agc	ctc		649
Ile	Ala	Ser	Phe	His	Arg	Thr	Phe	Arg	Glu	Cys	Glu	Arg	Lys	Ser	Leu		
				160					165					170			
cgt	cac	cac	ata	gac	tca	gcg	aat	gct	ctc	tac	acc	aaa	tgc	ctc	cag		697
Arg	His	His	Ile	Asp	Ser	Ala	Asn	Ala	Leu	Tyr	Thr	Lys	Cys	Leu	Gln		
			175					180					185				
cag	ctt	ctg	agg	gac	tct	cac	ctg	aaa	atg	ctc	gcc	aag	cag	gag	gcc		745
Gln	Leu	Leu	Arg	Asp	Ser	His	Leu	Lys	Met	Leu	Ala	Lys	Gln	Glu	Ala		
		190					195					200					
cag	atg	aac	ctg	atg	aag	cag	gca	gtg	gag	ata	tac	gtc	cat	cat	gaa		793
Gln	Met	Asn	Leu	Met	Lys	Gln	Ala	Val	Glu	Ile	Tyr	Val	His	His	Glu		
	205					210				215							
att	tac	aac	ctg	atc	ttt	aaa	tac	gtg	ggg	acc	atg	gag	gca	agt	gag		841
Ile	Tyr	Asn	Leu	Ile	Phe	Lys	Tyr	Val	Gly	Thr	Met	Glu	Ala	Ser	Glu		
220					225					230					235		
gat	gcg	gcc	ttt	aac	aaa	atc	aca	aga	agc	ctt	caa	gat	ctt	cag	cag		889
Asp	Ala	Ala	Phe		Lys	Ile	Thr	Arg	Ser	Leu	Gln	Asp	Leu	Gln	Gln		
			240						245					250			
aaa	gat	att	ggt	gtg	aaa	ccg	gag	ttc	agc	ttt	aac	ata	cct	cgt	gcc		937
Lys	Asp	Ile	Gly	Val	Lys	Pro	Glu	Phe	Ser	Phe	Asn	Ile	Pro	Arg	Ala		
			255					260					265				
aaa	aga	gag	ctg	gct	cag	ctg	aac	aaa	tgc	acc	tcc	cca	cag	cag	aag		985
Lys	Arg	Glu	Leu	Ala	Gln	Leu	Asn	Lys	Cys	Thr	Ser	Pro	Gln	Gln	Lys		
		270					275					280					
ctt	gtc	tgc	ttg	cga	aaa	gtg	gtg	cag	ctc	att	aca	cag	tct	cca	agc		1033
Leu	Val	Cys	Leu	Arg	Lys	Val	Val	Gln	Leu	Ile	Thr	Gln	Ser	Pro	Ser		
		285				290					295						
cag	aga	gtg	aac	ctg	gag	acc	atg	tgt	gct	gat	gat	ctg	cta	tca	gtc		1081
Gln	Arg	Val	Asn	Leu	Glu	Thr	Met	Cys	Ala	Asp	Asp	Leu	Leu	Ser	Val		
300					305					310					315		
ctg	tta	tac	ttg	ctt	gtg	aaa	acg	gag	atc	cct	aat	tgg	atg	gca	aat		1129
Leu	Leu	Tyr	Leu	Leu	Val	Lys	Thr	Glu	Ile	Pro	Asn	Trp	Met	Ala	Asn		
				320					325					330			
ttg	agt	tac	atc	aaa	aac	ttc	agg	ttt	agc	agc	ttg	gca	aag	gat	gaa		1177
Leu	Ser	Tyr	Ile	Lys	Asn	Phe	Arg	Phe	Ser	Ser	Leu	Ala	Lys	Asp	Glu		

335	340	345	
ctg gga tac tgc ctg acc tca ttc gaa gct gcc att gaa tat att cgg			1225
Leu Gly Tyr Cys Leu Thr Ser Phe Glu Ala Ala Ile Glu Tyr Ile Arg			
350	355	360	
caa gga agc ctc tct gct aaa ccc cct gag tct gag gga ttt gga gac			1273
Gln Gly Ser Leu Ser Ala Lys Pro Pro Glu Ser Glu Gly Phe Gly Asp			
365	370	375	
agg ctg ttc ctt aag cag aga atg agc tta ctc tct cag atg act tcg			1321
Arg Leu Phe Leu Lys Gln Arg Met Ser Leu Ser Gln Met Thr Ser			
380	385	390	395
tct ccc acc gac tgc ctg ttt aag cac att gca tca ggt aac cag aaa			1369
Ser Pro Thr Asp Cys Leu Phe Lys His Ile Ala Ser Gly Asn Gln Lys			
400	405	410	
gaa gtg gag aga ctt ctg agc caa gag gac cat gat aaa gat acc gtc			1417
Glu Val Glu Arg Leu Leu Ser Gln Glu Asp His Asp Lys Asp Thr Val			
415	420	425	
caa aag atg tgt cac cct ctc tgc ttc tgc gat gac tgt gag aaa ctc			1465
Gln Lys Met Cys His Pro Leu Cys Phe Cys Asp Asp Cys Glu Lys Leu			
430	435	440	
gtc tct ggg agg ttg aat gat ccc tca gtt gtc act cca ttc tcc aga			1513
Val Ser Gly Arg Leu Asn Asp Pro Ser Val Val Thr Pro Phe Ser Arg			
445	450	455	
gac gac agg ggg cac acc cct ctc cat gtg gct gct gtc tgt ggg cag			1561
Asp Asp Arg Gly His Thr Pro Leu His Val Ala Ala Val Cys Gly Gln			
460	465	470	475
gca tcc ctc atc gac ctc ctg gtt tcc aag ggc gcc atg gta aat gcc			1609
Ala Ser Leu Ile Asp Leu Leu Val Ser Lys Gly Ala Met Val Asn Ala			
480	485	490	
aca gac tac cat gga gcc act ccg ctc cac ctg gcc tgt cag aag ggc			1657
Thr Asp Tyr His Gly Ala Thr Pro Leu His Leu Ala Cys Gln Lys Gly			
495	500	505	
tac cag agc gtg acg ctg ctg ctg ctg cac tac aag gcc agc gcg gaa			1705
Tyr Gln Ser Val Thr Leu Leu Leu Leu His Tyr Lys Ala Ser Ala Glu			
510	515	520	
gtg cag gac aac aat ggg aat acg cca cat gta ttg cgg ccg ctc tag			1753
Val Gln Asp Asn Asn Gly Asn Thr Pro His Val Leu Arg Pro Leu			
525	530	535	
aggatcccag ctaacg			1769

<210> 47
 <211> 1501
 <212> DNA
 <213> Homo sapiens
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<221> CDS

<222> (749) .. (1447)

<400> 47

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caagctggca gacatgggtg ctctctggag ccgtcagaga gggcagagag ctctgtggttt      120
atggtgtaaa ggctgggagc ttggaggggg tctgtgtgtg ggctggactc tgaggcggcc      180
agaggcctag gaacgttatc ctgggcacac cgtgcgtggt gtgcagtctg agtcatgctc      240
cctgggtagg gcatccagct cccagcctgg gagtgctgag agccaaatcc accgtagagc      300
aggggtgaga gtcagggtcc cacctcctct atctgccggc aatccagtgg tgacctaggg      360
taaaagcttg agagtcccat acacacggtc atcccacgac atacctcaca ggccaggcag      420
ggacacacag cccctctccc tccctccag gtaccgtcat agctgctagt gtgactgaag      480
gcagtgtccc tggccccagc tgaagcaccg tagccagcca gcgggctcac gcaccttggc      540
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gaggctcccc tcttagactt ataagtct   atg gcc act ggc atc egg ctg cct      772
                                Met Ala Thr Gly Ile Arg Leu Pro
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gcc ctc cct gcc tcc ccc agg gtc cct tca gag ggt cct ggg ttt tct      820
Ala Leu Pro Ala Ser Pro Arg Val Pro Ser Glu Gly Pro Gly Phe Ser
    10                               15                               20

gaa cac cca gag ggg cct ccg gcg ctc cct cca gcc atc cct ttt agt      868
Glu His Pro Glu Gly Pro Pro Ala Leu Pro Pro Ala Ile Pro Phe Ser
    25                               30                               35                               40

ttc acc ctc ctg gtt caa gca gtg ttc ttt ctc tat cag gcc tgg tgg      916
Phe Thr Leu Leu Val Gln Ala Val Phe Phe Leu Tyr Gln Ala Trp Trp
                45                               50                               55

ctg ttg cat ggg gct ccc caa ggc aag ggg tgg ccc cag gcc agt ggg      964
Leu Leu His Gly Ala Pro Gln Gly Lys Gly Trp Pro Gln Ala Ser Gly
                60                               65                               70

ttg gaa gac agg gtg acc aga gaa gag gga agc ccg agg ggg ccg agc      1012
Leu Glu Asp Arg Val Thr Arg Glu Glu Gly Ser Pro Arg Gly Pro Ser
                75                               80                               85

atc agc ctg aat tgc ggg tgc cct gcc tgg gtg ccg tgt gag agg cca      1060
Ile Ser Leu Asn Cys Gly Cys Pro Ala Trp Val Pro Cys Glu Arg Pro
                90                               95                               100

gcg tgt gtg ggg tgg gga ggg ccg cca cag ccc cca ggc gct atc tgt      1108
Ala Cys Val Gly Trp Gly Gly Pro Pro Gln Pro Pro Gly Ala Ile Cys
    105                               110                               115                               120

gaa gct acg gct cct ccc tcc atc ttc ctc ccc ttt ccc ttc cag ccc      1156

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Glu	Ala	Thr	Ala	Pro	Pro	Ser	Ile	Phe	Leu	Pro	Phe	Pro	Phe	Gln	Pro		
				125					130					135			
ctt	ttc	cag	gaa	cct	tgc	cac	acc	cac	acc	tgc	agc	ctc	ccc	tcc	ccg		1204
Leu	Phe	Gln	Glu	Pro	Cys	His	Thr	His	Thr	Cys	Ser	Leu	Pro	Ser	Pro		
				140				145					150				
gcc	ctc	cca	cca	ctg	ctg	cgg	cgc	ggc	cgg	ccc	cgg	ccg	tgt	gct	gcg		1252
Ala	Leu	Pro	Pro	Leu	Leu	Arg	Arg	Gly	Arg	Pro	Arg	Pro	Cys	Ala	Ala		
				155				160					165				
ctt	gcc	tta	cca	gct	ctc	tcc	tcg	ctt	ttc	tct	ccc	gtt	ttc	tct	ctg		1300
Leu	Ala	Leu	Pro	Ala	Leu	Ser	Ser	Leu	Phe	Ser	Pro	Val	Phe	Ser	Leu		
				170				175				180					
ctt	tct	ctc	caa	ctg	cca	gcc	gat	cgg	gtc	agg	caa	gtc	cat	ccc	gtc		1348
Leu	Ser	Leu	Gln	Leu	Pro	Ala	Asp	Arg	Val	Arg	Gln	Val	His	Pro	Val		
				185		190				195					200		
ctg	aga	gcc	cca	ggc	ccc	cct	tcg	acc	tct	aaa	cag	atc	cct	cct	ctt		1396
Leu	Arg	Ala	Pro	Gly	Pro	Pro	Ser	Thr	Ser	Lys	Gln	Ile	Pro	Pro	Leu		
				205					210					215			
ctc	gga	gac	ctc	cct	ttc	caa	gcc	tgc	ctg	gac	ggc	tgt	tct	gtg	act		1444
Leu	Gly	Asp	Leu	Pro	Phe	Gln	Ala	Cys	Leu	Asp	Gly	Cys	Ser	Val	Thr		
				220				225						230			
tga	cagt	ggctccccca	gccccaaagc	cagccccctt	catctgtgac	ttaatctgtt											1501

<210> 48
 <211> 659
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (250)..(567)

<400> 48																	
tcccgtgtcg	acgatttcgt	ggctgccact	gtggggcttc	tgccggccgg	tagtccttgg												60
cgctgctgac	ccagcatcgg	cttttctacg	tcttgaacct	ggattcgcct	aggggttggg												120
aagggctgtg	gacggcggtg	ggggaggcct	gacgagatta	ataaagaact	cttcagaatt												180
cctggtgttt	catcatatat	acgactaaga	tatcaactct	tctagcttgc	tgtctctgga												240
ccaaaaaaa	atg acg tct att atc aaa tta act acc ctt tct ggg gtc																288
	Met Thr Ser Ile Ile Lys Leu Thr Thr Leu Ser Gly Val																
	1			5									10				
caa gaa gaa tct gcc ctt tgc tat ctt ctc caa gtt gat gag ttt aga																	336
Gln Glu Glu Ser Ala Leu Cys Tyr Leu Leu Gln Val Asp Glu Phe Arg																	
	15			20								25					

```

ttt tta ttg gac tgt ggc tgg gat gag cac ttt tct atg gat att att      384
Phe Leu Leu Asp Cys Gly Trp Asp Glu His Phe Ser Met Asp Ile Ile
 30                      35                      40                      45

gat tcc ctg agg aag cat gtt cac cag att gat gca gtg ctg ttg tct      432
Asp Ser Leu Arg Lys His Val His Gln Ile Asp Ala Val Leu Leu Ser
                      50                      55                      60

cac cct gat cct ctc cac ctt ggt gcc ctc ccg tat gct gtc gga aag      480
His Pro Asp Pro Leu His Leu Gly Ala Leu Pro Tyr Ala Val Gly Lys
                      65                      70                      75

ttg ggt ctg aac tgt gct atc tat gca act att cct gtt tat aaa atg      528
Leu Gly Leu Asn Cys Ala Ile Tyr Ala Thr Ile Pro Val Tyr Lys Met
                      80                      85                      90

gga cag atg ttc atg tat gat ctt tat cag gta att taa gcaattaa      577
Gly Gln Met Phe Met Tyr Asp Leu Tyr Gln Val Ile
                      95                      100                      105

aaattttgtt agcactcctt cagtgattgt ttttcacctt tatttgtgtt attccttttag      637

tctcgacaca atacagaaga tg      659

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<210> 49
 <211> 1486
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (187) .. (1188)

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<400> 49
ggaattccccg ggtcgacgat ttcgtgcgac ggctgctgtg tctcctggaa agggattccc      60

gaaagggtttt attccaaaag gagagggttg aagacatagc tcatctcctg ctgtgtatca      120

gccaaagaagg tgtgaggttg tggtccttgg ggatccgctt gcactactt ggggtggttt      180

tgaaac      atg aat ctt tcg ctc gtc ctg gct gcc ttt tgc ttg gga ata      228
      Met Asn Leu Ser Leu Val Leu Ala Ala Phe Cys Leu Gly Ile
              1                      5                      10

gcc tcc gct gtt cca aaa ttt gac caa aat ttg gat aca aag tgg tac      276
Ala Ser Ala Val Pro Lys Phe Asp Gln Asn Leu Asp Thr Lys Trp Tyr
 15                      20                      25                      30

cag tgg aag gca aca cac aga aga tta tat ggc gcg aat gaa gaa gga      324
Gln Trp Lys Ala Thr His Arg Arg Leu Tyr Gly Ala Asn Glu Glu Gly
                      35                      40                      45

tgg agg aga gca gtg tgg gaa aag aat atg aaa atg att gaa ctg cac      372
Trp Arg Arg Ala Val Trp Glu Lys Asn Met Lys Met Ile Glu Leu His
                      50                      55                      60

aat ggg gaa tac agc caa ggg aaa cac agc ttc aca atg gcc atg aat      420
Asn Gly Glu Tyr Ser Gln Gly Lys His Ser Phe Thr Met Ala Met Asn

```

65	70	75	
gcc ttt gga gac atg acc aat gaa gaa ttc agg cag gtg atg aat ggt Ala Phe Gly Asp Met Thr Asn Glu Glu Phe Arg Gln Val Met Asn Gly 80 85 90			468
ttt caa tac cag aag cac agg aag ggg aaa cag ttc cag gaa cgc ctg Phe Gln Tyr Gln Lys His Arg Lys Gly Lys Gln Phe Gln Glu Arg Leu 95 100 105 110			516
ctt ctt gag atc ccc aca tct gtg gac tgg aga gag aaa ggc tac atg Leu Leu Glu Ile Pro Thr Ser Val Asp Trp Arg Glu Lys Gly Tyr Met 115 120 125			564
act cct gtg aag gat cag ggt cag tgt ggc tct tgt tgg gct ttt agt Thr Pro Val Lys Asp Gln Gly Gln Cys Gly Ser Cys Trp Ala Phe Ser 130 135 140			612
gca act ggt gct ctg gaa ggg cag atg ttc tgg aaa aca ggc aaa ctt Ala Thr Gly Ala Leu Glu Gly Gln Met Phe Trp Lys Thr Gly Lys Leu 145 150 155			660
atc tca ctg aat gag cag aat ctg gta gac tgc tct ggg cct caa ggc Ile Ser Leu Asn Glu Gln Asn Leu Val Asp Cys Ser Gly Pro Gln Gly 160 165 170			708
aat gag ggc tgc aat ggt gac ttc atg gat aat ccc ttc cgg tat gtt Asn Glu Gly Cys Asn Gly Asp Phe Met Asp Asn Pro Phe Arg Tyr Val 175 180 185 190			756
cag gag aac gga ggc ctg gac tct gag gaa tcc tat cca tat gag gca Gln Glu Asn Gly Gly Leu Asp Ser Glu Glu Ser Tyr Pro Tyr Glu Ala 195 200 205			804
aca gaa gaa tcc tgt aag tac aat ccc aag tat tct gtt gct aat gac Thr Glu Glu Ser Cys Lys Tyr Asn Pro Lys Tyr Ser Val Ala Asn Asp 210 215 220			852
acc ggc ttt gtg gac atc cct aag cag gag aag gcc ctg atg aag gca Thr Gly Phe Val Asp Ile Pro Lys Gln Glu Lys Ala Leu Met Lys Ala 225 230 235			900
gtt gca act gtg ggg ccc att tct gtt gct att gat gca ggt cat gag Val Ala Thr Val Gly Pro Ile Ser Val Ala Ile Asp Ala Gly His Glu 240 245 250			948
tcc ttc ctg ttc tat aaa gaa ggc att tat ttt gag cca gac tgt agc Ser Phe Leu Phe Tyr Lys Glu Gly Ile Tyr Phe Glu Pro Asp Cys Ser 255 260 265 270			996
agt gaa gac atg gat cat ggt gtg ctg gtg gtt ggc tac gga ttt gaa Ser Glu Asp Met Asp His Gly Val Leu Val Val Gly Tyr Gly Phe Glu 275 280 285			1044
agc aca gaa tca gat aac aat aaa tat tgg ctg gtg aag aac agc tgg Ser Thr Glu Ser Asp Asn Asn Lys Tyr Trp Leu Val Lys Asn Ser Trp 290 295 300			1092
ggc gaa gaa tgg ggc atg ggt ggc tac gta aag atg gcc aaa gac cgg Gly Glu Glu Trp Gly Met Gly Gly Tyr Val Lys Met Ala Lys Asp Arg 305 310 315			1140

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aga aac cat tgt gga att gcc tca gca gcc agc tac ccc act gtg tga      1188
Arg Asn His Cys Gly Ile Ala Ser Ala Ala Ser Tyr Pro Thr Val
    320                      325                      330

gctggtggac ggtgatgagg aaggacttga ctggggatgg cgcattgcatg ggaggaattc      1248

atcttcagtc taccagcccc cgctgtgtcg gatacacact cgaatcattg aagatccgag      1308

tgtgatttga attctgtgat attttcacac tggtaaattgt tacctctatt ttaattactg      1368

ctataaatag gtttatatta ttgattcact tactgacttt gcatttttcgt ttttaaaagg      1428

atgtataaat ttttacctgt ttaaataaaa ttttaatttca aatgtaaaaa aaaaaaaaa      1486

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<210> 50
<211> 799
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (123) .. (749)

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<400> 50
tgcacgaggc gggaatgggc cccaggetct cgtcctgagc ggtcggctgg acgtggggggc      60

gccactgacc accgtggaga agcccggggg aggggaggtg ctttctggct gcacactgac      120

ct  atg ttg ggg tgc cag ggc agg atg tac acg ctg ctg tcg ggc ttg      167
    Met Leu Gly Cys Gln Gly Arg Met Tyr Thr Leu Leu Ser Gly Leu
        1              5              10              15

tac aag tac atg ttt cag aag gac gag tac tgc atc ctg atc ctg ggc      215
Tyr Lys Tyr Met Phe Gln Lys Asp Glu Tyr Cys Ile Leu Ile Leu Gly
        20              25              30

ctg gac aat gct ggg aag acg acc ttc ctg gag cag tcg aaa acc cga      263
Leu Asp Asn Ala Gly Lys Thr Thr Phe Leu Glu Gln Ser Lys Thr Arg
        35              40              45

ttt aac aag aac tac aag ggg atg agt cta tcc aaa atc acc acc acc      311
Phe Asn Lys Asn Tyr Lys Gly Met Ser Leu Ser Lys Ile Thr Thr Thr
        50              55              60

gtg ggc cta aac atc ggc act gtg gat gtg gga aag gct cgg ctc atg      359
Val Gly Leu Asn Ile Gly Thr Val Asp Val Gly Lys Ala Arg Leu Met
        65              70              75

ttc tgg gac tta gga ggg cag gaa gag ctg cag tct ttg tgg gac aag      407
Phe Trp Asp Leu Gly Gly Gln Glu Glu Leu Gln Ser Leu Trp Asp Lys
        80              85              90              95

tat tat gcg gag tgt cac ggc gtc atc tac gtc att gac tcc acc gac      455
Tyr Tyr Ala Glu Cys His Gly Val Ile Tyr Val Ile Asp Ser Thr Asp
        100              105              110

gag gag agg ctg gct gag tcc aag cag gcg ttt gag aag gtg gtg acc      503

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Glu	Glu	Arg	Leu	Ala	Glu	Ser	Lys	Gln	Ala	Phe	Glu	Lys	Val	Val	Thr		
			115					120					125				
agc	gag	gcg	ctg	tgc	ggt	gtc	ccc	gtc	ttg	gtg	ctg	gcc	aac	aag	cag		551
Ser	Glu	Ala	Leu	Cys	Gly	Val	Pro	Val	Leu	Val	Leu	Ala	Asn	Lys	Gln		
			130				135					140					
gat	gtg	gag	acg	tgc	ctc	tca	atc	cct	gac	atc	aag	acg	gcc	ttc	agc		599
Asp	Val	Glu	Thr	Cys	Leu	Ser	Ile	Pro	Asp	Ile	Lys	Thr	Ala	Phe	Ser		
			145				150				155						
gac	tgc	acc	agc	aag	atc	ggc	agg	cga	gat	tgc	ctg	acc	cag	gcc	tgc		647
Asp	Cys	Thr	Ser	Lys	Ile	Gly	Arg	Arg	Asp	Cys	Leu	Thr	Gln	Ala	Cys		
					165					170					175		
tcg	gcc	ctc	aca	ggc	aaa	ggg	gtg	cgc	gag	ggc	atc	gag	tgg	atg	gtg		695
Ser	Ala	Leu	Thr	Gly	Lys	Gly	Val	Arg	Glu	Gly	Ile	Glu	Trp	Met	Val		
				180					185					190			
aag	tgt	gtc	gtg	cgg	aat	gtg	cac	cgg	ccg	ccg	cgg	cag	agg	gac	atc		743
Lys	Cys	Val	Val	Arg	Asn	Val	His	Arg	Pro	Pro	Arg	Gln	Arg	Asp	Ile		
				195				200					205				
acg	tag	gcgcagccccg	cgcttgccccg	tccgggaacgg	ctgggtcccct	ggtgctggag											799
Thr																	

<210> 51
 <211> 1464
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (166) .. (855)

ctttgttcca	agtacagccc	cctaggactt	ttgaaatgca	gtctgccaca	tgggtgagaa												60
ggcatcaggg	cctggtaaca	ggcagtgagg	tatcagcagg	tgggaaataa	gttctctagt												120
gatggtaggg	ttggggaatg	ctcaagaaaa	ttgctaggct	gagaa	atg	cta	tca										174
						Met	Leu	Ser									1
gtg	gat	att	acc	agc	agg	tac	cgt	gca	ccc	agt	acc	tat	ctt	ctt	aac		222
Val	Asp	Ile	Thr	Ser	Arg	Tyr	Arg	Ala	Pro	Ser	Thr	Tyr	Leu	Leu	Asn		
			5			10					15						
tcc	ctg	aaa	gag	ggg	ctg	gaa	ggc	ctc	cat	ggt	gaa	tct	tgc	tct	tct		270
Ser	Leu	Lys	Glu	Gly	Leu	Glu	Gly	Leu	His	Gly	Glu	Ser	Cys	Ser	Ser		
			20		25				30						35		
ttt	ctc	ctg	ggg	ccc	tca	gtg	gcc	atg	aat	atg	cag	act	gca	ggg	ctt		318
Phe	Leu	Leu	Gly	Pro	Ser	Val	Ala	Met	Asn	Met	Gln	Thr	Ala	Gly	Leu		
				40					45					50			

gaa atg gac atc tgt gat ggg cat ttc cgc cag aat ggc ggc tgt ggc 366
 Glu Met Asp Ile Cys Asp Gly His Phe Arg Gln Asn Gly Gly Cys Gly
 55 60 65

tat gtg ctg aag cca gac ttc ctg cgt gat atc cag agt tct ttc cac 414
 Tyr Val Leu Lys Pro Asp Phe Leu Arg Asp Ile Gln Ser Ser Phe His
 70 75 80

cct gag aag ccc atc agc cct ttc aaa gcc cag act ctc tta atc cag 462
 Pro Glu Lys Pro Ile Ser Pro Phe Lys Ala Gln Thr Leu Leu Ile Gln
 85 90 95

gtg atc agc ggt cag caa ctc ccc aaa gtg gac aag acc aaa gag ggg 510
 Val Ile Ser Gly Gln Gln Leu Pro Lys Val Asp Lys Thr Lys Glu Gly
 100 105 110 115

tcc att gtg gat cca ctg gtg aaa gtg cag atc ttt ggc gtt cgt cta 558
 Ser Ile Val Asp Pro Leu Val Lys Val Gln Ile Phe Gly Val Arg Leu
 120 125 130

gac aca gca cgg cag gag acc aac tat gtg gag aac aat ggt ttt aat 606
 Asp Thr Ala Arg Gln Glu Thr Asn Tyr Val Glu Asn Asn Gly Phe Asn
 135 140 145

cca tac tgg ggg cag aca cta tgt ttc cgg gtg ctg gtg cct gaa ctt 654
 Pro Tyr Trp Gly Gln Thr Leu Cys Phe Arg Val Leu Val Pro Glu Leu
 150 155 160

gcc atg ctg cgt ttt gtg gta atg gat tat gac tgg aaa tcc cga aat 702
 Ala Met Leu Arg Phe Val Val Met Asp Tyr Asp Trp Lys Ser Arg Asn
 165 170 175

gac ttt att ggt cag tac acc ctg cct tgg acc tgc atg caa caa ggt 750
 Asp Phe Ile Gly Gln Tyr Thr Leu Pro Trp Thr Cys Met Gln Gln Gly
 180 185 190 195

tac cgc cac att cac ctg ctg tcc aaa gat ggc atc agc ctc cgc cca 798
 Tyr Arg His Ile His Leu Ser Lys Asp Gly Ile Ser Leu Arg Pro
 200 205 210

gct tcc atc ttt gtg tat atc tgc atc cag gaa ggc ctg gag ggg gat 846
 Ala Ser Ile Phe Val Tyr Ile Cys Ile Gln Glu Gly Leu Glu Gly Asp
 215 220 225

gag tcc tga ggtgggc atttcacggg aagggttggt gtgctggctt tagacgggga 902
 Glu Ser

gaaacatctg gaaggatgct cgagagaaca aatggagggtg gtgaaaatca agctttggat 962

tgtgcattcc taggcacaaa attacctcat tcttctaacc aagcaatctg ggacctgatt 1022

ttccaccttt tttctctttt cttcccttcc tttgttttca taagcctttg gtatctttcc 1082

tgcccttttc ctttgtgtac tctatactgg agttcccttc ttcctcttgc tgtaggctca 1142

atcccataacc gacatctaca actaatcttt cccatcaact ctgtgtgaag gcaggttgca 1202

actagaaatt cagaggggct tggaatagag aaacctaaag aagcatcatc cctccatcc 1262

ccaacttcct caaagcccaa agccaaggga aggataaatc aaggctcaag gcttcccag 1322

caaagattag ggaaagagac ttgaccccag gactgtacta cgactcttaa gagaacactg 1382
cacagcactc aaagtcccc actggactgc ttcctcctta gcccactgg tataaatata 1442
tctctctcca atttggttc aa 1464

<210> 52
<211> 1232
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (344)..(1015)

<400> 52
gttgtggaat tcaggggaag taacttgaag gtaggaaccc agcttgtgag cccctagcc 60
tctgggctgc tctgcatgtg cccctcttg ctggatcatc tggtagcagc cctgtgccct 120
gaggggtgatg ctctgaccta tgcagcccc ctccctgtcc tgagaaggct tccagctggg 180
ccttggagga caggggtccac ccctacctcc tgggtctcctt cctcagcttg gaagccccgg 240
agcctgccct gctgggaatc ggggaagcac tgcttacctg tctcctgctc ccttttcagg 300
tgctgtggc aggcagcacc ttgagccaac aggaaccatt gac atg cga ggc cca 355
Met Arg Gly Pro
1

ggg cag gca gac tgt gca gtg gcc att ggg cgg ccc ctc ggg gag gtg 403
Gly Gln Ala Asp Cys Ala Val Ala Ile Gly Arg Pro Leu Gly Glu Val
5 10 15 20

gtg acc ctc cgc gtc ctt gag agt tct ctc aac tgc agt gcg ggg gac 451
Val Thr Leu Arg Val Leu Glu Ser Ser Leu Asn Cys Ser Ala Gly Asp
25 30 35

atg ttg ctg ctt tgg ggc cgg ctc acc tgg agg aag atg tgc agg aag 499
Met Leu Leu Leu Trp Gly Arg Leu Thr Trp Arg Lys Met Cys Arg Lys
40 45 50

ctg ttg gac atg act ttc agc tcc aag acc aac acg ctg gtg gtg agg 547
Leu Leu Asp Met Thr Phe Ser Ser Lys Thr Asn Thr Leu Val Val Arg
55 60 65

cag cgc tgc ggg cgg cca gga ggt ggg gtg ctg ctg cgg tat ggg agc 595
Gln Arg Cys Gly Arg Pro Gly Gly Gly Val Leu Leu Arg Tyr Gly Ser
70 75 80

cag ctt gct cct gaa acc ttc tac aga gaa tgt gac atg cag ctc ttt 643
Gln Leu Ala Pro Glu Thr Phe Tyr Arg Glu Cys Asp Met Gln Leu Phe
85 90 95 100

ggg ccc tgg ggt gaa atc gtg agc ccc tgc ctg agt cca gcc acg agt 691
Gly Pro Trp Gly Glu Ile Val Ser Pro Ser Leu Ser Pro Ala Thr Ser
105 110 115

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aat gca ggg ggc tgc cgg ctc ttc att aat gtg gct ccg cac gca cgg      739
Asn Ala Gly Gly Cys Arg Leu Phe Ile Asn Val Ala Pro His Ala Arg
                120                125                130

att gcc atc cat gcc ctg gcc acc aac atg ggc gct ggg acc gag gga      787
Ile Ala Ile His Ala Leu Ala Thr Asn Met Gly Ala Gly Thr Glu Gly
                135                140                145

gcc aat gcc agc tac atc ttg atc cgg gac acc cac agc ttg agg acc      835
Ala Asn Ala Ser Tyr Ile Leu Ile Arg Asp Thr His Ser Leu Arg Thr
                150                155                160

aca gcg ttc cat ggg cag cag gtg ctc tac tgg gag tca gag agc agc      883
Thr Ala Phe His Gly Gln Gln Val Leu Tyr Trp Glu Ser Glu Ser Ser
                165                170                175                180

cag gct gag atg gag ttc agc gag ggc ttc ctg aag gct cag gcc agc      931
Gln Ala Glu Met Glu Phe Ser Glu Gly Phe Leu Lys Ala Gln Ala Ser
                185                190                195

ctg cgg ggc cag tac tgg aca ctc caa tca tgg gta ccg gag atg cag      979
Leu Arg Gly Gln Tyr Trp Thr Leu Gln Ser Trp Val Pro Glu Met Gln
                200                205                210

gac cct cag tcc tgg aag gga aag gaa gga acc tga gggt cattgaacat      1029
Asp Pro Gln Ser Trp Lys Gly Lys Glu Gly Thr
                215                220

ttgttccgtg tctggccagc cctggagggt tgaccctcctg tctcagtgc ttccaattcg      1089

aactttttcc aatcttaggt atctacttta gagtcttctc caatgtccaa aaggctaggg      1149

ggttggagggt ggggactctg gaaaagcagc cccatttcc tcgggtacca ataaataaaa      1209

catgcaggct gaaaaaaaaa aaa                                           1232

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<210> 53
<211> 934
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (375)..(596)

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<220>
<221> misc_feature
<222> (1)...(934)
<223> n = a,t,c or g

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<400> 53
cgcctgcggc accggtccgg aattcccggg tcgacgattt cgtgctaaga ccctgcttct      60
ccctggctcg tcctctactc gggcactacc cctggcctga ccctggtgag cctccacacg      120
cacgggcaat gccttgggtc ctagaccgtg ggctgggagc cacataaagg tcttgggtac      180

```

```

tcttaggagt aggtgcccgg gggagcacgc ccaggacata tcaggttccc tcaccaagct      240
tagccccctc tgccctctgt tgagtctcct gagtcccttt ggagtccctc tcttgctccc      300
atgcagacaa ctggaagcag gagctgacaa aattcatcag ccccgaccag ctgcctgtgg      360
agtttggggg gacc  atg act gac ccc gat ggc aac ccc aag tgc ctg acc      410
                Met Thr Asp Pro Asp Gly Asn Pro Lys Cys Leu Thr
                  1                5                10

aag atc aac tac ggg ggt gag gtg ccc aag agc tac tac ctg tgc aag      458
Lys Ile Asn Tyr Gly Gly Glu Val Pro Lys Ser Tyr Tyr Leu Cys Lys
          15                20                25

cag gtg agg ctg cag tat gag cac acg agg tcc gtg ggc cgc ggc tcc      506
Gln Val Arg Leu Gln Tyr Glu His Thr Arg Ser Val Gly Arg Gly Ser
          30                35                40

tcc ctg cag gtg gag aac gag atc ctg ttc ccg ggc tgt gtg ctc aga      554
Ser Leu Gln Val Glu Asn Glu Ile Leu Phe Pro Gly Cys Val Leu Arg
          45                50                55                60

tgt cct gag gtt tta caa cac cta cag cct ggt tca ttc taa acgcatc      603
Cys Pro Glu Val Leu Gln His Leu Gln Pro Gly Ser Phe
          65                70

agctacaccg tggaggtact gctcccagac caaaccttca tggagaagat ggagaaattc      663
taggtgaacc tcatggtccc cacaccctcc tctttgatct ctgaatccac aatgagttca      723
cagccttccc tggccagacc ctgttcaacc tctcaggaac agggattcta caacagcagg      783
tcacagccta tgcatacag ctggcccaact cctcaagaac ggctgggaca gtgtcctagt      843
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<220>
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 <222> (48)..(656)

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tat tta gct tcg ata ttc ggg act gag aag gac aag gtt aac tgc tct      104
Tyr Leu Ala Ser Ile Phe Gly Thr Glu Lys Asp Lys Val Asn Cys Ser
          5                10                15

ttt tac ttt aag atc ggg gtc tgc cgg cac ggg gac cgg tgc tcc cgg      152
Phe Tyr Phe Lys Ile Gly Val Cys Arg His Gly Asp Arg Cys Ser Arg

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20	25	30	35	
ctt cac aac aag ccg aca ttc agc cag gag gtg ttc aca gaa ctg cag				200
Leu His Asn Lys Pro Thr Phe Ser Gln Glu Val Phe Thr Glu Leu Gln	40	45	50	
gag aag tat ggg gag att gaa gag atg aat gtg tgc gac aac ctt ggg				248
Glu Lys Tyr Gly Glu Ile Glu Glu Met Asn Val Cys Asp Asn Leu Gly	55	60	65	
gac cac ctg gtg ggc aac gtc tat gtc aag ttc cgg agg gag gag gat				296
Asp His Leu Val Gly Asn Val Tyr Val Lys Phe Arg Arg Glu Glu Asp	70	75	80	
gga gag cgg gcc gtg gct gaa ctg agt aac cgc tgg ttc aac ggg cag				344
Gly Glu Arg Ala Val Ala Glu Leu Ser Asn Arg Trp Phe Asn Gly Gln	85	90	95	
gct gtg cac ggg aat gta ccc gag gtg gct tct gca act tca tgc atc				392
Ala Val His Gly Asn Val Pro Glu Val Ala Ser Ala Thr Ser Cys Ile	100	105	110	115
tgc ggc cca ttt ccc aga acc tcc aga ggc agc tct atg ggc ggg gac				440
Cys Gly Pro Phe Pro Arg Thr Ser Arg Gly Ser Ser Met Gly Gly Asp	120	125	130	
cca ggc gca ggt cac ccc cga ggt tcc ata ctg gcc acc atc ccc gag				488
Pro Gly Ala Gly His Pro Arg Gly Ser Ile Leu Ala Thr Ile Pro Glu	135	140	145	
aga gga acc atc ggt gtt ccc ctg atc act ggc atg gcc gct tct gag				536
Arg Gly Thr Ile Gly Val Pro Leu Ile Thr Gly Met Ala Ala Ser Glu	150	155	160	
gcc ctg gcc ccc tta ccc ttc acc ccc aac agg gac aga tgt tcc tgg				584
Ala Leu Ala Pro Leu Pro Phe Thr Pro Asn Arg Asp Arg Cys Ser Trp	165	170	175	
cag gac ctg tcc tca aag ccc cct tca ctg tcc tgc ccc atc ctt ccc				632
Gln Asp Leu Ser Ser Lys Pro Pro Ser Leu Ser Cys Pro Ile Leu Pro	180	185	190	195
agg ctg ccg ggc tcc ata atg taa tctgttcagc atggagacct tcttctaccg				686
Arg Leu Pro Gly Ser Ile Met	200			
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 <213> Homo sapiens

<220>
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 <222> (48) .. (773)
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Tyr Leu Ala Ser Ile Phe Gly Thr Glu Lys Asp Lys Val Asn Cys Ser		
5 10 15		
ttt tac ttt aag att ggc gcc tgc cgg cac ggg gac cgg tgc tcc cga		152
Phe Tyr Phe Lys Ile Gly Ala Cys Arg His Gly Asp Arg Cys Ser Arg		
20 25 30 35		
ctt cac aac aaa ccg act ttc agc cag acc ata gtc ctg ctc aac ttg		200
Leu His Asn Lys Pro Thr Phe Ser Gln Thr Ile Val Leu Leu Asn Leu		
40 45 50		
tac cgg aat cca cag aac aca gcc caa act gca gac gga tca cac tgt		248
Tyr Arg Asn Ser Pro Gln Asn Thr Ala Gln Thr Ala Asp Gly Ser His Cys		
55 60 65		
cat gtg agc gac gtg gag gtg cag gag cac tat gat agc ttc ttc gag		296
His Val Ser Asp Val Glu Val Gln Glu His Tyr Asp Ser Phe Phe Glu		
70 75 80		
gag gtg ttc aca gaa ctg cag gag aag tat ggg gag att gaa gag atg		344
Glu Val Phe Thr Glu Leu Gln Glu Lys Tyr Gly Glu Ile Glu Glu Met		
85 90 95		
aat gtg tgc gac aac ctt ggg gac cac ctc gtg ggc aac gtc tat gtc		392
Asn Val Cys Asp Asn Leu Gly Asp His Leu Val Gly Asn Val Tyr Val		
100 105 110 115		
aag ttc cgg agg gag gag gat gga gag cgg gcc gtg gct gaa ctc agt		440
Lys Phe Arg Arg Glu Glu Asp Gly Glu Arg Ala Val Ala Glu Leu Ser		
120 125 130		
aac cgc tgg ttc aac ggg cag gct gtg cac ggg aat gta ccc gag gtg		488
Asn Arg Trp Phe Asn Gly Gln Ala Val His Gly Asn Val Pro Glu Val		
135 140 145		
gct tct gca act tca tgc atc tgc ggc cca ttt ccc aga acc tcc aga		536
Ala Ser Ala Thr Ser Cys Ile Cys Gly Pro Phe Pro Arg Thr Ser Arg		
150 155 160		
ggc agc tct atg ggc ggg gac cca ggc gca ggt cac ccc cga ggt tcc		584
Gly Ser Ser Met Gly Gly Asp Pro Gly Ala Gly His Pro Arg Gly Ser		
165 170 175		
ata ctg gcc acc atc ccc gag aga gga acc atc gtt gtt ccc ctg atc		632
Ile Leu Ala Thr Ile Pro Glu Arg Gly Thr Ile Val Val Pro Leu Ile		
180 185 190 195		
act ggc atg gcc gct tct gag gcc ctg gcc ccc tta ccc ttc acc ccc		680
Thr Gly Met Ala Ala Ser Glu Ala Leu Ala Pro Leu Pro Phe Thr Pro		
200 205 210		
aac agg gac aga tgt tcc tgg cag gac ctc tcc tca aag ccc cct tca		728
Asn Arg Asp Arg Cys Ser Trp Gln Asp Leu Ser Ser Lys Pro Pro Ser		
215 220 225		
ctc tcc tgc ccc atc ctt ccc agg ctc ccg ggc tcc ata atg taa tct		776

Leu Ser Cys Pro Ile Leu Pro Arg Leu Pro Gly Ser Ile Met
 230 235 240

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 <211> 3068
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (128)..(2512)

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 ccaagcc atg ctg tgc ggc cgc tgg agg cgt tgc cgc cgc ccg ccc gag 169
 Met Leu Cys Gly Arg Trp Arg Arg Cys Arg Arg Pro Pro Glu
 1 5 10
 gag ccc cca gtg gcc gcc cag gtc gca gcc caa gtc gcg gcg ccg gtc 217
 Glu Pro Pro Val Ala Ala Gln Val Ala Ala Gln Val Ala Ala Pro Val
 15 20 25 30
 gct ctc ccg tcc ccg ccg act ccc tcc gat ggc ggc acc aag agg ccc 265
 Ala Leu Pro Ser Pro Pro Thr Pro Ser Asp Gly Gly Thr Lys Arg Pro
 35 40 45
 ggg ctg cgg gcg ctg aag aag atg ggc ctg acg gag gac gag gac gtg 313
 Gly Leu Arg Ala Leu Lys Lys Met Gly Leu Thr Glu Asp Glu Asp Val
 50 55 60
 cgc gcc atg ctg cgg ggc tcc cgg ctc cgc aag atc cgc tcg cgc acg 361
 Arg Ala Met Leu Arg Gly Ser Arg Leu Arg Lys Ile Arg Ser Arg Thr
 65 70 75
 tgg cac aag gag cgg ctg tac cgg ctg cag gag gac ggc ctg agc gtg 409
 Trp His Lys Glu Arg Leu Tyr Arg Leu Gln Glu Asp Gly Leu Ser Val
 80 85 90
 tgg ttc cag cgg cgc atc ccg cgt gcg cca tcg cag cac atc ttc ttc 457
 Trp Phe Gln Arg Arg Ile Pro Arg Ala Pro Ser Gln His Ile Phe Phe
 95 100 105 110
 gtg cag cac atc gag gcg gtc cgc gag ggc cac cag tcc gag ggc ctg 505
 Val Gln His Ile Glu Ala Val Arg Glu Gly His Gln Ser Glu Gly Leu
 115 120 125
 cgg cgc ttc ggg ggt gcc ttc gcg cca gcg cgc tgc ctc acc atc gcc 553
 Arg Arg Phe Gly Gly Ala Phe Ala Pro Ala Arg Cys Leu Thr Ile Ala
 130 135 140
 ttc aag ggc cgc cgc aag aac ctg gac ctg gcg gcg ccc acg gct gag 601

Phe Lys Gly Arg Arg Lys Asn Leu Asp Leu Ala Ala Pro Thr Ala Glu	
145 150 155	
gaa gcg cag cgc tgg gtg cgc ggt ctg acc aag ctc cgc gcg cgc ctg	649
Glu Ala Gln Arg Trp Val Arg Gly Leu Thr Lys Leu Arg Ala Arg Leu	
160 165 170	
gac gcc atg agc cag cgc gag cgg cta gac cac tgg atc cac tcc tat	697
Asp Ala Met Ser Gln Arg Glu Arg Leu Asp His Trp Ile His Ser Tyr	
175 180 185 190	
ctg cac cgg gct gac tcc aac cag gac agc aag atg agc ttc aag gag	745
Leu His Arg Ala Asp Ser Asn Gln Asp Ser Lys Met Ser Phe Lys Glu	
195 200 205	
atc aag agc ctg ctg aga atg gtc aac gtg gac atg aac gac atg tac	793
Ile Lys Ser Leu Leu Arg Met Val Asn Val Asp Met Asn Asp Met Tyr	
210 215 220	
gcc tac ctc ctc ttc aag gag tgt gac cac tcc aac aac gac cgt cta	841
Ala Tyr Leu Leu Phe Lys Glu Cys Asp His Ser Asn Asn Asp Arg Leu	
225 230 235	
gag ggg gct gag atc gag gag ttc ctg cgg cgg ctg ctg aag cgg ccg	889
Glu Gly Ala Glu Ile Glu Glu Phe Leu Arg Arg Leu Leu Lys Arg Pro	
240 245 250	
gag ctg gag gag atc ttc cat cag tac tgc ggc gag gac cgc gtg ctg	937
Glu Leu Glu Glu Ile Phe His Gln Tyr Ser Gly Glu Asp Arg Val Leu	
255 260 265 270	
agt gcc cct gag ctg ctg gag ttc ctg gag gac cag ggc gag gag ggc	985
Ser Ala Pro Glu Leu Leu Glu Phe Leu Glu Asp Gln Gly Glu Glu Gly	
275 280 285	
gcc aca ctg gcc cgc gcc cag cag ctc att cag acc tat gag ctc aac	1033
Ala Thr Leu Ala Arg Ala Gln Gln Leu Ile Gln Thr Tyr Glu Leu Asn	
290 295 300	
gag aca gcc aag cag cat gag ctg atg aca ctg gat ggc ttc atg atg	1081
Glu Thr Ala Lys Gln His Glu Leu Met Thr Leu Asp Gly Phe Met Met	
305 310 315	
tac ctg ttg tgc ccg gag ggg gct gcc ttg gac aac acc cac acg tgt	1129
Tyr Leu Leu Ser Pro Glu Gly Ala Ala Leu Asp Asn Thr His Thr Cys	
320 325 330	
gtg ttc cag gac atg aac cag ccc ctt gcc cac tac ttc atc tct tcc	1177
Val Phe Gln Asp Met Asn Gln Pro Leu Ala His Tyr Phe Ile Ser Ser	
335 340 345 350	
tcc cac aac acc tat ctg act gac tcc cag atc ggg ggg ccc agc agc	1225
Ser His Asn Thr Tyr Leu Thr Asp Ser Gln Ile Gly Gly Pro Ser Ser	
355 360 365	
acc gag gcc tat gtt agg tac tgt agc agg ggg gcc ttt gcc cag gga	1273
Thr Glu Ala Tyr Val Arg Tyr Cys Ser Arg Gly Ala Phe Ala Gln Gly	
370 375 380	
tgc cgc tgc gtg gag ctg gac tgc tgg gag ggg cca gga ggg gag ccc	1321
Cys Arg Cys Val Glu Leu Asp Cys Trp Glu Gly Pro Gly Gly Glu Pro	

385	390	395	
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gtg gtc caa gcc gtg cgc gac cat gcc ttc acg ctg tcc cct tac cct Val Val Gln Ala Val Arg Asp His Ala Phe Thr Leu Ser Pro Tyr Pro 415 420 425 430			1417
gtc atc cta tcc ctg gag aac cac tgc ggg ctg gag cag cag gct gcc Val Ile Leu Ser Leu Glu Asn His Cys Gly Leu Glu Gln Gln Ala Ala 435 440 445			1465
atg gcc cgc cac ctc tgc acc atc ctg ggg gac atg ctg gtg aca cag Met Ala Arg His Leu Cys Thr Ile Leu Gly Asp Met Leu Val Thr Gln 450 455 460			1513
gcg ctg gac tcc cca aat ccc gag gag ctg cca tcc cca gag cag ctg Ala Leu Asp Ser Pro Asn Pro Glu Glu Leu Pro Ser Pro Glu Gln Leu 465 470 475			1561
aag ggc cgg gtc ctg gtg aag gga aag aag ctg ccc gct gct cgg agc Lys Gly Arg Val Leu Val Lys Gly Lys Lys Leu Pro Ala Ala Arg Ser 480 485 490			1609
gag gat ggc cgg gct ctg tcg gat cgg gag gag gag gag gag gat gac Glu Asp Gly Arg Ala Leu Ser Asp Arg Glu Glu Glu Glu Glu Asp Asp 495 500 505 510			1657
gag gag gaa gaa gag gag gtg gag gct gca gcg cag agg cgg ctg gcc Glu Glu Glu Glu Glu Glu Val Glu Ala Ala Ala Gln Arg Arg Leu Ala 515 520 525			1705
aag cag atc tcc ccg gag ctg tcg gcc ctg gct gtg tac tgc cac gcc Lys Gln Ile Ser Pro Glu Leu Ser Ala Leu Ala Val Tyr Cys His Ala 530 535 540			1753
acc cgc ctg cgg acc ctg cac cct gcc ccc aac gcc cca caa ccc tgc Thr Arg Leu Arg Thr Leu His Pro Ala Pro Asn Ala Pro Gln Pro Cys 545 550 555			1801
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gca ggg aac agc ttt gtc agg cac aat gcc cgc cag ctg acc cgc gtg Ala Gly Asn Ser Phe Val Arg His Asn Ala Arg Gln Leu Thr Arg Val 575 580 585 590			1897
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atg tgg aac tcg ggc tgt cag ctg gtg gcc ttg aac ttc cag acg cca Met Trp Asn Ser Gly Cys Gln Leu Val Ala Leu Asn Phe Gln Thr Pro 610 615 620			1993
ggc tac gag atg gac ctc aat gcc ggg cgc ttc cta gtc aat ggg cag Gly Tyr Glu Met Asp Leu Asn Ala Gly Arg Phe Leu Val Asn Gly Gln 625 630 635			2041

tgt ggc tac gtc cta aaa cct gcc tgc ctg cgg caa cct gac tgc acc Cys Gly Tyr Val Leu Lys Pro Ala Cys Leu Arg Gln Pro Asp Ser Thr 640 645 650	2089
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gtg ctg act gca cag cag ctg ccc aag ctg aat gcc gag aag cca cac Val Leu Thr Ala Gln Gln Leu Pro Lys Leu Asn Ala Glu Lys Pro His 675 680 685	2185
tcc att gtg gac ccc ctg gtg cgc att gag atc cat ggg gtg ccc gca Ser Ile Val Asp Pro Leu Val Arg Ile Glu Ile His Gly Val Pro Ala 690 695 700	2233
gac tgt gcc cgg cag gag act gac tac gtg ctc aac aat ggc ttc aac Asp Cys Ala Arg Gln Glu Thr Asp Tyr Val Leu Asn Asn Gly Phe Asn 705 710 715	2281
ccc cgc tgg ggg cag acc ctg cag ttc cag ctg cgg gct ccg gag ctg Pro Arg Trp Gly Gln Thr Leu Gln Phe Gln Leu Arg Ala Pro Glu Leu 720 725 730	2329
gca ctg gtc cgg ttt gtg gtg gaa gat tat gac gcc acc tcc ccc aat Ala Leu Val Arg Phe Val Val Glu Asp Tyr Asp Ala Thr Ser Pro Asn 735 740 745 750	2377
gac ttt gtg ggc cag ttt aca ctg cct ctt agc agc cta aag caa ggg Asp Phe Val Gly Gln Phe Thr Leu Pro Leu Ser Ser Leu Lys Gln Gly 755 760 765	2425
tac cgc cac ata cac ctg ctt tcc aag gac ggg gcc tca ctg tca cca Tyr Arg His Ile His Leu Leu Ser Lys Asp Gly Ala Ser Leu Ser Pro 770 775 780	2473
gcc acg ctc ttc atc caa atc cgc atc cag cgc tcc tga gggccacct Ala Thr Leu Phe Ile Gln Ile Arg Ile Gln Arg Ser 785 790	2522
cactcgccctt ggggttctgc gagtgccagt ccacatcccc tgcagagccc tctcctcctc	2582
tggagtcagg tgggtgggagt accagcccc cagcccaccc acttggccca ctcagcccat	2642
tcaccaggcg ctggtctcac ctgggtgctg agggctgcct gggccctcc tgaagaacag	2702
aaaggtgttc atgtgacttc agtgagctcc aaccctgggg ccctgagatg gccccagctc	2762
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cccctaagcc ctccctttacc ccaggccttc ctggactcct ccctccagct ccggaacctg	3002
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tggcag	3068

<210> 57
 <211> 719
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (343)..(690)

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gccctgtgcc cagtgacccc actagctttt ccctctactt tccccgcctg gctgtgctcc      180
ccttgattcg tgccatttgg ccgtgcccac agtctctccc aagctcaaag ttcacctctt      240
tctccagatc ccctgggggtc cccaagcctg actcagtgtg tctggggggg tcccttctga      300
gccacgcac cgacccagct cctcttccct gcagttgtgg cc  atg gcg gct gtg      354
                                         Met Ala Ala Val
                                         1

ccc atg gtg ctc agt gcc atg ggc ttc act gcg gcg gga atc gcc tcg      402
Pro Met Val Leu Ser Ala Met Gly Phe Thr Ala Ala Gly Ile Ala Ser
   5                10                15                20

tcc tcc ata gca gcc aag atg atg tcc gca gca gcc att gcc aac ggg      450
Ser Ser Ile Ala Ala Lys Met Met Ser Ala Ala Ala Ile Ala Asn Gly
                25                30                35

ggg ggt gtt tct gcg ggg agc ctg gtg gct act ctg cag tcc gtg ggg      498
Gly Gly Val Ser Ala Gly Ser Leu Val Ala Thr Leu Gln Ser Val Gly
                40                45                50

gca gct gga ctc tcc aca tca tcc aac atc ctc ctg gcc tct gtt ggg      546
Ala Ala Gly Leu Ser Thr Ser Ser Asn Ile Leu Leu Ala Ser Val Gly
                55                60                65

tca gtg ttg ggg gcc tgc ttg ggg aat tca cct tct tct tct ctc cca      594
Ser Val Leu Gly Ala Cys Leu Gly Asn Ser Pro Ser Ser Ser Leu Pro
                70                75                80

gct gaa ccc gag gct aaa gaa gat gag gca aga gaa aat gta ccc caa      642
Ala Glu Pro Glu Ala Lys Glu Asp Glu Ala Arg Glu Asn Val Pro Gln
                85                90                95                100

ggg gaa cct cca aaa ccc cca ctc aag tca gag aaa cat gag gaa taa      690
Gly Glu Pro Pro Lys Pro Pro Leu Lys Ser Glu Lys His Glu Glu
                105                110                115

aggtcacatg cagatgcaaa aaaaaaaaaa      719

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<210> 58

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<211> 1256
<212> DNA
<213> Homo sapiens

<220>
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<222> (137) .. (1021)

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tgcagctgct gtcagc      atg gcc cag gct cct gct gac ccg ggc aga gaa      169
                        Met Ala Gln Ala Pro Ala Asp Pro Gly Arg Glu
                        1              5              10

gcc aag agg ccc cag caa cat gca gct aca att cca gag acc cct ggc      217
Ala Lys Arg Pro Gln Gln His Ala Ala Thr Ile Pro Glu Thr Pro Gly
                        15              20              25

cct cag ttc agc caa caa cgg gag gaa gac atc tac agg ttt ctc aaa      265
Pro Gln Phe Ser Gln Gln Arg Glu Glu Asp Ile Tyr Arg Phe Leu Lys
                        30              35              40

gac aat ggt ccc cag agg gcc ctg gtc atc gcc caa gca ctg gga atg      313
Asp Asn Gly Pro Gln Arg Ala Leu Val Ile Ala Gln Ala Leu Gly Met
                        45              50              55

agg aca gca aaa gat gtg aac cga gac ttg tac agg atg aag agc agg      361
Arg Thr Ala Lys Asp Val Asn Arg Asp Leu Tyr Arg Met Lys Ser Arg
                        60              65              70              75

cac ctt ctg gac atg gat gag cag tcc aaa gca tgg acg att tac cgc      409
His Leu Leu Asp Met Asp Glu Gln Ser Lys Ala Trp Thr Ile Tyr Arg
                        80              85              90

cca gaa gat tct gga aga aga gca aag tca gcc tca att att tac cag      457
Pro Glu Asp Ser Gly Arg Arg Ala Lys Ser Ala Ser Ile Ile Tyr Gln
                        95              100              105

cac aat cca atc aac atg atc tgc cag aat gga ccc aac agc tgg att      505
His Asn Pro Ile Asn Met Ile Cys Gln Asn Gly Pro Asn Ser Trp Ile
                        110              115              120

tcc att gca aac tcc gaa gcc atc cag att gga cac ggg aac atc att      553
Ser Ile Ala Asn Ser Glu Ala Ile Gln Ile Gly His Gly Asn Ile Ile
                        125              130              135

aca aga cag aca gtc tcc agg gag gac ggt tcc gcc ggt cca cgc cac      601
Thr Arg Gln Thr Val Ser Arg Glu Asp Gly Ser Ala Gly Pro Arg His
                        140              145              150              155

ctc cct tca atg gca cca ggt gat tcc tca act tgg ggg acc cta gtt      649
Leu Pro Ser Met Ala Pro Gly Asp Ser Ser Thr Trp Gly Thr Leu Val
                        160              165              170

gat ccc tgg ggg ccc cag gac atc cac atg gag cgg tcc ata ctg aga      697
Asp Pro Trp Gly Pro Gln Asp Ile His Met Glu Arg Ser Ile Leu Arg
                        175              180              185

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cgg gtc cag ctg gga cac agc aat gag atg agg ctc cac ggc gtc ccg	745
Arg Val Gln Leu Gly His Ser Asn Glu Met Arg Leu His Gly Val Pro	
190 195 200	
tcc gag ggc cct gcc cac atc ccc cct ggc agc ccc cca gtc tct gcc	793
Ser Glu Gly Pro Ala His Ile Pro Pro Gly Ser Pro Pro Val Ser Ala	
205 210 215	
act gct gcc ggc cca gaa gct tcg ttt gaa gca aga att ccc agt cca	841
Thr Ala Ala Gly Pro Glu Ala Ser Phe Glu Ala Arg Ile Pro Ser Pro	
220 225 230 235	
gga act cac cct gag ggg gaa gcc gcc cag aga atc cac atg aaa tcg	889
Gly Thr His Pro Glu Gly Glu Ala Ala Gln Arg Ile His Met Lys Ser	
240 245 250	
tgc ttt ctc gag gac gcc acc atc ggc aac agc aac aaa atg tct atc	937
Cys Phe Leu Glu Asp Ala Thr Ile Gly Asn Ser Asn Lys Met Ser Ile	
255 260 265	
cag ccc agg ggt ggc tgg ccc agg agg agt cgc agg gtc tgg aga ggg	985
Gln Pro Arg Gly Gly Trp Pro Arg Arg Ser Arg Arg Val Trp Arg Gly	
270 275 280	
gga gcc agg gga gga cgc agt tgc tgc ctt cac tga agtc ttgaaccct	1035
Gly Ala Arg Gly Gly Arg Ser Cys Cys Leu His	
285 290	
caaagtcatt catgaaatctt ggaatcaact tcttccagac tcctgtgaat gttgatagtt	1095
tgacctcttc ccatgaatca caaatgttct taacggcatg tagattgggtg atcttttcca	1155
gaagattttc aacttacttt gccagatcc atctgaggaa tcactctgtg ttgcacttat	1215
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<210> 59

<211> 1129

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (115)..(1101)

<400> 59

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caccaggtg cattggtgcc agcatcttca ctgaaaggag gtaatctggg ctct	117
Met	
1	

tca gtc cgt tct aaa ttg cca aat tct cca gca gca tct tct cat ccc	165
Ser Val Arg Ser Lys Leu Pro Asn Ser Pro Ala Ala Ser Ser His Pro	
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Lys Leu Lys Ser Ser Lys Gly Ile Thr Lys Lys Pro Gln Ala Pro Ser	

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His Ser Thr Lys Gly Pro Pro Arg Ser Gly Lys Thr Pro Ala Ser Ile
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agg aaa cca ccc tca tct gtt aag gat gca gat agt gga gat aaa aaa      1029
Arg Lys Pro Pro Ser Ser Val Lys Asp Ala Asp Ser Gly Asp Lys Lys
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Met Ala Pro Thr Leu Phe Gln Lys Leu Phe Ser Lys Arg
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Thr Gly Leu Gly Ala Pro Gly Arg Asp Ala Arg Asp Pro Asp Cys Gly
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Phe Ser Trp Pro Leu Pro Glu Phe Asp Pro Ser Gln Ile Arg Leu Ile
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Val Tyr Gln Asp Cys Glu Arg Arg Gly Arg Asn Val Leu Phe Asp Ser
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Ser Val Lys Arg Arg Asn Glu Asp Ile Ser Val Ser Asp Leu Asn Thr
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Ile Tyr Ser Tyr Leu His Gly Met Glu Ile Leu Ser Asn Leu Arg Glu
    80                                85                                90

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His Gln Leu Arg Leu Met Ser Ala Arg Ala Arg Tyr Glu Arg Tyr Ser
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Asn Ser Ala Ser Gly Gln Asp Pro Gly Gly Arg Arg Arg Ala Trp Ala
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Glu Leu Leu Ala Gly Arg Val Lys Arg Glu Lys Tyr Asn Pro Glu Arg
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Ser Val Gly Gln Ile Cys Thr Ala Pro Ala Glu Thr Ser His Pro Val
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Met Leu Arg Ala Val Gly
1 5
agc cta ctg cgc ctt ggc cgc ggg cta aca gtc cgc tgc ggc ccc ggg 221
Ser Leu Leu Arg Leu Gly Arg Gly Leu Thr Val Arg Cys Gly Pro Gly
10 15 20
gcg cct ctc gag gcc acg cga cgg ccc gca ccg gct ctt ccg ccc cgg 269
Ala Pro Leu Glu Ala Thr Arg Arg Pro Ala Pro Ala Leu Pro Pro Arg
25 30 35
ggc ctc ccc tgc tac tcc agc ggc ggg gcc ccc agc aat tct ggg ccc 317
Gly Leu Pro Cys Tyr Ser Ser Gly Gly Ala Pro Ser Asn Ser Gly Pro
40 45 50
caa ggt cac ggg gag att cac cga gtc ccc acg cag cgc agg cct tcg 365
Gln Gly His Gly Glu Ile His Arg Val Pro Thr Gln Arg Arg Pro Ser

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gag gag atc ccg cct cgg atc ccg cca gaa atg ata gac acc gca aga				461
Glu Glu Ile Pro Pro Arg Ile Pro Pro Glu Met Ile Asp Thr Ala Arg				
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Asn Lys Ala Arg Val Lys Ala Cys Tyr Ile Met Ile Gly Leu Thr Ile				
	105	110	115	
atc gcc tgc ttt gct gtg ata gtg tca gcc aaa agg gct gta gaa cga				557
Ile Ala Cys Phe Ala Val Ile Val Ser Ala Lys Arg Ala Val Glu Arg				
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cat gaa tcc tta aca agt tgg aac ttg gca aag aaa gct aag tgg cgt				605
His Glu Ser Leu Thr Ser Trp Asn Leu Ala Lys Lys Ala Lys Trp Arg				
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Glu Glu Ala Ala Leu Ala Ala Gln Ala Lys Ala Lys				
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gccttcaggg tctaccgaat gctgccccta tcagaacggc cttctaagaa aggaaagaaa	180
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acagcaacat tgagaatcaa gagattgtca ccaatccgcc agacatttgc caagttgtag	300
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tctccccctgt gtcttcctat gcagaaagcg aaacgactga tagtggtgccc agcgatgaag	420
agagtgccga gggacggcca cactggcgga agaggagcag ataaactcca acacgatccc	480
ggggctcaag tggcttaaca aggaaaagaa gattttttcag atcccctgg atg cat	535
	Met His
	1
gcg gct aga cat ggg tgg gat gtg gaa aaa gat gca cca ctc ttt aga	583
Ala Ala Arg His Gly Trp Asp Val Glu Lys Asp Ala Pro Leu Phe Arg	
5 10 15	
aac tgg gca atc cat aca gga aag cat caa cca gga gta gat aaa cct	631
Asn Trp Ala Ile His Thr Gly Lys His Gln Pro Gly Val Asp Lys Pro	
20 25 30	
gat ccc aaa aca tgg aag gcg aat ttc aga tgc gcc atg aat tcc ttg	679
Asp Pro Lys Thr Trp Lys Ala Asn Phe Arg Cys Ala Met Asn Ser Leu	
35 40 45 50	
cct gat att gaa gaa gtc aag gat aaa agc ata aag aaa gga aat aat	727
Pro Asp Ile Glu Glu Val Lys Asp Lys Ser Ile Lys Lys Gly Asn Asn	
55 60 65	
gcc ttc agg gtc tac cga atg ctg ccc cta tca gaa cgg cct tct aag	775
Ala Phe Arg Val Tyr Arg Met Leu Pro Leu Ser Glu Arg Pro Ser Lys	
70 75 80	
aaa gga aag aaa cca aag aca gaa aaa gaa gac aaa gtt aag cac atc	823
Lys Gly Lys Lys Pro Lys Thr Glu Lys Glu Asp Lys Val Lys His Ile	
85 90 95	
aag caa gaa cca gtt gag tca tct ctg ggg ctt agt aat gga gta agt	871
Lys Gln Glu Pro Val Glu Ser Ser Leu Gly Leu Ser Asn Gly Val Ser	
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Asp Leu Ser Pro Glu Tyr Ala Val Leu Thr Ser Thr Ile Lys Asn Glu	
115 120 125 130	
gtg gat agt acg gtg aac atc ata gtt gta gga cag tcc cat ctg gac	967
Val Asp Ser Thr Val Asn Ile Ile Val Val Gly Gln Ser His Leu Asp	
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Gln Val Val Glu Val Thr Thr Glu Ser Asp Glu Gln Pro Val Ser Met	
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agc gag ctc tac cct ctg cag atc tcc ccc gtg tct tcc tat gca gaa	1111
Ser Glu Leu Tyr Pro Leu Gln Ile Ser Pro Val Ser Ser Tyr Ala Glu	
180 185 190	
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Ser	Glu	Thr	Thr	Asp	Ser	Val	Pro	Ser	Asp	Glu	Glu	Ser	Ala	Glu	Gly		
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cgg	cca	cac	tgg	cgg	aag	agg	aat	att	gaa	ggc	aaa	cag	tac	ctc	agc		1207
Arg	Pro	His	Trp	Arg	Lys	Arg	Asn	Ile	Glu	Gly	Lys	Gln	Tyr	Leu	Ser		
				215					220					225			
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Asn	Met	Gly	Thr	Arg	Gly	Ser	Tyr	Leu	Leu	Pro	Gly	Met	Ala	Ser	Phe		
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gtc	act	tcc	aac	aaa	ccg	gac	ctc	cag	gtc	acc	atc	aaa	gag	gag	agc		1303
Val	Thr	Ser	Asn	Lys	Pro	Asp	Leu	Gln	Val	Thr	Ile	Lys	Glu	Glu	Ser		
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aat	ccg	gtg	cct	tac	aac	agc	tcc	tgg	ccc	cct	ttt	caa	gac	ctc	ccc		1351
Asn	Pro	Val	Pro	Tyr	Asn	Ser	Ser	Trp	Pro	Pro	Phe	Gln	Asp	Leu	Pro		
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ctt	tct	tcc	tcc	atg	acc	cca	gca	tcc	agc	agc	agt	cgg	cca	gac	cgt		1399
Leu	Ser	Ser	Ser	Met	Thr	Pro	Ala	Ser	Ser	Ser	Ser	Arg	Pro	Asp	Arg		
	275				280					285				290			
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Glu	Thr	Arg	Ala	Ser	Val	Ile	Lys	Lys	Thr	Ser	Asp	Ile	Thr	Gln	Ala		
			295					300						305			
cgc	gtc	aag	agc	tgt	taa	gcctct	gactctccgc	ggcgggtgtt	ggggccttctt								1501
Arg	Val	Lys	Ser	Cys													
			310														
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taaaattcta	aataaaaatat	aattgttttt	tatcttttct	acagcaaatt	tataatttta												2341
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<212> DNA
<213> Homo sapiens
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<222> (37) .. (669)
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185	190	195	
aca tcg gat atc acc cag gcc cgc gtc aag agc tgt taa gcctctgact			679
Thr Ser Asp Ile Thr Gln Ala Arg Val Lys Ser Cys			
200	205	210	
ctccgcggtg gttgttgggg cttcttggct ttgttttgtt gtttgtttgt attttatttt			739
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gattgctgtg tccaactcca gtacctggag cttctcttta actcaggact ccagccatt			859
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	Met Tyr Lys Arg Asn Gly Leu Met Ala Ser Val Leu Val Thr		

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Ser Ala Thr Pro Gln Gly Ser Ser Ser Ser Asp Ser Leu Glu Gly Gln			
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agc tgc gac tat gcc agc aag agc tat gat gcc gtt gtc ttc gat gtc			203
Ser Cys Asp Tyr Ala Ser Lys Ser Tyr Asp Ala Val Val Phe Asp Val			
35	40	45	
ttg aaa gtg acc cca gag gag ttt gct agc cag att aca tta atg gat			251
Leu Lys Val Thr Pro Glu Glu Phe Ala Ser Gln Ile Thr Leu Met Asp			
50	55	60	
ata cct gtg ttt aaa gct atc cag ccg gag gaa cta gcc agc tgt gga			299
Ile Pro Val Phe Lys Ala Ile Gln Pro Glu Glu Leu Ala Ser Cys Gly			
65	70	75	
tgg agt aag aag gag aaa cac agt ctt gcc cct aac gtt gtg gcc ttt			347
Trp Ser Lys Lys Glu Lys His Ser Leu Ala Pro Asn Val Val Ala Phe			
80	85	90	
acc cgg agg ttt aac cag gtc agt ttt tgg gtt gta cga gaa att cta			395
Thr Arg Arg Phe Asn Gln Val Ser Phe Trp Val Val Arg Glu Ile Leu			
95	100	105	110
aca gca cag act tta aaa ata agg gca gaa atc ctc agc cat ttt gtg			443
Thr Ala Gln Thr Leu Lys Ile Arg Ala Glu Ile Leu Ser His Phe Val			
115	120	125	
aaa ata gcc aag aaa ctt cta gaa ctc aac aac ctt cat tct ctc atg			491
Lys Ile Ala Lys Lys Leu Leu Glu Leu Asn Asn Leu His Ser Leu Met			
130	135	140	
tct gtg gta tca gca tta caa agt gct ccc atc ttc agg ctg aca aaa			539
Ser Val Val Ser Ala Leu Gln Ser Ala Pro Ile Phe Arg Leu Thr Lys			
145	150	155	
acc tgg gct ctt tta aat cga aaa gac aag act acc ttt gag aaa ttg			587
Thr Trp Ala Leu Leu Asn Arg Lys Asp Lys Thr Thr Phe Glu Lys Leu			
160	165	170	
gac tac ctg atg tgc aaa gaa gat aat tac aag cgg aca cgg gaa tat			635
Asp Tyr Leu Met Ser Lys Glu Asp Asn Tyr Lys Arg Thr Arg Glu Tyr			
175	180	185	190
atc cga agc ctg aag atg gtt cca agt att ccc tat cta gga atc tat			683
Ile Arg Ser Leu Lys Met Val Pro Ser Ile Pro Tyr Leu Gly Ile Tyr			
195	200	205	
ctt ctg gat tta atc tac att gat tct gca tat cct gcc tca ggc agt			731
Leu Leu Asp Leu Ile Tyr Ile Asp Ser Ala Tyr Pro Ala Ser Gly Ser			
210	215	220	
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Ile Met Glu Asn Glu Gln Arg Ser Asn Gln Met Asn Asn Ile Leu Arg			
225	230	235	
ata att gct gat tta caa gtt tcc tgc agc tat gat cac ctc acc acc			827
Ile Ile Ala Asp Leu Gln Val Ser Cys Ser Tyr Asp His Leu Thr Thr			
240	245	250	

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Leu Gln Lys Phe Val Glu Asp Asp Asn Tyr Lys Leu Ser Leu Arg Ile	
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Glu Pro Gly Ser Ser Ser Pro Arg Leu Val Ser Ser Lys Glu Asp Leu	
290 295 300	
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Ala Gly Pro Ser Ala Gly Ser Gly Ser Ala Arg Phe Ser Arg Arg Pro	
305 310 315	
acc tgt cct gac aca tct gtt gct ggc agc ctc ccc aca cct cca gtc	1067
Thr Cys Pro Asp Thr Ser Val Ala Gly Ser Leu Pro Thr Pro Pro Val	
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ccc aga cac agg aag agc cac agc cta ggc aac aac agg gga cgt ctc	1115
Pro Arg His Arg Lys Ser His Ser Leu Gly Asn Asn Arg Gly Arg Leu	
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tat gcc acc ctg ggg ccc aac tgg cgg gtt cca gtt agg aat tct ccc	1163
Tyr Ala Thr Leu Gly Pro Asn Trp Arg Val Pro Val Arg Asn Ser Pro	
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aga acc cgg agc tgt gtc tac agc ccc acc ggc ccg tgc atc tgt tct	1211
Arg Thr Arg Ser Cys Val Tyr Ser Pro Thr Gly Pro Cys Ile Cys Ser	
370 375 380	
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Leu Gly Asn Ser Ala Ala Val Pro Thr Met Glu Gly Pro Leu Arg Arg	
385 390 395	
aaa acc ctg ctc aag gaa ggg cgg aag cct gcg ctg tcc tcg tgg acc	1307
Lys Thr Leu Leu Lys Glu Gly Arg Lys Pro Ala Leu Ser Ser Trp Thr	
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Arg Tyr Trp Val Ile Leu Ser Gly Ser Thr Leu Leu Tyr Tyr Gly Ala	
415 420 425 430	
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Lys Ser Leu Arg Gly Thr Asp Arg Lys His Val Ser Ile Val Gly Trp	
435 440 445	
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Met Val Gln Leu Pro Asp Asp Pro Glu His Pro Asp Ile Phe Gln Leu	
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Asn Asn Pro Asp Lys Gly Asn Val Tyr Lys Phe Gln Thr Gly Ser Arg	
465 470 475	
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Phe His Ala Ile Leu Trp His Lys His Leu Asp Asp Ala Cys Lys Ser	
480 485 490	

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aac agg cct cag gaa gcc gga gca gct cca ggt cca aca gga act gac      1595
Asn Arg Pro Gln Glu Ala Gly Ala Ala Pro Gly Pro Thr Gly Thr Asp
495                      500                      505                      510

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Ser His Glu Val Asp His Leu Glu Gly Gly Ala Gly Lys Glu Ala Gly
515                      520                      525

ccc tgt gcc tga agc ctgggcacca tgggtggcccc agtcaggagc aacagtggta      1698
Pro Cys Ala

gccctgagta aaacccattg tccctctttg gaggagcggc cagaggatga cagcagcccc      1758
agcaggcagc agtgccctggg caggctgata cagcagagca ctaatgggtc agtttcatgt      1818
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cagacctgga ggaggggatt tttcttcccta ctttccccct tttttatttc taatttactt      1938
tcaaccaaatt attcccacta tgtgtctatat gtaataataa aaagttgaca acaactgaaa      1998
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                                         Met Ala Glu Glu Gln
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caa cag ccg cca cca cag cag cct gat gcc cat cag cag ctt ccc ccc      162
Gln Gln Pro Pro Pro Gln Gln Pro Asp Ala His Gln Gln Leu Pro Pro
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agc gcc ccc aac tcg ggg gtg gcc ctg cca gcc ctt gtg ccc ggg ctg      210
Ser Ala Pro Asn Ser Gly Val Ala Leu Pro Ala Leu Val Pro Gly Leu
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cca ggg aca gag gcc agc gcg ctg caa cac aag atc aag aac tcc atc      258
Pro Gly Thr Glu Ala Ser Ala Leu Gln His Lys Ile Lys Asn Ser Ile
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tgc aaa act gta caa tct aaa gtg gac tgc att ttg caa gaa gtt gag      306
Cys Lys Thr Val Gln Ser Lys Val Asp Cys Ile Leu Gln Glu Val Glu
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Gly Leu Ser Asn Gly Glu Lys Ser Asp Gln Asn Ala Met Ser Ser Ser	
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cgg gca caa caa atg cat gcc ttt tcc tgg att cgg aat acc cta gag	450
Arg Ala Gln Gln Met His Ala Phe Ser Trp Ile Arg Asn Thr Leu Glu	
105 110 115	
gaa cat ccg gag act tca ctg ccc aaa cag gaa gtc tat gat gag tac	498
Glu His Pro Glu Thr Ser Leu Pro Lys Gln Glu Val Tyr Asp Glu Tyr	
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Lys Ser Tyr Cys Asp Asn Leu Gly Tyr His Pro Leu Ser Ala Ala Asp	
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Phe Gly Lys Ile Met Lys Asn Val Phe Pro Asn Met Lys Ala Arg Arg	
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Lys Ala Phe Val His Met Pro Thr Leu Pro Asn Leu Asp Phe His Lys	
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Ala Gln Lys Val Leu Ser Gln Pro Phe Asp Thr Val Leu Glu Leu Ala	
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Arg Phe Leu Val Lys Ser His Tyr Ile Gly Thr Lys Ser Met Ala Ala	
250 255 260	
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Leu Thr Val Met Ala Ala Pro Ala Gly Met Lys Gly Ile Thr Gln	
265 270 275	
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Pro Ser Ala Phe Ile Pro Thr Ala Glu Ser Asn Ser Phe Gln Pro Gln	
280 285 290	
gtg aag act ttg cca tct cca att gat gct aaa cag cag ttg caa cgg	1026
Val Lys Thr Leu Pro Ser Pro Ile Asp Ala Lys Gln Gln Leu Gln Arg	
295 300 305	
aaa atc cag aag aag cag caa gaa cag aaa cta caa tcc cct ttg cca	1074

Lys	Ile	Gln	Lys	Lys	Gln	Gln	Glu	Gln	Lys	Leu	Gln	Ser	Pro	Leu	Pro		
310					315					320					325		
gga	gaa	tct	gca	gca	aaa	aag	tca	gaa	agt	gct	aca	agc	aat	gga	gtg	1122	
Gly	Glu	Ser	Ala	Ala	Lys	Lys	Ser	Glu	Ser	Ala	Thr	Ser	Asn	Gly	Val		
				330					335					340			
act	aat	ctt	cct	aat	gga	aat	cct	tca	atc	ctt	tct	cct	caa	cct	att	1170	
Thr	Asn	Leu	Pro	Asn	Gly	Asn	Pro	Ser	Ile	Leu	Ser	Pro	Gln	Pro	Ile		
			345					350					355				
ggt	atc	gtt	atg	gca	gct	gtc	cct	agt	ccc	att	ccg	gtc	cag	cgg	act	1218	
Gly	Ile	Val	Met	Ala	Ala	Val	Pro	Ser	Pro	Ile	Pro	Val	Gln	Arg	Thr		
		360					365					370					
agg	cat	ttg	gta	act	tca	ccg	agt	cca	atg	agt	tct	tct	gac	ggc	aaa	1266	
Arg	His	Leu	Val	Thr	Ser	Pro	Ser	Pro	Met	Ser	Ser	Ser	Asp	Gly	Lys		
		375				380					385						
gtt	ctt	ccc	ctc	aat	gta	cag	gtg	tca	ctc	agc	aca	tgc	agt	ctg	tga	1314	
Val	Leu	Pro	Leu	Asn	Val	Gln	Val	Ser	Leu	Ser	Thr	Cys	Ser	Leu			
390					395				400								
aacaggcacc	aaagactccc	cagaacgttc	cagccagtc	tggtggggat	cgttctgccc	1374											
ggcaccgtta	ccctcagatc	ttacccaaac	cagcgaacac	cagtgcactc	accattcgct	1434											
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ggagtgttcc	acagatcaag	aatggttctg	tcgtgtcgct	tcagtctcct	gggtccagga	1674											
acagcagtg	ggggggaaca	tatgctgtgg	aagtcaaagt	ggaacccgaa	acatcatcag	1734											
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gtgccctttt	ggggcagaaa	agtaatacag	acggagccct	gcagaaacct	tcaaataag	1854											
gtgtcattga	aataaaagca	actaaggtct	gtgaccagag	gaccaaagt	aaaagtcgct	1914											
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<211> 946

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (135) .. (608)

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cgccgcccgc atattcccgt ggcattcttc ttactttgtc catcctccgg actcgcgac 120

ttccttccgg agcc atg tca gaa gga gtg gac ttg att gat ata tat gct 170
Met Ser Glu Gly Val Asp Leu Ile Asp Ile Tyr Ala
1 5 10

gac gag gag ttc aac cag gac cca gag ttc aac aat aca gat cag att 218
Asp Glu Glu Phe Asn Gln Asp Pro Glu Phe Asn Asn Thr Asp Gln Ile
15 20 25

gac ctg tat gat gat gtg ctg aca gcc acc tca cag ccc tca gat gac 266
Asp Leu Tyr Asp Asp Val Leu Thr Ala Thr Ser Gln Pro Ser Asp Asp
30 35 40

aga agc agc agc act gaa cca cct cct cct gtt cgc cag gag cca tct 314
Arg Ser Ser Ser Thr Glu Pro Pro Pro Pro Val Arg Gln Glu Pro Ser
45 50 55 60

ccc aag ccc aac aac aag acc cct gca att ctg tat acc tac agt ggc 362
Pro Lys Pro Asn Asn Lys Thr Pro Ala Ile Leu Tyr Thr Tyr Ser Gly
65 70 75

ctg cgt aat aga cga gct gcc gtt tat gtg ggc agc ttc tcc tgg tgg 410
Leu Arg Asn Arg Arg Ala Ala Val Tyr Val Gly Ser Phe Ser Trp Trp
80 85 90

acc aca gac cag cag ctg atc cag gtt att cgc tct ata gga gtc tat 458
Thr Thr Asp Gln Gln Leu Ile Gln Val Ile Arg Ser Ile Gly Val Tyr
95 100 105

gat gtg gtg gag ttg aaa ttt gca gag aat cga gca aat ggc cag tcc 506
Asp Val Val Glu Leu Lys Phe Ala Glu Asn Arg Ala Asn Gly Gln Ser
110 115 120

aaa ggg tat gct gag gtg gtg gta gcc tct gaa aac tct gtc cac aaa 554
Lys Gly Tyr Ala Glu Val Val Val Ala Ser Glu Asn Ser Val His Lys
125 130 135 140

ttg ttg gaa ctc cta cca ggg aaa gtt ctt aac tgg cag aaa aag tgg 602
Leu Leu Glu Leu Leu Pro Gly Lys Val Leu Asn Trp Gln Lys Lys Trp
145 150 155

acg tga gtgccggcca ccctggcaga acctgtcaca gtttgaggca caggctcgga 658
Thr

aacgaatacc tccacgggcc cattcccag attctagtga ttctgctgat ggactgggcc 718

acaccctctg agaaccttgt accctcatct gctcgtgtgg ataagccccc cagtgtgctg 778

ccctacttca atacgtccta ccttacggcc cttacacctg atgagtacta gccaccacaa 838

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cttgatctac cactaacaga atctcaatgc cccacctcac taattacc 946

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Leu Ala Leu Leu Gly Ala Met Ser Gly Gly Glu Ala Leu His Leu Ile
      10           15           20

ctc tta cct gct aca ggc aat gtg gca gag aat tct cca cct ggg act      147
Leu Leu Pro Ala Thr Gly Asn Val Ala Glu Asn Ser Pro Pro Gly Thr
      25           30           35

tca gtg cac aag ttt tct gtg aag tta tca gca tca ttg tca cct gtg      195
Ser Val His Lys Phe Ser Val Lys Leu Ser Ala Ser Leu Ser Pro Val
      40           45           50           55

atc cca gga ttt ccc cag ata gtc aac tca aat ccc ctc act gaa gct      243
Ile Pro Gly Phe Pro Gln Ile Val Asn Ser Asn Pro Leu Thr Glu Ala
      60           65           70

ttt agg gtg aat tgg ctg tca ggc acc tac ttt gag gtt gtc acc act      291
Phe Arg Val Asn Trp Leu Ser Gly Thr Tyr Phe Glu Val Val Thr Thr
      75           80           85

ggg atg gaa caa cta gat ttt gaa aca gga cca aac ata ttt gat ttg      339
Gly Met Glu Gln Leu Asp Phe Glu Thr Gly Pro Asn Ile Phe Asp Leu
      90           95           100

cag att tat gtg aag gat gag gtt ggt gtc aca gac ctt caa gtc ctg      387
Gln Ile Tyr Val Lys Asp Glu Val Gly Val Thr Asp Leu Gln Val Leu
      105           110           115

act gtc cag gta aca gat gtg aac gag cca cct cag ttt caa ggc aac      435
Thr Val Gln Val Thr Asp Val Asn Glu Pro Pro Gln Phe Gln Gly Asn
      120           125           130           135

ttg gca gaa ggt cta cac ctc tac ata gta gaa aga gca aac cct gga      483
Leu Ala Glu Gly Leu His Leu Tyr Ile Val Glu Arg Ala Asn Pro Gly
      140           145           150

ttc att tac cag gtt gag gcc ttc gat cca gaa gac aca agc cga aac      531
Phe Ile Tyr Gln Val Glu Ala Phe Asp Pro Glu Asp Thr Ser Arg Asn
      155           160           165

att ccc ctc agt tat ttc ctg att tct ccc cca aag agc ttc aga atg      579
Ile Pro Leu Ser Tyr Phe Leu Ile Ser Pro Pro Lys Ser Phe Arg Met
      170           175           180

tct gct aat ggc acc ctc ttc tcc aca aca gaa ttg gac ttt gaa gca      627
Ser Ala Asn Gly Thr Leu Phe Ser Thr Thr Glu Leu Asp Phe Glu Ala
      185           190           195

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Gly His Arg Ser Phe His Leu Ile Val Glu Val Arg Asp Ser Gly Gly
200                      205                      210                      215

ctc aaa gcc tcc aca gag ctc cag gtg aac atc gtg aac ctc aac gac      723
Leu Lys Ala Ser Thr Glu Leu Gln Val Asn Ile Val Asn Leu Asn Asp
                      220                      225                      230

gaa gtc cct cgc ttt acc agc ccg aca cga gtg tac aca gtc ctg gag      771
Glu Val Pro Arg Phe Thr Ser Pro Thr Arg Val Tyr Thr Val Leu Glu
                      235                      240                      245

gaa ctg agt cca gga acc atc gtg gcc aat atc aca gcg gag gat cct      819
Glu Leu Ser Pro Gly Thr Ile Val Ala Asn Ile Thr Ala Glu Asp Pro
                      250                      255                      260

gat gat gaa ggt ttt ccc agc cac ctc ctc tac agc att acc act gtt      867
Asp Asp Glu Gly Phe Pro Ser His Leu Leu Tyr Ser Ile Thr Thr Val
265                      270                      275

agc aaa tat ttc atg ata aat cag ttg act ggt aca atc caa gtg gcc      915
Ser Lys Tyr Phe Met Ile Asn Gln Leu Thr Gly Thr Ile Gln Val Ala
280                      285                      290                      295

caa agg ata gac cga gat gca ggt gaa ttg aga caa aat ccc acc att      963
Gln Arg Ile Asp Arg Asp Ala Gly Glu Leu Arg Gln Asn Pro Thr Ile
                      300                      305                      310

tcc ctg gaa gtt cta gtg aag gac aga cca tat ggg ggt cag gag aat      1011
Ser Leu Glu Val Leu Val Lys Asp Arg Pro Tyr Gly Gly Gln Glu Asn
                      315                      320                      325

cgc atc cag ata acc ttc att gtg gaa gac gtc aac gac aat cct gcc      1059
Arg Ile Gln Ile Thr Phe Ile Val Glu Asp Val Asn Asp Asn Pro Ala
                      330                      335                      340

aca tgc caa aag ttc acc ttc aga tgg agg aac tga aacc tggagacatg      1109
Thr Cys Gln Lys Phe Thr Phe Arg Trp Arg Asn
345                      350

agaaagcccc tcaatgaatg gaagtctcaa ggtgttcatt ggtcttctctc agagcctcct      1169

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<212> DNA
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	Met Lys Leu Cys Pro Arg Tyr	
	1 5	
aat tcc caa gaa gaa act tta gag ttt gta gca gat tac agt gga caa		161
Asn Ser Gln Glu Glu Thr Leu Glu Phe Val Ala Asp Tyr Ser Gly Gln		
10 15 20		
gat aat ttc tta caa cga gtg gga caa aat ggc tta aag aat tgc gag		209
Asp Asn Phe Leu Gln Arg Val Gly Gln Asn Gly Leu Lys Asn Ser Glu		
25 30 35		
aag gag tcc act gtc aac agc atc ttt cag gtc atc cgg agc tgc aat		257
Lys Glu Ser Thr Val Asn Ser Ile Phe Gln Val Ile Arg Ser Cys Asn		
40 45 50 55		
cga agt ctg gag aca gac gag gag gac agc ccc agt gaa gga aac agc		305
Arg Ser Leu Glu Thr Asp Glu Glu Asp Ser Pro Ser Glu Gly Asn Ser		
60 65 70		
tcc agg aaa agc tcc ttg aag gat aaa agc cga tgg cag ttt ata att		353
Ser Arg Lys Ser Ser Leu Lys Asp Lys Ser Arg Trp Gln Phe Ile Ile		
75 80 85		
gga gat ttg ttg gat tca gac aat gac atc ttt gag caa tcc aaa gaa		401
Gly Asp Leu Leu Asp Ser Asp Asn Asp Ile Phe Glu Gln Ser Lys Glu		
90 95 100		
tac gac tct cat ggt tca gag gac tca cag aag gcc ttc gac cat ggg		449
Tyr Asp Ser His Gly Ser Glu Asp Ser Gln Lys Ala Phe Asp His Gly		
105 110 115		
acg gag ctc atc cct tgg tac gtg ctg tcc atc caa gcc gat gtg cac		497
Thr Glu Leu Ile Pro Trp Tyr Val Leu Ser Ile Gln Ala Asp Val His		
120 125 130 135		
cag ttc ctg ctg cag ggg gcc acg gtc atc cac tac gac cag gac aca		545
Gln Phe Leu Leu Gln Gly Ala Thr Val Ile His Tyr Asp Gln Asp Thr		
140 145 150		
cac ctc tct gcc cgc tgc ttc ctc cag ctt cag ccc gac aat agc acc		593
His Leu Ser Ala Arg Cys Phe Leu Gln Leu Gln Pro Asp Asn Ser Thr		
155 160 165		
ttg acc tgg gta aag ccc aca act gcc tcc cca gcc agc agt aaa gca		641
Leu Thr Trp Val Lys Pro Thr Thr Ala Ser Pro Ala Ser Ser Lys Ala		
170 175 180		
aaa ctt ggt gta ctt aat aac aca gct gag cct gga aaa ttc cca cta		689
Lys Leu Gly Val Leu Asn Asn Thr Ala Glu Pro Gly Lys Phe Pro Leu		
185 190 195		
ctg ggt aat gct gga tta agt agc ctg acg gaa ggg gtc ttg gat ctt		737
Leu Gly Asn Ala Gly Leu Ser Ser Leu Thr Glu Gly Val Leu Asp Leu		
200 205 210 215		
ttt gca gtg aag gct gta tac atg ggc cac cct ggc att gat ata cac		785
Phe Ala Val Lys Ala Val Tyr Met Gly His Pro Gly Ile Asp Ile His		
220 225 230		
act gtg tgt gtt cag aac aaa ctg ggt agc atg ttc ctg tca gag act		833

Thr	Val	Cys	Val	Gln	Asn	Lys	Leu	Gly	Ser	Met	Phe	Leu	Ser	Glu	Thr	
			235					240					245			
ggt	gtg	aca	ttg	ctc	tat	ggg	ctt	cag	acc	aca	gac	aac	aga	tta	ttg	881
Gly	Val	Thr	Leu	Leu	Tyr	Gly	Leu	Gln	Thr	Thr	Asp	Asn	Arg	Leu	Leu	
		250					255					260				
cac	ttc	gtg	gca	cca	aag	cac	aca	gct	aaa	atg	ctc	ttc	agc	gga	tta	929
His	Phe	Val	Ala	Pro	Lys	His	Thr	Ala	Lys	Met	Leu	Phe	Ser	Gly	Leu	
	265					270					275					
ttg	gaa	ctc	act	aga	gct	gtg	aga	aag	atg	agg	aaa	ttc	cct	gac	caa	977
Leu	Glu	Leu	Thr	Arg	Ala	Val	Arg	Lys	Met	Arg	Lys	Phe	Pro	Asp	Gln	
280					285				290						295	
aga	cag	cag	tgg	ctg	cgg	aaa	cag	tac	gtc	agc	ctt	tat	cag	gag	gat	1025
Arg	Gln	Gln	Trp	Leu	Arg	Lys	Gln	Tyr	Val	Ser	Leu	Tyr	Gln	Glu	Asp	
				300					305					310		
gga	cgg	tat	gaa	ggc	cca	act	ttg	gct	cac	gct	gtg	gag	ttg	ttt	ggt	1073
Gly	Arg	Tyr	Glu	Gly	Pro	Thr	Leu	Ala	His	Ala	Val	Glu	Leu	Phe	Gly	
			315					320					325			
ggc	aga	cgg	tgg	agt	gct	cga	aac	ccc	agc	ccc	gga	aca	tca	gca	aag	1121
Gly	Arg	Arg	Trp	Ser	Ala	Arg	Asn	Pro	Ser	Pro	Gly	Thr	Ser	Ala	Lys	
		330					335					340				
aat	gct	gag	aag	ccc	aat	atg	cag	aga	aac	aat	acc	ctg	ggc	ata	agc	1169
Asn	Ala	Glu	Lys	Pro	Asn	Met	Gln	Arg	Asn	Asn	Thr	Leu	Gly	Ile	Ser	
	345					350					355					
act	acc	aag	aaa	aag	aag	aaa	atc	ctc	atg	agg	ggt	gag	agt	gga	gag	1217
Thr	Thr	Lys	Lys	Lys	Lys	Lys	Ile	Leu	Met	Arg	Gly	Glu	Ser	Gly	Glu	
360					365				370						375	
gta	act	gac	gat	gag	atg	gca	acc	cga	aag	gcc	aag	atg	cac	aaa	gag	1265
Val	Thr	Asp	Asp	Glu	Met	Ala	Thr	Arg	Lys	Ala	Lys	Met	His	Lys	Glu	
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tgt	cga	agc	cgg	agt	ggt	tct	gat	cct	caa	gac	att	aat	gaa	caa	gaa	1313
Cys	Arg	Ser	Arg	Ser	Gly	Ser	Asp	Pro	Gln	Asp	Ile	Asn	Glu	Gln	Glu	
			395					400					405			
gaa	tca	gag	gtg	aat	gcc	atc	gct	aac	cct	cca	aac	ccc	ctc	cct	tcc	1361
Glu	Ser	Glu	Val	Asn	Ala	Ile	Ala	Asn	Pro	Pro	Asn	Pro	Leu	Pro	Ser	
		410					415					420				
aga	aga	gcc	cac	tct	ttg	acc	aca	gct	ggg	tcc	ccc	aac	ttg	gct	gcc	1409
Arg	Arg	Ala	His	Ser	Leu	Thr	Ala	Gly	Ser			Asn	Leu	Ala	Ala	
		425				430					435					
ggg	acg	tca	tct	ccc	atc	agg	cca	gtg	tcc	tcc	cct	gtg	ctg	tct	tct	1457
Gly	Thr	Ser	Ser	Pro	Ile	Arg	Pro	Val	Ser	Ser	Pro	Val	Leu	Ser	Ser	
440					445				450						455	
tca	aac	aag	agc	cca	tcc	agt	gct	tgg	agc	agt	agt	agc	tgg	cac	ggg	1505
Ser	Asn	Lys	Ser	Pro	Ser	Ser	Ala	Trp	Ser	Ser	Ser	Ser	Trp	His	Gly	
				460					465					470		
cgg	atc	aaa	ggc	ggc	atg	aag	gga	ttt	cag	agc	ttc	atg	gtt	tca	gat	1553
Arg	Ile	Lys	Gly	Gly	Met	Lys	Gly	Phe	Gln	Ser	Phe	Met	Val	Ser	Asp	

475	480	485	
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ggg gtg ggc ata ctt cag ctg aac gat ttc ctg gtg aat tgc caa gga Gly Val Gly Ile Leu Gln Leu Asn Asp Phe Leu Val Asn Cys Gln Gly 600 605 610 615			1937
gaa cac tgc act tat gat gaa atc ctg agc atc atc cag aag ttc gag Glu His Cys Thr Tyr Asp Glu Ile Leu Ser Ile Ile Gln Lys Phe Glu 620 625 630			1985
cct agc atc agt atg tgt cat cag gga cta atg tca ttt gaa ggg ttt Pro Ser Ile Ser Met Cys His Gln Gly Leu Met Ser Phe Glu Gly Phe 635 640 645			2033
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tat cat gga cat acg ctg aca acc aag atc ccc ttc aag gaa gtg gtt	2321
Tyr His Gly His Thr Leu Thr Thr Lys Ile Pro Phe Lys Glu Val Val	
730 735 740	
gaa gcc att gat cgc agt gcc ttc atc aac tct gac ctg cca atc atc	2369
Glu Ala Ile Asp Arg Ser Ala Phe Ile Asn Ser Asp Leu Pro Ile Ile	
745 750 755	
ata tcg att gag aac cac tgt tca ttg cct cag caa cga aaa atg gca	2417
Ile Ser Ile Glu Asn His Cys Ser Leu Pro Gln Gln Arg Lys Met Ala	
760 765 770 775	
gaa att ttc aag act gtg ttt gga gaa aag ctg gtg act aaa ttc tta	2465
Glu Ile Phe Lys Thr Val Phe Gly Glu Lys Leu Val Thr Lys Phe Leu	
780 785 790	
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Phe Glu Thr Asp Phe Ser Asp Asp Pro Met Leu Pro Ser Pro Asp Gln	
795 800 805	
ctc aga aag aaa gtt ctt ctt aaa aac aag aag cta aaa gcc cat cag	2561
Leu Arg Lys Lys Val Leu Leu Lys Asn Lys Lys Leu Lys Ala His Gln	
810 815 820	
acg cca gtg gat atc tta aag caa aag gct cat cag tta gca tct atg	2609
Thr Pro Val Asp Ile Leu Lys Gln Lys Ala His Gln Leu Ala Ser Met	
825 830 835	
caa gtg cag gct tat aat ggt ggg aat gcc aac ccc cga cct gcc aat	2657
Gln Val Gln Ala Tyr Asn Gly Gly Asn Ala Asn Pro Arg Pro Ala Asn	
840 845 850 855	
aat gag gaa gag gaa gat gag gag gac gaa tat gat tat gac tat gaa	2705
Asn Glu Glu Glu Glu Asp Glu Glu Asp Glu Tyr Asp Tyr Asp Tyr Glu	
860 865 870	
tcc ctt tct gat gac aac att ctg gaa gac aga cct gaa aat aaa tca	2753
Ser Leu Ser Asp Asp Asn Ile Leu Glu Asp Arg Pro Glu Asn Lys Ser	
875 880 885	
tgt aat gac aag ctt cag ttt gaa tat aat gaa gaa atc cca aag agg	2801
Cys Asn Asp Lys Leu Gln Phe Glu Tyr Asn Glu Glu Ile Pro Lys Arg	
890 895 900	
ata aag aaa gca gat aac tct gct tgc aac aaa gga aag gtt tat gat	2849
Ile Lys Lys Ala Asp Asn Ser Ala Cys Asn Lys Gly Lys Val Tyr Asp	
905 910 915	
atg gaa ctg gga gaa gaa ttt tat ctt gat cag aat aaa aag gaa agc	2897
Met Glu Leu Gly Glu Glu Phe Tyr Leu Asp Gln Asn Lys Lys Glu Ser	
920 925 930 935	
aga cag att gca cca gag ctt tct gac ctt gta atc tat tgt caa gca	2945
Arg Gln Ile Ala Pro Glu Leu Ser Asp Leu Val Ile Tyr Cys Gln Ala	
940 945 950	
gta aaa ttt cca gga ctg tca act cta aat gca tct ggc tct agc aga	2993
Val Lys Phe Pro Gly Leu Ser Thr Leu Asn Ala Ser Gly Ser Ser Arg	
955 960 965	

gga aaa gaa agg aaa agc agg aag tcc att ttt ggc aac aat ccg ggc	3041
Gly Lys Glu Arg Lys Ser Arg Lys Ser Ile Phe Gly Asn Asn Pro Gly	
970 975 980	
aga atg agc cca ggg gag aca gca tca ttt aac aaa aca tct gga aaa	3089
Arg Met Ser Pro Gly Glu Thr Ala Ser Phe Asn Lys Thr Ser Gly Lys	
985 990 995	
agt tcc tgt gaa ggc att cga cag acc tgg gag gaa tct tct tcc cct	3137
Ser Ser Cys Glu Gly Ile Arg Gln Thr Trp Glu Glu Ser Ser Ser Pro	
1000 1005 1010 1015	
ctc aac cca acc acg tcc ctc agt gct atc att aga act ccc aaa tgt	3185
Leu Asn Pro Thr Thr Ser Leu Ser Ala Ile Ile Arg Thr Pro Lys Cys	
1020 1025 1030	
tat cat atc tcg tcg ctg aat gaa aat gcc gcc aaa cgt ctg tgt cgc	3233
Tyr His Ile Ser Ser Leu Asn Glu Asn Ala Ala Lys Arg Leu Cys Arg	
1035 1040 1045	
agg tat tct cag aaa ctg acc cag cac acc gcc tgt cag ctg ctg aga	3281
Arg Tyr Ser Gln Lys Leu Thr Gln His Thr Ala Cys Gln Leu Leu Arg	
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act tac cct gct gcc acc cgc atc gac tct tcc aac ccg aac ccc ctc	3329
Thr Tyr Pro Ala Ala Thr Arg Ile Asp Ser Ser Asn Pro Asn Pro Leu	
1065 1070 1075	
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Met Phe Trp Leu His Gly Ile Gln Leu Val Ala Leu Asn Tyr Gln Thr	
1080 1085 1090 1095	
gat gat ctc cct tta cat tta aat gct gca atg ttt gag gca aat ggt	3425
Asp Asp Leu Pro Leu His Leu Asn Ala Ala Met Phe Glu Ala Asn Gly	
1100 1105 1110	
ggt tgt ggt tat gta ttg aaa cct cca gtt ctg tgg gac aag aac tgc	3473
Gly Cys Gly Tyr Val Leu Lys Pro Pro Val Leu Trp Asp Lys Asn Cys	
1115 1120 1125	
ccc atg tat cag aag ttt tct cca cta gaa aga gat ctg gac agc atg	3521
Pro Met Tyr Gln Lys Phe Ser Pro Leu Glu Arg Asp Leu Asp Ser Met	
1130 1135 1140	
gat cct gca gtc tat tct tta act att gtc tct ggt cag aat gtg tgc	3569
Asp Pro Ala Val Tyr Ser Leu Thr Ile Val Ser Gly Gln Asn Val Cys	
1145 1150 1155	
ccc agt aat agc atg gga agc ccg tgc att gaa gtc gac gtc ctg ggc	3617
Pro Ser Asn Ser Met Gly Ser Pro Cys Ile Glu Val Asp Val Leu Gly	
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atg cct ctg gac agc tgc cat ttc cgc aca aag ccc atc cat cga aac	3665
Met Pro Leu Asp Ser Cys His Phe Arg Thr Lys Pro Ile His Arg Asn	
1180 1185 1190	
acc ctg aac ccc atg tgg aac gag cag ttt ctg ttc cgc gtt cac ttc	3713
Thr Leu Asn Pro Met Trp Asn Glu Gln Phe Leu Phe Arg Val His Phe	
1195 1200 1205	
gaa gat ctt gta ttt ctt cgt ttt gca gtt gtg gaa aac aat agt tca	3761

Glu Asp Leu Val Phe Leu Arg Phe Ala Val Val Glu Asn Asn Ser Ser	
1210 1215 1220	
gcg gta act gct cag aga atc att cca ctg aaa gct tta aaa cga gga	3809
Ala Val Thr Ala Gln Arg Ile Ile Pro Leu Lys Ala Leu Lys Arg Gly	
1225 1230 1235	
tat cga cat ctt cag ctg cga aac ctt cac aat gaa gtc ttg gag att	3857
Tyr Arg His Leu Gln Leu Arg Asn Leu His Asn Glu Val Leu Glu Ile	
1240 1245 1250 1255	
tct agt tta ttc att aac agc aga agg atg gaa gaa aat tcc tct ggc	3905
Ser Ser Leu Phe Ile Asn Ser Arg Arg Met Glu Glu Asn Ser Ser Gly	
1260 1265 1270	
aat acc atg tca gcc tct tcg atg ttt aat aca gaa gaa aga aaa tgt	3953
Asn Thr Met Ser Ala Ser Ser Met Phe Asn Thr Glu Glu Arg Lys Cys	
1275 1280 1285	
ttg cag act cac aga gtc acg gtg cat ggg gtc cca ggg cca gag ccc	4001
Leu Gln Thr His Arg Val Thr Val His Gly Val Pro Gly Pro Glu Pro	
1290 1295 1300	
ttt acc gtt ttc act att aat gga ggc acc aag gca aag cag ctt ctg	4049
Phe Thr Val Phe Thr Ile Asn Gly Gly Thr Lys Ala Lys Gln Leu Leu	
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cag caa att ctg aca aat gaa caa gac atc aaa cct gtt acc aca gac	4097
Gln Gln Ile Leu Thr Asn Glu Gln Asp Ile Lys Pro Val Thr Thr Asp	
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Tyr Phe Leu Met Glu Glu Lys Tyr Phe Ile Ser Lys Glu Lys Asn Glu	
1340 1345 1350	
tgt agg aaa caa cca ttc cag aga gcc att ggt cca gaa gag gag atc	4193
Cys Arg Lys Gln Pro Phe Gln Arg Ala Ile Gly Pro Glu Glu Glu Ile	
1355 1360 1365	
atg caa att tta agc agc tgg ttt cca gaa gag gga tac atg ggc agg	4241
Met Gln Ile Leu Ser Ser Trp Phe Pro Glu Glu Gly Tyr Met Gly Arg	
1370 1375 1380	
att gtc tta aaa acc cag cag gaa aac cta gaa gag aaa aac att gtt	4289
Ile Val Leu Lys Thr Gln Gln Glu Asn Leu Glu Glu Lys Asn Ile Val	
1385 1390 1395	
caa gat gac aaa gag gtg atc ttg agc tca gag gag gag agt ttc ttt	4337
Gln Asp Asp Lys Glu Val Ile Leu Ser Ser Glu Glu Glu Ser Phe Phe	
1400 1405 1410 1415	
gtc caa gtg cat gat gtt tct cca gag caa cct cga aca gtc atc aaa	4385
Val Gln Val His Asp Val Ser Pro Glu Gln Pro Arg Thr Val Ile Lys	
1420 1425 1430	
gca ccc cgc gtc agc act gca cag gat gtc att cag cag acc tta tgc	4433
Ala Pro Arg Val Ser Thr Ala Gln Asp Val Ile Gln Gln Thr Leu Cys	
1435 1440 1445	
aaa gcc aaa tat tcc tac agc atc ctg agc aac ccc aat cca agc gac	4481
Lys Ala Lys Tyr Ser Tyr Ser Ile Leu Ser Asn Pro Asn Pro Ser Asp	

1450	1455	1460	
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Tyr Val Leu Leu Glu Glu Val Val Lys Asp Thr Thr Asn Lys Lys Thr			
1465	1470	1475	
acc aca cca aag tcc tct cag cgg gtc ctt ctg gat cag gag tgt gtg			4577
Thr Thr Pro Lys Ser Ser Gln Arg Val Leu Leu Asp Gln Glu Cys Val			
1480	1485	1490	1495
ttt caa gcc caa agc aag tgg aaa ggt gca gga aaa ttc atc ctt aag			4625
Phe Gln Ala Gln Ser Lys Trp Lys Gly Ala Gly Lys Phe Ile Leu Lys			
1500	1505	1510	
cta aag gag cag gtg cag gca tct cga gaa gat aaa aag aaa ggc att			4673
Leu Lys Glu Gln Val Gln Ala Ser Arg Glu Asp Lys Lys Lys Gly Ile			
1515	1520	1525	
tct ttc gca agt gaa ctc aag aag ctc acc aag tca act aaa cag ccc			4721
Ser Phe Ala Ser Glu Leu Lys Lys Leu Thr Lys Ser Thr Lys Gln Pro			
1530	1535	1540	
cga gga ctt aca tca cct tct cag ctc ttg acc tca gaa agt atc caa			4769
Arg Gly Leu Thr Ser Pro Ser Gln Leu Leu Thr Ser Glu Ser Ile Gln			
1545	1550	1555	
acc aag gag gag aaa cct gtg ggt ggc ttg tcc tcc agt gac aca atg			4817
Thr Lys Glu Glu Lys Pro Val Gly Gly Leu Ser Ser Ser Asp Thr Met			
1560	1565	1570	1575
gat tac cga cag tga ctaagggcag catgtttaac ccaggtgaag atctttaacc			4872
Asp Tyr Arg Gln			
aagaagttaa agagtgaaca tgggtggaaaa aatataatta ttttcatcag acttaaaactg			4932
gaaattgatg atttctgaag ccttcacaca tgtgagatcc atgctgagga gaagcaaaat			4992
ggcacagggc tagttgccac caaccaattt actgatgaat gaagcccagg ggactgccat			5052
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gcttgtctgt aaagggccaa acagtaaata ttttagggct gggggccata aaatatgttg			5172
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 <213> Homo sapiens

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<400> 71

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ctg gcg gcc ggc tgg ctg ggg cct gag gcc tgg ggc tca ccc acg ccc	96
Leu Ala Ala Gly Trp Leu Gly Pro Glu Ala Trp Gly Ser Pro Thr Pro	
20 25 30	
ccg ccg acg cct gcc gcg ccg ccg cca ccc ccg cca ccc gga gcc ccg	144
Pro Pro Thr Pro Ala Ala Pro Pro Pro Pro Pro Pro Gly Ala Pro	
35 40 45	
ggt ggc tgc cag gac acc tgt acg tgc tgc ggc ggc ttc cgg cgg cca	192
Gly Gly Ser Gln Asp Thr Cys Thr Ser Cys Gly Gly Phe Arg Arg Pro	
50 55 60	
gag gag ctc ggc cga gtg gac ggc gac ttc ctg gag gcg gtg aag cgg	240
Glu Glu Leu Gly Arg Val Asp Gly Asp Phe Leu Glu Ala Val Lys Arg	
65 70 75 80	
cac atc ttg agc cgc ctg cag atg cgg ggc cgg ccc aac atc acg cac	288
His Ile Leu Ser Arg Leu Gln Met Arg Gly Arg Pro Asn Ile Thr His	
85 90 95	
gcc gtg cct aag gcc gcc atg gtc acg gcc ctg cgc aag ctg cac gcg	336
Ala Val Pro Lys Ala Ala Met Val Thr Ala Leu Arg Lys Leu His Ala	
100 105 110	
ggc aag gtg cgc gag gac ggc cgc gtg gag atc ccg cac ctc gac ggc	384
Gly Lys Val Arg Glu Asp Gly Arg Val Glu Ile Pro His Leu Asp Gly	
115 120 125	
cac gcc agc ccg ggc gcc gac ggc cag gag cgc gtt tcc gaa atc atc	432
His Ala Ser Pro Gly Ala Asp Gly Gln Glu Arg Val Ser Glu Ile Ile	
130 135 140	
agc ttc gcc gag aca gat ggc ctc gcc tcc tcc cgg gtc cgc cta tac	480
Ser Phe Ala Glu Thr Asp Gly Leu Ala Ser Ser Arg Val Arg Leu Tyr	
145 150 155 160	
ttc ttc atc tcc aac gaa ggc aac cag aac ctg ttt gtg gtc cag gcc	528
Phe Phe Ile Ser Asn Glu Gly Asn Gln Asn Leu Phe Val Val Gln Ala	
165 170 175	
agc ctg tgg ctt tac ctg aaa ctc ctg ccc tac gtc ctg gag aag ggc	576
Ser Leu Trp Leu Tyr Leu Lys Leu Leu Pro Tyr Val Leu Glu Lys Gly	
180 185 190	
agc cgg cgg aag gtg cgg gtc aaa gtg tac ttc cag gag cag ggc cac	624
Ser Arg Arg Lys Val Arg Val Lys Val Tyr Phe Gln Glu Gln Gly His	
195 200 205	
ggt gac agg tgg aac atg gtg gag aag agg gtg gac ctc aag cgc agc	672
Gly Asp Arg Trp Asn Met Val Glu Lys Arg Val Asp Leu Lys Arg Ser	
210 215 220	
ggc tgg cat acc ttc cca ctc acg gag gcc atc cag gcc ttg ttt gag	720
Gly Trp His Thr Phe Pro Leu Thr Glu Ala Ile Gln Ala Leu Phe Glu	
225 230 235 240	
cgg ggc gag cgg cga ctc aac cta gac gtg cag tgt gac agc tgc cag	768

Arg Gly Glu Arg Arg Leu Asn Leu Asp Val Gln Cys Asp Ser Cys Gln	
245 250 255	
gag ctg gcc gtg gtg ccg gtg ttc gtg gac cca ggc gaa gag tcg cac	816
Glu Leu Ala Val Val Pro Val Phe Val Asp Pro Gly Glu Glu Ser His	
260 265 270	
cga ccc ttt gtg gtg gtg cag gct cgg ctg ggc gac agc agg cac cgc	864
Arg Pro Phe Val Val Val Gln Ala Arg Leu Gly Asp Ser Arg His Arg	
275 280 285	
att cgc aag cga ggc ctg gag tgc gat ggc cgg acc aac ctc tgt tgc	912
Ile Arg Lys Arg Gly Leu Glu Cys Asp Gly Arg Thr Asn Leu Cys Cys	
290 295 300	
agg caa cag ttc ttc att gac ttc cgc ctc atc ggc tgg aac gac tgg	960
Arg Gln Gln Phe Phe Ile Asp Phe Arg Leu Ile Gly Trp Asn Asp Trp	
305 310 315 320	
atc ata gca ccc acc ggc tac tac ggc aac tac tgt gag ggc agc tgc	1008
Ile Ile Ala Pro Thr Gly Tyr Tyr Gly Asn Tyr Cys Glu Gly Ser Cys	
325 330 335	
cca gcc tac ctg gca ggg gtc ccc ggc tct gcc tcc tcc ttc cac acg	1056
Pro Ala Tyr Leu Ala Gly Val Pro Gly Ser Ala Ser Ser Phe His Thr	
340 345 350	
gct gtg gtg aac cag tac cgc atg cgg ggt ctg aac ccc ggc acg gtg	1104
Ala Val Val Asn Gln Tyr Arg Met Arg Gly Leu Asn Pro Gly Thr Val	
355 360 365	
aac tcc tgc tgc att ccc acc aag ctg agc acc atg tcc atg ctg tac	1152
Asn Ser Cys Cys Ile Pro Thr Lys Leu Ser Thr Met Ser Met Leu Tyr	
370 375 380	
ttc gat gat gag tac aac atc gtc aag cgg gac gtg ccc aac atg att	1200
Phe Asp Asp Glu Tyr Asn Ile Val Lys Arg Asp Val Pro Asn Met Ile	
385 390 395 400	
gtg gag gag tgc ggc tgc gcc tga cagtgcgaagg cagggggcacg gtgggtggggc	1254
Val Glu Glu Cys Gly Cys Ala	
405	
acggaggggca gtcccgggtg ggcttcttcc agcccccgcg ggaacggggg tacacgggtg	1314
gctgagtaca gtcattctgt tgggctgtgg agatagtgcc aggggtgcggc ctgagatatt	1374
tttctacagc ttcataagagc aaccagtcaa aaccagagcg agaaccctca actgacatga	1434
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cgaagttgcg ccttcccag cacaataaaa agcacaaga cagagacgca gagagagaga	1674
gagagccacg gagaggaaaa gcagatgcag ggggtggggag cgcagctcgg cggaggctgc	1734
gtgtgccccg tggcttttac caggcctgct ctgcctggct cgatgtctgc ttcttcccca	1794

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gcctgggatac cttcgtgctt caaggcctgg ggagcctgtc cttccatgcc cttgtcgagg 1854
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aagggttgac ccacactaga cgaaactgga ctcgtacgac tctttttata ttttttatac 2634
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<210> 72
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (70)..(1293)

<220>
 <221> misc_feature
 <222> (1)..(1494)
 <223> n = a,t,c or g

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             Met Ala Leu Gly Val Gly Arg Ala Arg Pro Gly Leu Ser
             1             5             10

tgt gga gtc atc tca ccg ccg tgc gca ccc act cgt aac tcg cac ccg 156
Cys Gly Val Ile Ser Pro Pro Cys Ala Pro Thr Arg Asn Ser His Pro
             15             20             25

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ggt cct ggc tgc acc gca tcc cct cct gca ccc cct gga tgg ccc ttc Gly Pro Gly Cys Thr Ala Ser Pro Pro Ala Pro Pro Gly Trp Pro Phe 30 35 40 45	204
agc caa cgg ggg cct ggg cga tgg tgg acc acg gag ctg cgc aag gaa Ser Gln Arg Gly Pro Gly Arg Trp Ser Thr Thr Glu Leu Arg Lys Glu 50 55 60	252
aag tcc cgg gat gcg gcc cgc agc cgg cgc agc cag gag acc gag gtg Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg Ser Gln Glu Thr Glu Val 65 70 75	300
ctg tac cag ctg gct cac acg ctg ccc ttc gcc cgc ggc gtc agc gcc Leu Tyr Gln Leu Ala His Thr Leu Pro Phe Ala Arg Gly Val Ser Ala 80 85 90	348
cac ctg gac aag gcc tct atc atg cgc ctc acc atc agc tac ctg cgc His Leu Asp Lys Ala Ser Ile Met Arg Leu Thr Ile Ser Tyr Leu Arg 95 100 105	396
atg cac cgc ctc tgc gcc gca ggg gag tgg aac cag gtg gga gca ggg Met His Arg Leu Cys Ala Ala Gly Glu Trp Asn Gln Val Gly Ala Gly 110 115 120 125	444
gga gaa cca ctg gat gcc tgc tac ctg aag gcc ctg gag ggc ttc gtc Gly Glu Pro Leu Asp Ala Cys Tyr Leu Lys Ala Leu Glu Gly Phe Val 130 135 140	492
atg gtg ctc acc gcc gag gga gac atg gct tac ctg tgg gag aat gtc Met Val Leu Thr Ala Glu Gly Asp Met Ala Tyr Leu Ser Glu Asn Val 145 150 155	540
agc aaa cac ctg ggc ctc agt cag ctg gag ctc att gga cac agc atc Ser Lys His Leu Gly Leu Ser Gln Leu Glu Leu Ile Gly His Ser Ile 160 165 170	588
ttt gat ttc atc cac ccc tgt gac caa gag gag ctt cag gac gcc ctg Phe Asp Phe Ile His Pro Cys Asp Gln Glu Glu Leu Gln Asp Ala Leu 175 180 185	636
acc ccc cag cag acc ctg tcc agg agg aag gtg gag gcc ccc acg gag Thr Pro Gln Gln Thr Leu Ser Arg Arg Lys Val Glu Ala Pro Thr Glu 190 195 200 205	684
cgg tgc ttc tcc ttg cgc atg aag agt acg ctc acc agc cgc ggg cgc Arg Cys Phe Ser Leu Arg Met Lys Ser Thr Leu Thr Ser Arg Gly Arg 210 215 220	732
acc ctc aac ctc aag gcg gcc acc tgg aag gtg ctg aac tgc tct gga Thr Leu Asn Leu Lys Ala Ala Thr Trp Lys Val Leu Asn Cys Ser Gly 225 230 235	780
cat atg agg gcc tac aag cca cct gcg cag act tct cca gct ggg agc His Met Arg Ala Tyr Lys Pro Pro Ala Gln Thr Ser Pro Ala Gly Ser 240 245 250	828
cct gac tca gag ccc ccg ctg cag tgc ctg gtg ctc atc tgc gaa gcc Pro Asp Ser Glu Pro Pro Leu Gln Cys Leu Val Leu Ile Cys Glu Ala 255 260 265	876

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atc ccc cac cca ggc agc ctg gag ccc cca ctg ggc cga ggg gcc ttc      924
Ile Pro His Pro Gly Ser Leu Glu Pro Pro Leu Gly Arg Gly Ala Phe
270                               275                               280                               285

ctc agc cgc cac agc ctg gac atg aag ttc acc tac tgt gac gac agg      972
Leu Ser Arg His Ser Leu Asp Met Lys Phe Thr Tyr Cys Asp Asp Arg
                               290                               295                               300

att gca gaa gtg gct ggc tat agt ccc gat gac ctg atc ggc tgt tcc      1020
Ile Ala Glu Val Ala Gly Tyr Ser Pro Asp Asp Leu Ile Gly Cys Ser
                               305                               310                               315

gcc tac gag tac atc cac gcg ctg gac tcc gac gcg gtc agc aag agc      1068
Ala Tyr Glu Tyr Ile His Ala Leu Asp Ser Asp Ala Val Ser Lys Ser
                               320                               325                               330

atc cac acc tgt atg tat ccc att tcc cca ggt gcg aag cca gct gcc      1116
Ile His Thr Cys Met Tyr Pro Ile Ser Pro Gly Ala Lys Pro Ala Ala
                               335                               340                               345

aca tgg ccc cca gct gac acc agg acc ccc cag ctc ccc ata ccc cag      1164
Thr Trp Pro Pro Ala Asp Thr Arg Thr Pro Gln Leu Pro Ile Pro Gln
350                               355                               360                               365

gat gca ctg cct ccc cac ctc aac acc agc tcc ctg ctc ccc aag ccc      1212
Asp Ala Leu Pro Pro His Leu Asn Thr Ser Ser Leu Leu Pro Lys Pro
                               370                               375                               380

caa gga act gtc tcc ttc ctt gcc ccc tca tac cca gtc ccc aga tct      1260
Gln Gly Thr Val Ser Phe Leu Ala Pro Ser Tyr Pro Val Pro Arg Ser
                               385                               390                               395

ttc tct ccc cat ttg ccc cct tgg tgg ccc tga tccctccc gatccccctc      1311
Phe Ser Pro His Leu Pro Pro Trp Trp Pro
                               400                               405

ctcagtgctg agcaagggcc aggcagtaac agggcagtat cgcttctctgg cccggagtgg      1371

tggctacctg tggacccaga cccagggccac agtgggtgtca gggggacggg gcccccagtc      1431

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<210> 73
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 <213> Homo sapiens

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Glu Glu Phe Asn Gln Asp Pro Glu Phe Asn Asn Thr Asp Gln Ile Asp		
15 20 25		
ctg tat gat gat gtg ctg aca gcc acc tca cag ccc tca gat gac aga	265	
Leu Tyr Asp Asp Val Leu Thr Ala Thr Ser Gln Pro Ser Asp Asp Arg		
30 35 40 45		
agc agc agc act gaa cca cct cct cct gtt cgc cag gag cca tct ccc	313	
Ser Ser Ser Thr Glu Pro Pro Pro Pro Val Arg Gln Glu Pro Ser Pro		
50 55 60		
aag ccc aac aac aag acc cct gca att ctg tat acc tac agt ggc ctg	361	
Lys Pro Asn Asn Lys Thr Pro Ala Ile Leu Tyr Thr Tyr Ser Gly Leu		
65 70 75		
cgt aat aga cga gct gcc gtt tat gtg ggc agc ttc tcc tgg tgg acc	409	
Arg Asn Arg Arg Ala Ala Val Tyr Val Gly Ser Phe Ser Trp Trp Thr		
80 85 90		
aca gac cag cag ctg atc cag gtt att cgc tct ata gga gtc tat gat	457	
Thr Asp Gln Gln Leu Ile Gln Val Ile Arg Ser Ile Gly Val Tyr Asp		
95 100 105		
gtg gtg gag ttg aaa ttt gca gag aat cga gca aat ggc cag tcc aaa	505	
Val Val Glu Leu Lys Phe Ala Glu Asn Arg Ala Asn Gly Gln Ser Lys		
110 115 120 125		
ggg tat gct gag gtg gtg gta gcc tct gaa aac tct gtc cac aaa ttg	553	
Gly Tyr Ala Glu Val Val Val Ala Ser Glu Asn Ser Val His Lys Leu		
130 135 140		
ttg gaa ctg cta cca ggg aaa gtt ctt aat gga gaa aaa gtg gac gtg	601	
Leu Glu Leu Leu Pro Gly Lys Val Leu Asn Gly Glu Lys Val Asp Val		
145 150 155		
agg ccg gcc acc cgg cag aac ctg tca cag ttt gag gca cag gct cgg	649	
Arg Pro Ala Thr Arg Gln Asn Leu Ser Gln Phe Glu Ala Gln Ala Arg		
160 165 170		
aaa cgt gag tgt gtc cga gtc cca aga ggg gga ata cct cca cgg gcc	697	
Lys Arg Glu Cys Val Arg Val Pro Arg Gly Gly Ile Pro Pro Arg Ala		
175 180 185		
cat tcc cga gat tct agt gat tct gct gat gga cgg gcc aca ccc tct	745	
His Ser Arg Asp Ser Ser Asp Ser Ala Asp Gly Arg Ala Thr Pro Ser		
190 195 200 205		
gag aac ctt gta ccc tca tct gct cgt gtg gat aag ccc ccc agt gtg	793	
Glu Asn Leu Val Pro Ser Ser Ala Arg Val Asp Lys Pro Pro Ser Val		
210 215 220		
ctg ccc tac ttc aat cgt cct cct tgg gcc ctt ccc ctg atg ggt ctg	841	
Leu Pro Tyr Phe Asn Arg Pro Pro Ser Ala Leu Pro Leu Met Gly Leu		
225 230 235		
ccc cca cca cca att cca ccc cca cca cct ctc tcc tca agc ttt ggg	889	

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<210> 74
<211> 2184
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (40)..(2124)

<400> 74
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				Met Gly Ala Pro Ala	
				1 5	
tgc gcc ctc gcg ctc tgc gtg gcc gtg gcc atc gtg gcc ggc gcc tcc	102				
Cys Ala Leu Ala Leu Cys Val Ala Val Ala Ile Val Ala Gly Ala Ser					
	10		15	20	
tgc gag tcc ttg ggg acg gag cag cgc gtc gtg ggg cga gcg gca gaa	150				
Ser Glu Ser Leu Gly Thr Glu Gln Arg Val Val Gly Arg Ala Ala Glu					
	25		30	35	
gtc ccg ggc cca gag ccc ggc cag cag gag cag ttg gtc ttc ggc agc	198				
Val Pro Gly Pro Glu Pro Gly Gln Gln Glu Gln Leu Val Phe Gly Ser					
	40		45	50	
ggg gat gct gtg gag ctg agc tgt ccc ccg ccc ggg ggt ggt ccc atg	246				
Gly Asp Ala Val Glu Leu Ser Cys Pro Pro Pro Gly Gly Gly Pro Met					
	55		60	65	
ggg ccc act gtc tgg gtc aag gat ggc aca ggg ctg gtg ccc tcg gag	294				
Gly Pro Thr Val Trp Val Lys Asp Gly Thr Gly Leu Val Pro Ser Glu					
	70		75	80	85
cgt gtc ctg gtg ggg ccc cag cgg ctg cag gtg ctg aat gcc tcc cac	342				
Arg Val Leu Val Gly Pro Gln Arg Leu Gln Val Leu Asn Ala Ser His					
	90		95	100	
gag gac tcc ggg gcc tac agc tgc cgg cag cgg ctg acg cag cgc gta	390				
Glu Asp Ser Gly Ala Tyr Ser Cys Arg Gln Arg Leu Thr Gln Arg Val					
	105		110	115	
ctg tgc cac ttc agt gtg cgg gtg aca gac gct cca tcc tcg gga gat	438				
Leu Cys His Phe Ser Val Arg Val Thr Asp Ala Pro Ser Ser Gly Asp					
	120		125	130	
gac gaa gac ggg gag gac gag gct gag gac aca ggt gtg gac aca ggg	486				
Asp Glu Asp Gly Glu Asp Glu Ala Glu Asp Thr Gly Val Asp Thr Gly					
	135		140	145	
gcc cct tac tgg aca cgg ccc gag cgg atg gac aag aag ctg ctg gcc	534				
Ala Pro Tyr Trp Thr Arg Pro Glu Arg Met Asp Lys Lys Leu Leu Ala					
	150		155	160	165
gtg ccg gcc gcc aac acc gtc cgc ttc cgc tgc cca gcc gct ggc aac	582				
Val Pro Ala Ala Asn Thr Val Arg Phe Arg Cys Pro Ala Ala Gly Asn					
	170		175	180	
ccc act ccc tcc atc tcc tgg ctg aag aac ggc agg gag ttc cgc ggc	630				
Pro Thr Pro Ser Ile Ser Trp Leu Lys Asn Gly Arg Glu Phe Arg Gly					
	185		190	195	
gag cac cgc att gga ggc atc aag ctg cgg cat cag cag tgg agc ctg	678				
Glu His Arg Ile Gly Gly Ile Lys Leu Arg His Gln Gln Trp Ser Leu					
	200		205	210	
gtc atg gaa agc gtg gtg ccc tcg gac cgc ggc aac tac acc tgc gtc	726				
Val Met Glu Ser Val Val Pro Ser Asp Arg Gly Asn Tyr Thr Cys Val					
	215		220	225	
gtg gag aac aag ttt ggc agc atc cgg cag acg tac acg ctg gac gtg	774				

Val 230	Glu	Asn	Lys	Phe	Gly 235	Ser	Ile	Arg	Gln	Thr 240	Tyr	Thr	Leu	Asp	Val 245	
ctg	gag	cgc	tcc	ccg	cac	cgg	ccc	atc	ctg	cag	gcg	ggg	ctg	ccg	gcc	822
Leu	Glu	Arg	Ser	Pro	His 250	Arg	Pro	Ile	Leu 255	Gln	Ala	Gly	Leu	Pro	Ala 260	
aac	cag	acg	gcg	gtg	ctg	ggc	agc	gac	gtg	gag	ttc	cac	tgc	aag	gtg	870
Asn	Gln	Thr	Ala 265	Val	Leu	Gly	Ser	Asp 270	Val	Glu	Phe	His	Cys 275	Lys	Val	
tac	agt	gac	gca	cag	ccc	cac	atc	cag	tgg	ctc	aag	cac	gtg	gag	gtg	918
Tyr	Ser	Asp 280	Ala	Gln	Pro	His	Ile 285	Gln	Trp	Leu	Lys	His	Val 290	Glu	Val	
aac	ggc	agc	aag	gtg	ggc	ccg	gac	ggc	aca	ccc	tac	gtt	acc	gtg	ctc	966
Asn	Gly 295	Ser	Lys	Val	Gly	Pro	Asp 300	Gly	Thr	Pro	Tyr	Val 305	Thr	Val	Leu	
aag	gtg	tcc	ctg	gag	tcc	aac	gcg	tcc	atg	agc	tcc	aac	aca	cca	ctg	1014
Lys	Val	Ser	Leu	Glu	Ser 315	Asn	Ala	Ser	Met	Ser 320	Ser	Asn	Thr	Pro	Leu 325	
gtg	cgc	atc	gca	agg	ctg	tcc	tca	ggg	gag	ggc	ccc	acg	ctg	gcc	aat	1062
Val	Arg	Ile	Ala 330	Arg	Leu	Ser	Ser	Gly	Glu 335	Gly	Pro	Thr	Leu	Ala	Asn 340	
gtc	tcc	gag	ctc	gag	ctg	cct	gcc	gac	ccc	aaa	tgg	gag	ctg	tct	cgg	1110
Val	Ser	Glu	Leu 345	Glu	Leu	Pro	Ala	Asp 350	Pro	Lys	Trp	Glu	Leu 355	Ser	Arg	
gcc	cgg	ctg	acc	ctg	ggc	aag	ccc	ctt	ggg	gag	ggc	tgc	ttc	ggc	cag	1158
Ala	Arg	Leu 360	Thr	Leu	Gly	Lys	Pro 365	Leu	Gly	Glu	Gly	Cys 370	Phe	Gly	Gln	
gtg	gtc	atg	gcg	gag	gcc	atc	ggc	att	gac	aag	gac	cgg	gcc	gcc	aag	1206
Val	Val	Met	Ala	Glu	Ala 380	Ile	Gly	Ile	Asp	Lys 385	Asp	Arg	Ala	Ala	Lys	
cct	gtc	acc	gta	gcc	gtg	aag	atg	ctg	aaa	gac	gat	gcc	act	gac	aag	1254
Pro	Val	Thr	Val	Ala	Val 395	Lys	Met	Leu	Lys 400	Asp	Asp	Ala	Thr	Asp 405	Lys	
gac	ctg	tcg	gac	ctg	gtg	tct	gag	atg	gag	atg	atg	aag	atg	atc	ggg	1302
Asp	Leu	Ser	Asp 410	Leu	Val	Ser	Glu	Met	Glu 415	Met	Met	Lys	Met	Ile 420	Gly	
aaa	cac	aaa	aac	atc	atc	aac	ctg	ctg	ggc	gcc	tgc	acg	cag	ggc	ggg	1350
Lys	His	Lys	Asn 425	Ile	Ile	Asn	Leu	Leu 430	Gly	Ala	Cys	Thr	Gln 435	Gly	Gly	
ccc	ctg	tac	gtg	ctg	gtg	gag	tac	gcg	gcc	aag	ggt	aac	ctg	cgg	gag	1398
Pro	Leu	Tyr 440	Val	Leu	Val	Glu	Tyr 445	Ala	Ala	Lys	Gly	Asn 450	Leu	Arg	Glu	
ttt	ctg	cgg	gcg	cgg	cgg	ccc	ccg	ggc	ctg	gac	tac	tcc	ttc	gac	acc	1446
Phe	Leu	Arg	Ala 455	Arg	Arg	Pro	Pro 460	Gly	Leu	Asp	Tyr 465	Ser	Phe	Asp	Thr	
tgc	aag	ccg	ccc	gag	gag	cag	ctc	acc	ttc	aag	gac	ctg	gtg	tcc	tgt	1494
Cys	Lys	Pro	Pro	Glu	Glu	Gln	Leu	Thr	Phe	Lys	Asp	Leu	Val	Ser	Cys	

470	475	480	485	
gcc tac cag gtg gcc cgg ggc atg gag tac ttg gcc tcc cag aag tgc Ala Tyr Gln Val Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys	490	495	500	1542
atc cac agg gac ctg gct gcc cgc aat gtg ctg gtg acc gag gac aac Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn	505	510	515	1590
gtg atg aag atc gca gac ttc ggg ctg gcc cgg gac gtg cac aac ctc Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Val His Asn Leu	520	525	530	1638
gac tac tac aag aag aca acc aac ggc cgg ctg ccc gtg aag tgg atg Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met	535	540	545	1686
gcg cct gag gcc ttg ttt gac cga gtc tac act cac cag agt gac gtc Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val	550	555	560	1734
tgg tcc ttt ggg gtc ctg ctc tgg gag atc ttc acg ctg ggg ggc tcc Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser	570	575	580	1782
ccg tac ccc ggc atc cct gtg gag gag ctc ttc aag ctg ctg aag gag Pro Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu	585	590	595	1830
ggc cac cgc atg gac aag ccc gcc aac tgc aca cac gac ctg tac atg Gly His Arg Met Asp Lys Pro Ala Asn Cys Thr His Asp Leu Tyr Met	600	605	610	1878
atc atg cgg gag tgc tgg cat gcc gcg ccc tcc cag agg ccc acc ttc Ile Met Arg Glu Cys Trp His Ala Ala Pro Ser Gln Arg Pro Thr Phe	615	620	625	1926
aag cag ctg gtg gag gac ctg gac cgt gtc ctt acc gtg acg tcc acc Lys Gln Leu Val Glu Asp Leu Asp Arg Val Leu Thr Val Thr Ser Thr	630	635	640	1974
gac gag tac ctg gac ctg tcg gcg cct ttc gag cag tac tcc ccg ggt Asp Glu Tyr Leu Asp Leu Ser Ala Pro Phe Glu Gln Tyr Ser Pro Gly	650	655	660	2022
ggc cag gac acc ccc agc tcc agc tcc tca ggg gac gac tcc gtg ttt Gly Gln Asp Thr Pro Ser Ser Ser Ser Gly Asp Asp Ser Val Phe	665	670	675	2070
gcc cac gac ctg ctg ccc ccg gcc cca ccc agc agt ggg ggc tcg cgg Ala His Asp Leu Leu Pro Pro Ala Pro Pro Ser Ser Gly Gly Ser Arg	680	685	690	2118
acg tga agggccactg gtccccaaca atgtgagggg tccctagcag ccctccctgc Thr				2174
tgctggtgca				2184

<210> 75
 <211> 806
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (487) .. (648)

<400> 75
 ctctgacttc tggcttgcac tgtttccagt gagaaatctg ctactatttt tatcttagtg 60
 tctctgtagt gtgtcttggc tgccttttagg attttctctt ttcattggcc ttgagtcctt 120
 ccttcttccc ctacacatgtg gggactttta attccatgta tattaggctg catgaagctt 180
 cccacaacc tactgatgct cttttcatta gaaacatttc ttactctgcg tttcattttg 240
 gatagtttct attcctatgt tttcaaacc accaataaaa gattctgcaa catctgacct 300
 gccattaatc ccgtccagtg tatttttcat ctctgtatt gtagttttca tctctacaat 360
 ccagcttgag cctttgggta tatcttccat gttgctcctg cactgtttga acatgcagaa 420
 tggctagtgg ggcagtgagc tgaggagaag ggacagaggg gaagctcggc tgttgggtct 480
 acgggt atg atg gag acc atg cag ctg aaa gta aac cgt cac ccc ttc 528
 Met Met Glu Thr Met Gln Leu Lys Val Asn Arg His Pro Phe
 1 5 10
 tgc ttc agt gtg aaa ggc cag gtg aag atg ctg cag ctg atg agg ctg 576
 Cys Phe Ser Val Lys Gly Gln Val Lys Met Leu Gln Leu Met Arg Leu
 15 20 25 30
 ggc ctt agg gtg cgg ggg gtg gtg gaa tct gct tgt .ggg cgg gag atg 624
 Gly Leu Arg Val Arg Gly Val Val Glu Ser Ala Cys Gly Arg Glu Met
 35 40 45
 tgg cta tgt ggc tat aaa gga tga agatgaacgc cctgtttgct tttcagcctc 678
 Trp Leu Cys Gly Tyr Lys Gly
 50
 gcttggatca aggttaaaag gccggttggt gccttcttgg tggaagaaag agagagataa 738
 ggcactgtcc tccccttcgg aggggtctggg gatacactaa tccatcaaaa ccactgaggg 798
 ctgggcgt 806

<210> 76
 <211> 357
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (80) .. (208)

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<400> 76
gcaagagagg ggaaccagag aggacccaga ggggagagac agagcagcaa gcagtggatt      60
gctccttgac gacgccagc atg agc tcc ttc tcc acc acc acc gtg agc ttc      112
                Met Ser Ser Phe Ser Thr Thr Thr Val Ser Phe
                  1                5                10

ctc ctt tta ctg gca ttc cag ctc cta ggt cag acc aga gct aat ccc      160
Leu Leu Leu Leu Ala Phe Gln Leu Leu Gly Gln Thr Arg Ala Asn Pro
                15                20                25

atg tac aat gcc gtg tcc aac gca gac ctg tta ctg aaa gtg gtt tga      208
Met Tyr Asn Ala Val Ser Asn Ala Asp Leu Leu Leu Lys Val Val
                30                35                40

aagtgaataa acttcagcac catggacaga agacaaatgc ctgcgttggt gtgctttctt      268
tcttcttggg aagagaattc aggccgatat tccttgtcgt ttactcttt gtcagaggaa      328
agaatgctga gtttttcttc ttcttttca      357

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<210> 77
<211> 1297
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (80)..(949)

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<400> 77
cgcccggaat tcccgggtcg aggcaacgct tcgatttaga atcctgcagc accccaccat      60
ctaagagcaa gagccaaag atg ttt gtc ttg ctc tat gtt aca agt ttt gcc      112
                Met Phe Val Leu Leu Tyr Val Thr Ser Phe Ala
                  1                5                10

att tgt gcc agt gga caa ccc cgg ggt aat cag ttg aaa gga gag aac      160
Ile Cys Ala Ser Gly Gln Pro Arg Gly Asn Gln Leu Lys Gly Glu Asn
                15                20                25

tac tcc ccc agg tat atc tgc agc att cct ggc ttg cct gga cct cca      208
Tyr Ser Pro Arg Tyr Ile Cys Ser Ile Pro Gly Leu Pro Gly Pro Pro
                30                35                40

ggg ccc cct gga gca aat ggt tcc cct ggg ccc cat ggt cgc atc ggc      256
Gly Pro Pro Gly Ala Asn Gly Ser Pro Gly Pro His Gly Arg Ile Gly
                45                50                55

ctt cca gga aga gat ggt aga gac ggc agg aaa gga gag aaa ggt gaa      304
Leu Pro Gly Arg Asp Gly Arg Asp Gly Arg Lys Gly Glu Lys Gly Glu
                60                65                70                75

aag gga act gca ggt ttg aga ggt aag act gga ccg cta ggt ctt gcc      352
Lys Gly Thr Ala Gly Leu Arg Gly Lys Thr Gly Pro Leu Gly Leu Ala
                80                85                90

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ggt gag aaa ggg gac caa gga gag act ggg aag aaa gga ccc ata gga 400
 Gly Glu Lys Gly Asp Gln Gly Glu Thr Gly Lys Lys Gly Pro Ile Gly
 95 100 105

cca gag gga gag aaa gga gaa gta ggt cca att ggt cct cct gga cca 448
 Pro Glu Gly Glu Lys Gly Glu Val Gly Pro Ile Gly Pro Pro Gly Pro
 110 115 120

aag gga gac aga gga gaa caa ggg gac ccg ggg ctg cct gga gtt tgc 496
 Lys Gly Asp Arg Gly Glu Gln Gly Asp Pro Gly Leu Pro Gly Val Cys
 125 130 135

aga tgt gga agc atc gtg ctc aaa tcc gcc ttt tct gtt ggc atc aca 544
 Arg Cys Gly Ser Ile Val Leu Lys Ser Ala Phe Ser Val Gly Ile Thr
 140 145 150 155

acc agc tac cca gaa gaa aga cta cct att ata ttt aac aag gtc ctc 592
 Thr Ser Tyr Pro Glu Glu Arg Leu Pro Ile Ile Phe Asn Lys Val Leu
 160 165 170

ttc aac gag gga gag cac tac aac cct gcc aca ggg aag ttc atc tgt 640
 Phe Asn Glu Gly Glu His Tyr Asn Pro Ala Thr Gly Lys Phe Ile Cys
 175 180 185

gct ttc cca ggg atc tat tac ttt tct tat gat atc aca ttg gct aat 688
 Ala Phe Pro Gly Ile Tyr Tyr Phe Ser Tyr Asp Ile Thr Leu Ala Asn
 190 195 200

aag cat ctg gca atc gga ctg gta cac aat ggg caa tac cgg ata aag 736
 Lys His Leu Ala Ile Gly Leu Val His Asn Gly Gln Tyr Arg Ile Lys
 205 210 215

acc ttc gac gcc aac aca gga aac cat gat gtg gct tcg ggg tcc aca 784
 Thr Phe Asp Ala Asn Thr Gly Asn His Asp Val Ala Ser Gly Ser Thr
 220 225 230 235

gtc atc tat ctg cag cca gaa gat gaa gtc tgg ctg gag att ttc ttc 832
 Val Ile Tyr Leu Gln Pro Glu Asp Glu Val Trp Leu Glu Ile Phe Phe
 240 245 250

aca gac cag aat ggc ctc ttc tca gac cca ggt tgg gca gac agc tta 880
 Thr Asp Gln Asn Gly Leu Phe Ser Asp Pro Gly Trp Ala Asp Ser Leu
 255 260 265

ttc tcc ggg ttt ctc tta tac gtt gac aca gat tac cta gat tcc ata 928
 Phe Ser Gly Phe Leu Leu Tyr Val Asp Thr Asp Tyr Leu Asp Ser Ile
 270 275 280

tca gaa gat gat gaa ttg tga tc aggaccaaga tccctgtggt aaacactctg 981
 Ser Glu Asp Asp Glu Leu
 285

attgaatctg gggttccaga aggtggaaca agcaggaatg ggatccaaag agactccac 1041

tcagattcta aagcatttaa agacaattct agcagaattt atcaaaacaa gatgaaacac 1101

agaaaagtgt aaaccacaac aaaatgaatt ctattaaaga atagccccag atataaattc 1161

tcttgaaagc aatgttcata aatatttaag caaattaaag acaatgttaa caaattttct 1221

attaaatgcc ctgagtgata aaaccagttg gcaataatat tgccttatta aatcttcaaa 1281

aaataaaaaa aaaaaa

1297

<210> 78
 <211> 943
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (189)..(701)

<400> 78
 gcattcccgg gtcgactacg ctgtgcacga gcgcccgcga taagacgact gactatacgc 60
 gactccgccc gcctcccat tcaactgggaa ctaacacccg gcgcccgcga gacatctcta 120
 ttcccgccctc tccgacccgg tctcacttcg ctctctgggca gctgcgcgga gaactggggc 180
 tcaccgtc atg gat gct cta tca gaa gca aat ggc aca ttt gca tta aac 230
 Met Asp Ala Leu Ser Glu Ala Asn Gly Thr Phe Ala Leu Asn
 1 5 10
 ctt ttg aaa aag cta ggg gaa aac aac tca aac aac tta ttt ttt tcc 278
 Leu Leu Lys Lys Leu Gly Glu Asn Asn Ser Asn Asn Leu Phe Phe Ser
 15 20 25 30
 cca ctg agc ata tca tca gcc ttg gcc atg gtt ttc atg ggg gca aag 326
 Pro Leu Ser Ile Ser Ser Ala Leu Ala Met Val Phe Met Gly Ala Lys
 35 40 45
 gga aac act gca gct cag atg tct cag gca ctt tgt ttt agt aaa atc 374
 Gly Asn Thr Ala Ala Gln Met Ser Gln Ala Leu Cys Phe Ser Lys Ile
 50 55 60
 gga ggt gaa gat gga gat att cat cga ggt ttt cag tca ctt ctt gtt 422
 Gly Gly Glu Asp Gly Asp Ile His Arg Gly Phe Gln Ser Leu Leu Val
 65 70 75
 gca att aac aga act gac act gaa tat gtg ctt aga act gcc aac ggg 470
 Ala Ile Asn Arg Thr Asp Thr Glu Tyr Val Leu Arg Thr Ala Asn Gly
 80 85 90
 ctg ttt gga gaa aag tct tat gat ttc ctg aca ggt ttt aca gat tcc 518
 Leu Phe Gly Glu Lys Ser Tyr Asp Phe Leu Thr Gly Phe Thr Asp Ser
 95 100 105 110
 tgt ggc aaa ttt tac caa gca acg ata aaa cag cta gac ttt gtg aat 566
 Cys Gly Lys Phe Tyr Gln Ala Thr Ile Lys Gln Leu Asp Phe Val Asn
 115 120 125
 gat aca gag aag tcc aca aca cgt gta aac tcc tgg gtt gct gat aaa 614
 Asp Thr Glu Lys Ser Thr Thr Arg Val Asn Ser Trp Val Ala Asp Lys
 130 135 140
 act aaa ggt gaa aat ata ttg tta ttc tat ttc gat aat att tta aac 662
 Thr Lys Gly Glu Asn Ile Leu Leu Phe Tyr Phe Asp Asn Ile Leu Asn
 145 150 155

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agt ttt ata gtc agt tct tta caa aac tgt caa ata taa aaaggagtcc      711
Ser Phe Ile Val Ser Ser Leu Gln Asn Cys Gln Ile
    160                      165                      170

ttttttctct aaacaactat gcaaacatta aaacctttct ttggaaatat agccaactcg      771

agtccttttc tctagctata gcttttccct tatcaagtat ctgtgatgtc tctctagatg      831

aaataatctc ttgcagggtt ttcacttggt aatattaggt agtacttctt atcacaaata      891

gcgtgtaaga taggaagtta acgaatcggt gacagcgaag tcgacccggg aa          943

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<210> 79
<211> 1370
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (302)..(940)

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<400> 79
tcgggtctat ccacgcatcc gaacacaagc caggtgagtc ttcatgctgg tgtttaaaag      60

tttcctccac atcagtatag ccacgctgat gtctactctg ttgaagccag gtgcgcagtg      120

atctactgac taatggattc tccaattggt aagcctatgt tacaggacaa aggccgtcgc      180

tttgtaaaag cttgaagtgc agtttgctgc tgagtacaga agacctttgc aaacagagag      240

gggagatttt ctctgtaagg ttgcaaacaa gagcagggtcc tggaagataa gattccccgc      300

c   atg tta tcc tcc gtg gtg ttt tgg gga cta att gcc ctc att ggc      346
    Met Leu Ser Ser Val Val Phe Trp Gly Leu Ile Ala Leu Ile Gly
      1                      5                      10                      15

act tcc agg ggc tca tac ccc ttc agt cac tca atg aag cct cac cta      394
Thr Ser Arg Gly Ser Tyr Pro Phe Ser His Ser Met Lys Pro His Leu
      20                      25                      30

cat cca cgc ctg tac cac ggc tgc tat ggg gac atc atg acc atg aag      442
His Pro Arg Leu Tyr His Gly Cys Tyr Gly Asp Ile Met Thr Met Lys
      35                      40                      45

acc tct ggg gcc act tgt gat gca aac agt gtg atg aac tgc ggg atc      490
Thr Ser Gly Ala Thr Cys Asp Ala Asn Ser Val Met Asn Cys Gly Ile
      50                      55                      60

cgt ggt tct gaa atg ttt gct gag atg gat ttg agg gcc ata aaa cct      538
Arg Gly Ser Glu Met Phe Ala Glu Met Asp Leu Arg Ala Ile Lys Pro
      65                      70                      75

tac cag act ctg atc aaa gaa gtc ggg cag aga cat tgc gtg gac cct      586
Tyr Gln Thr Leu Ile Lys Glu Val Gly Gln Arg His Cys Val Asp Pro
      80                      85                      90                      95

gct gtc atc gca gcc atc atc tcc agg gaa agc cat ggc gga tct gtc      634

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Ala Val Ile Ala Ala Ile Ile Ser Arg Glu Ser His Gly Gly Ser Val	
100 105 110	
ctg caa gac ggc tgg gac cac agg gga ctt aaa ttt ggc ttg atg cag	682
Leu Gln Asp Gly Trp Asp His Arg Gly Leu Lys Phe Gly Leu Met Gln	
115 120 125	
ctt gat aaa caa acg tac cac cct gtc ggt gcc tgg gat agc aaa gag	730
Leu Asp Lys Gln Thr Tyr His Pro Val Gly Ala Trp Asp Ser Lys Glu	
130 135 140	
cac ctt tca cag gct act ggg att cta aca gag aga att aag gca atc	778
His Leu Ser Gln Ala Thr Gly Ile Leu Thr Glu Arg Ile Lys Ala Ile	
145 150 155	
cag aaa aaa ttc ccc acg tgg agt gtt gct cag cac ctc aaa ggt ggt	826
Gln Lys Lys Phe Pro Thr Trp Ser Val Ala Gln His Leu Lys Gly Gly	
160 165 170 175	
ctc tca gct ttt aag tca gga att gaa gcg att gcc acc cca tcg gac	874
Leu Ser Ala Phe Lys Ser Gly Ile Glu Ala Ile Ala Thr Pro Ser Asp	
180 185 190	
ata gac aat gac ttc gtc aat gat atc att gct cga gct aag ttc tat	922
Ile Asp Asn Asp Phe Val Asn Asp Ile Ile Ala Arg Ala Lys Phe Tyr	
195 200 205	
aaa aga caa agc ttc tag gcaaag ctctgtgggt gggccagggtt ggcagagtgc	976
Lys Arg Gln Ser Phe	
210	
tcagatggcc gcctttgaga gttttacgtg aatgtgttgt atacaacact ggcacagaaa	1036
tgattaaaat catgaaagaa aattcatttc ccaattttct gaatgaaaat aatcattgaa	1096
aaaaggaaag aaaaataaaa gaaatccatc cagttcacaa tatggttcct aggaaacgga	1156
catagacata tatataacta ctttgagta aatgtgaata tcatggcaaa tgggtccctag	1216
gtattccagc caggcttcac tttagcctgt gattccaatg cccacctact cctgtctac	1276
cagaattgct aacaagttaa gtaagcctta cccgagcctt tgtctttttt ccagtatctg	1336
cccagagccc tcaagctttg cttatgagaa gttc	1370

<210> 80

<211> 1960

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (161) .. (1906)

<400> 80

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cgcgcgggccc	ggccccgcggg	gctccccggcc	gccgcagctg	atg	gtg	ttc	cgc	aac	175
				Met	Val	Phe	Arg	Asn	
				1				5	
gtg	ggt	cgg	ccg	ccg	gag	gag	gag	gac	223
Val	Gly	Arg	Pro	Pro	Glu	Glu	Glu	Asp	
			10					15	20
gga	ccc	tcg	gaa	ctg	ctg	tgt	ccc	cgg	271
Gly	Pro	Ser	Glu	Leu	Leu	Cys	Pro	Arg	
			25				30		35
aag	gcc	ctg	ccg	ccg	ggc	ttg	gcg	ctc	319
Lys	Ala	Leu	Pro	Pro	Gly	Leu	Ala	Leu	
		40				45		50	
gct	gga	cta	gag	gcg	cag	ttg	gcg	gct	367
Ala	Gly	Leu	Glu	Ala	Gln	Leu	Ala	Ala	
		55			60			65	
ggg	ccg	ggg	gtc	aag	aca	gtc	ggg	ggg	415
Gly	Pro	Gly	Val	Lys	Thr	Val	Gly	Gly	
		70			75			80	85
ccc	cct	cag	ccg	ccc	cct	ccg	cag	ccc	463
Pro	Pro	Gln	Pro	Pro	Pro	Pro	Gln	Pro	
			90				95		100
cag	gcc	ggg	gag	gac	ccc	acg	gaa	acg	511
Gln	Ala	Gly	Glu	Asp	Pro	Thr	Glu	Thr	
			105				110		115
gag	ggc	ttg	gaa	tcg	gag	gcc	gag	agc	559
Glu	Gly	Leu	Glu	Ser	Glu	Ala	Glu	Ser	
		120				125		130	
gaa	gag	gag	ctc	agc	agc	ccg	ggg	cgc	607
Glu	Glu	Glu	Leu	Ser	Ser	Pro	Gly	Arg	
		135				140		145	
ctt	ctg	ctg	cag	ccc	cca	ggc	cct	gaa	655
Leu	Leu	Leu	Gln	Pro	Pro	Gly	Pro	Glu	
				155				160	165
ctg	cag	gac	ttg	gtc	cct	ctg	ggg	cgc	703
Leu	Gln	Asp	Leu	Val	Pro	Leu	Gly	Arg	
				170			175		180
cag	cag	cag	cag	cag	caa	cct	ccc	ccg	751
Gln	Gln	Gln	Gln	Gln	Gln	Pro	Pro	Pro	
			185				190		195
ctc	cgg	cca	ctc	gcg	ggg	cct	tct	cgg	799
Leu	Arg	Pro	Leu	Ala	Gly	Pro	Ser	Arg	
		200				205		210	
ctc	agt	cgc	ctc	ttt	cgc	acc	aag	agc	847
Leu	Ser	Arg	Leu	Phe	Arg	Thr	Lys	Ser	
		215				220		225	

ggg gat ggg acc ggc aag agg cct tct gga gag ctg gct gct tca gct Gly Asp Gly Thr Gly Lys Arg Pro Ser Gly Glu Leu Ala Ala Ser Ala 230 235 240 245	895
gcg agc ctg aca gac atg gga ggc tct gcg ggc cgg gag ctg gac gcg Ala Ser Leu Thr Asp Met Gly Gly Ser Ala Gly Arg Glu Leu Asp Ala 250 255 260	943
ggg agg aaa ccc aag ttg aca aga act caa agt gcc ttt tct ccg gtc Gly Arg Lys Pro Lys Leu Thr Arg Thr Gln Ser Ala Phe Ser Pro Val 265 270 275	991
tcc ttc agc ccc ctg ttc aca ggt gaa act gtg tcg ctt gtg gat gtg Ser Phe Ser Pro Leu Phe Thr Gly Glu Thr Val Ser Leu Val Asp Val 280 285 290	1039
gac att tct cag cgg ggc ctg acc tct cca cac cct cca act ccc cct Asp Ile Ser Gln Arg Gly Leu Thr Ser Pro His Pro Pro Thr Pro Pro 295 300 305	1087
cct cct ccg aga aga agc ctc agc ctc cta gat gat atc agt ggg acg Pro Pro Pro Arg Arg Ser Leu Ser Leu Leu Asp Asp Ile Ser Gly Thr 310 315 320 325	1135
ctg cct aca tct gtc ctt gtg gct ccg atg ggg tct tcc ttg cag tct Leu Pro Thr Ser Val Leu Val Ala Pro Met Gly Ser Ser Leu Gln Ser 330 335 340	1183
ttc ccc cta cct ccg cct cct cca ccc cat gcc cca gat gca ttt ccc Phe Pro Leu Pro Pro Pro Pro Pro His Ala Pro Asp Ala Phe Pro 345 350 355	1231
cgg att gct ccc atc cga gca gct gaa tcc ctg cac agc caa ccc cca Arg Ile Ala Pro Ile Arg Ala Ala Glu Ser Leu His Ser Gln Pro Pro 360 365 370	1279
cag cac ctc cag tgt ccc ctc tac cgg cct gac tcg agc agc ttt gca Gln His Leu Gln Cys Pro Leu Tyr Arg Pro Asp Ser Ser Ser Phe Ala 375 380 385	1327
gcc agc ctt cga gag ttg gag aag tgt ggt tgg tat tgg ggg cca atg Ala Ser Leu Arg Glu Leu Glu Lys Cys Gly Trp Tyr Trp Gly Pro Met 390 395 400 405	1375
aat tgg gaa gat gca gag atg aag ctg aaa ggg aaa cca gat ggt tct Asn Trp Glu Asp Ala Glu Met Lys Leu Lys Gly Lys Pro Asp Gly Ser 410 415 420	1423
ttc ctg gta cga gac agt tct gat cct cgt tac atc ctg agc ctc agt Phe Leu Val Arg Asp Ser Ser Asp Pro Arg Tyr Ile Leu Ser Leu Ser 425 430 435	1471
ttc cga tca cag ggt atc acc cac cac act aga atg gag cac tac aga Phe Arg Ser Gln Gly Ile Thr His His Thr Arg Met Glu His Tyr Arg 440 445 450	1519
gga acc ttc agc ctg tgg tgt cat ccc aag ttt gag gac cgc tgt caa Gly Thr Phe Ser Leu Trp Cys His Pro Lys Phe Glu Asp Arg Cys Gln 455 460 465	1567
tct gtt gta gag ttt att aag aga gcc att atg cac tcc aag aat gga	1615

Ser Val Val Glu Phe Ile Lys Arg Ala Ile Met His Ser Lys Asn Gly	
470 475 480 485	
aag ttt ctc tat ttc tta aga tcc agg gtt cca gga ctg cca cca act	1663
Lys Phe Leu Tyr Phe Leu Arg Ser Arg Val Pro Gly Leu Pro Pro Thr	
490 495 500	
cct gtc cag ctg ctc tat cca gtg tcc cga ttc agc aat gtc aaa tcc	1711
Pro Val Gln Leu Leu Tyr Pro Val Ser Arg Phe Ser Asn Val Lys Ser	
505 510 515	
ctc cag cac ctt tgc aga ttc cgg ata cga cag ctc gtc agg ata gat	1759
Leu Gln His Leu Cys Arg Phe Arg Ile Arg Gln Leu Val Arg Ile Asp	
520 525 530	
cac atc cca gat ctc cca ctg cct aaa cct ctg atc tct tat atc cga	1807
His Ile Pro Asp Leu Pro Leu Pro Lys Pro Leu Ile Ser Tyr Ile Arg	
535 540 545	
aag ttc tac tac tat gat cct cag gaa gag gta tac ctg tct cta aag	1855
Lys Phe Tyr Tyr Tyr Asp Pro Gln Glu Glu Val Tyr Leu Ser Leu Lys	
550 555 560 565	
gaa gcg cag ctc att tcc aaa cag aag caa gag gtg gaa ccc tcc acg	1903
Glu Ala Gln Leu Ile Ser Lys Gln Lys Gln Glu Val Glu Pro Ser Thr	
570 575 580	
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<210> 81
 <211> 1774
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (313) .. (576)

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gtatatataa tgcttatgta atatagaatg gatctccaat gatttttttg tgtgtttttc	120
acatatatttg catatgtgtg tgatactgct cagtgccagg catctcttac acacagtagt	180
caagaatctt ttttggcctc tgcctaacca gattcctcct gcctccaggt agattttata	240
cttattttcaa ggcagaaact tggtggaagg aggtaatctg tcgctaattg gtattttattc	300
cttcattgcat gt atg cat tca tac cct ggg att ttt ttc ttc cct tta	348
Met His Ser Tyr Pro Gly Ile Phe Phe Phe Pro Leu	
1 5 10	
gct gtg ttc cag atc atc tcc ctg gta att tac ccc gtg aag tac acc	396
Ala Val Phe Gln Ile Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr Thr	

15	20	25	
cag acc ttc acc ctt cac gat aac cct gct gtt aat tac atc tat aac			444
Gln Thr Phe Thr Leu His Asp Asn Pro Ala Val Asn Tyr Ile Tyr Asn			
30	35	40	
tgg gcc tat ggc ttc gga tgg gcg gcc acc atc atc ttg att ggt tgt			492
Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly Cys			
45	50	55	60
tcc ttc ttc ttc tgc tgc ctc ccc aac tac gag gat gac ctt ttg ggg			540
Ser Phe Phe Phe Cys Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly			
65	70	75	
gcc gcc aag ccc agg tac ttc tat ccc cca gcc taa tgtg ggaggaagag			590
Ala Ala Lys Pro Arg Tyr Phe Tyr Pro Pro Ala			
80	85		
cctgagaaaa gcctgctgca agatggatct gaggaggaaa ctgttctcca aggcacaagg			650
aacctacgtt tgggcaatgt tcatatgatac agaaatgcta gaataaatgc taaagaaaat			710
tcttcataat tagtgtaag tttcatgtat gtcgtgtgga gttaaaaaga cttgaattct			770
gtttgctaag tatatgctaa tttttcctta tgtcaattct ataccattta agcttcattt			830
gttaagaat atgcctgtga aacttgataa ggtagaaatg tagcagcctc tcatttaata			890
atctgatggg gettctgttt ttccacatag aatgggttgt ttctgctaag ggctacagag			950
gaggaaagtc actggcaaaa cttccgtgac caaatatcct gaaattagta tttttttaa			1010
aagaccttat tttgagtttt cagttacata aaaaagcaga agcagattgg tttcctaagt			1070
gagcatcggt tgtgagaatt tttagtcagt gttttgaaca attattgttt ttctaagctt			1130
cgtgttgact ttctctgatg cgtagaaaag tgttctaacg tagccaaggt taagccgctg			1190
tcactactga aatgctaaga attttcctct tttcccgtag tgtagagggg taggggtgtg			1250
gaagaagccg tgtagcaca tctgtagtat tctgtgtgta tgcttagaac cagcgtagac			1310
cggatgggag gatggactag gcctaataccc tcccactgg tggatgtgaa gaggtcaggt			1370
aggaaggcac aggagggtca ccaactgtcac agcagtgcc tgcagacatc ctaggagaag			1430
acatggcagt gtttcttctc agtgcttctt cccttaactg agctctgctc acagacagct			1490
agaatagatt ttaactgtaa cagaaacct aatgtaatta aaacctggtc ttccttggt			1550
agcagactta aaatatctgt atagtacatg caagtggaaa atttggaat gcgtgtctct			1610
gaatacatc cggaagggt actattacct tttccttacc atttatactt acctaatgga			1670
aacgagcttg ttttaactat cagaacacta ttttgtaagg tgctgcaaag acagttgaag			1730
ttttcattac caacttcccc aataaaccag gtgttcaaaa aaaa			1774

<210> 82
 <211> 1870
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (91)..(672)

<400> 82
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 ctccgctccg cgcccgccgc caccgaacgac atg ctg cgc tgc ggc ctg gcc 111
 Met Leu Arg Cys Gly Leu Ala
 1 5
 tgc gag cgc tgc agg tgg atc ctg ccc ctg ctg ctc ctc agc gcc atc 159
 Cys Glu Arg Cys Arg Trp Ile Leu Pro Leu Leu Leu Leu Ser Ala Ile
 10 15 20
 gcc ttc gac atc atc gcg ctg gcc ggc cgc ggc tgg ctg cag tct agc 207
 Ala Phe Asp Ile Ile Ala Leu Ala Gly Arg Gly Trp Leu Gln Ser Ser
 25 30 35
 aac cac atc cag aca tcg tcg ctt tgg tgg agg tgt ttc gac gag ggc 255
 Asn His Ile Gln Thr Ser Ser Leu Trp Trp Arg Cys Phe Asp Glu Gly
 40 45 50 55
 ggc ggc agc ggc tcc tac gac gat ggc tgc cag agc ctc atg gag tac 303
 Gly Gly Ser Gly Ser Tyr Asp Asp Gly Cys Gln Ser Leu Met Glu Tyr
 60 65 70
 gca tgg gga cga gca gct gca gcc acg ctt ttc tgt ggc ttt atc atc 351
 Ala Trp Gly Arg Ala Ala Ala Ala Thr Leu Phe Cys Gly Phe Ile Ile
 75 80 85
 ctg tgc atc tgc ttc att ctc tcg ttc ttc gcc ctg tgt gga ccc cag 399
 Leu Cys Ile Cys Phe Ile Leu Ser Phe Phe Ala Leu Cys Gly Pro Gln
 90 95 100
 atg ctt gtt ttc ctg aga gtc att gga ggc ctc ctc gca ctg gct gcc 447
 Met Leu Val Phe Leu Arg Val Ile Gly Gly Leu Leu Ala Leu Ala Ala
 105 110 115
 ata ttc cag atc atc tcc ctg gta att tac ccc gtg aag tac acc cag 495
 Ile Phe Gln Ile Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr Thr Gln
 120 125 130 135
 acc ttc acc ctt cac gat aac cct gct gtt aat tac atc tat aac tgg 543
 Thr Phe Thr Leu His Asp Asn Pro Ala Val Asn Tyr Ile Tyr Asn Trp
 140 145 150
 gcc tat ggc ttc gga tgg gcg gcc acc atc atc ttg att ggt tgt tcc 591
 Ala Tyr Gly Phe Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly Cys Ser
 155 160 165
 ttc ttc ttc tgc tgc ctc ccc aac tac gag gat gac ctt ttg ggg gcc 639
 Phe Phe Phe Cys Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly Ala
 170 175 180
 gcc aag ccc agg tac ttc tat ccc cca gcc taa tgtgggag gaagagcctg 690

Ala Lys Pro Arg Tyr Phe Tyr Pro Pro Ala
185 190

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agaaaagcct gctgcaagat ggatctgagg aggaaactgt tctccaaggc acaaggaacc 750
tacgtttggg caatgttcat atgatcagaa atgctagaat aaatgctaaa gaaaattctt 810
cataattagt gttaagtttc atgtatgtcg tgtggagtta aaaagacttg aattctgttt 870
gctaagtata tgctaatttt tccttatgtc aattctatac catttaagct tcatttggtta 930
aagaatatgc ctgtgaaact tgataaggta gaaatgtagc agcctctcat ttaataatct 990
gatggggcct ctgtttttcc acatagaatg ggttggtttct gctaagggct acagaggagg 1050
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ccttattttg agttttcagt tacataaaaa agcagaagca gattgggttc ctaagtgagc 1170
atcgtttgtg agaattttta gtcagtgttt tgaacaatta ttgtttttct aagcttcgtg 1230
ttgactttct ctgatgcgta gaaaagtgtt ctaacgtagc caaggttaag ccgctgtcac 1290
tactgaaatg ctaagaatth tcctcttttc ccgtagtgta gaggggtagg gtgtgggaag 1350
aagccgtgtt agcacatctg tagtattctg tgtgtatgct tagaaccagc gtagaccgga 1410
tgaggaggat gactaggcct aatccctccc aactgggtga tgtgaagagg tcaggtagga 1470
aggcacagga gggtcaccac tgtcacagca gtgccatgca gacatcctag gagaagacat 1530
ggcagtgttt cttctcagtg cttcttccct taactgagct ctgtcacag acagctagaa 1590
tagatthtaa ctgtaacaga aacctaaatg taattaaaac ctgggtcttc ttggtaagca 1650
gacttaaaat atctgtatag tacatgcaag tggaaaattt gggaatgcgt gtctctgaat 1710
acataccgga agggctacta ttaccttttc cttaccattt atacttacct aatggaaacg 1770
agcttgthtt aactatcaga acactattht gtaagggtgct gcaaagacag ttgaagthtt 1830
cattaccaac ttccccaata aaccagggtg tcaaaaaaaa 1870

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<210> 83
<211> 1294
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (647)..(910)

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<400> 83
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aaacttgatg tttcagcagg cgctgcctct aagccccga ctctaccgg aggaaataaa 120
taggaaacct taagctaaaa taagtaacca agagagaatt actcatccta ttcagtctca 180

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cccctacctc atcaaatact tttatcggtc ctacctctcc ttttaagcca aatattaaaa 240
ctttttaatg gaaattatct actacgccac ccgtgtggga attgctttac tcaactctact 300
atttgacagta ggactatata ctgtagcacc ctcagggtta aatatcagac acagaatctc 360
aattaccata gcatttcgct taattattat cctcatagcg ggaataatgg ttactaacag 420
aaaataacac atgggccttt ccaaaccagc acctctgcct cttattagga aaggaatggt 480
gtttctatat cagccaatca gacctagtaa aaagcgctat taaaaaaaaa aagctaaaaa 540
gctaaggagt accaaaaaca acaaacagat tcttggtttg ggaacaaaat catagatagc 600
atgggtcatc ccattcctgg gccctctcct aataatatac ctaatt atg gga cta 655
                                         Met Gly Leu
                                         1

atg ttc tta ccc tgc cta att aac ctt ttt cag aga ttt ttt aaa ctg 703
Met Phe Leu Pro Cys Leu Ile Asn Leu Phe Gln Arg Phe Phe Lys Leu
      5              10              15

aca gga tca tgg cca ttt cac aga caa cta ccc aaa aat atc tac aga 751
Thr Gly Ser Trp Pro Phe His Arg Gln Leu Pro Lys Asn Ile Tyr Arg
      20              25              30              35

cgg cac tgc tcc tac caa cac gat acc aga gaa ctc tct gtc ccc tcg 799
Arg His Cys Ser Tyr Gln His Asp Thr Arg Glu Leu Ser Val Pro Ser
              40              45              50

tca gca gga agt agc cag aaa gaa cat gcc gcc cct cgt cct ttt tat 847
Ser Ala Gly Ser Ser Gln Lys Glu His Ala Ala Pro Arg Pro Phe Tyr
              55              60              65

aac tat gag gtc tgg att gac aga gca gaa gca tca cca ttg tgg ata 895
Asn Tyr Glu Val Trp Ile Asp Arg Ala Glu Ala Ser Pro Leu Trp Ile
              70              75              80

agc gcc tca ttt taa aattcacctt aatcaaaaac tgcctaaatc caaagggcat 950
Ser Ala Ser Phe
      85

cagcctaattg gctaagggtca gcatgatcac aaaccacaaa taacatctcc aaccaaaaac 1010
attccagaca cctccacag agaaatgcta gcctcgggat aaccctctc ctgccggaaa 1070
gatgtcacc ccaagataac caccctccg ccagaacat tccaaccctg ccacaaactt 1130
ctccccaca cagaaacatt ccaagcttgt aataagctcc ctcaccctaa aaccaacgta 1190
cattcttagt ctgcaaggaa aagtgtcct gactgaccag ccagaatcct ctctcaggtc 1250
ttttctataa taaacctgtc ttgtactgtc aaaaaaaaaa aaaa 1294

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<210> 84
 <211> 633
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (148)..(399)

<400> 84

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cttgtaagaa gtaaatagaag cttcctt      atg agt ctg tta aga ctc cat aga      171
                                   Met Ser Leu Leu Arg Leu His Arg
                                   1                               5

ttg tca ata ata tgg aaa aat ttg ata ttt cat cag gaa tat gaa cat      219
Leu Ser Ile Ile Trp Lys Asn Leu Ile Phe His Gln Glu Tyr Glu His
   10                               15                               20

gtg ttt cag gta gag aat gcc aaa gat aat gaa gat agt att cta caa      267
Val Phe Gln Val Glu Asn Ala Lys Asp Asn Glu Asp Ser Ile Leu Gln
   25                               30                               35                               40

aga gaa att cct gcc aga caa tcc cga aga aga ttt cgg aaa att aac      315
Arg Glu Ile Pro Ala Arg Gln Ser Arg Arg Arg Phe Arg Lys Ile Asn
                               45                               50                               55

tat aaa gga gag cgc caa acc att act gat gat gtg gag gtt aac agc      363
Tyr Lys Gly Glu Arg Gln Thr Ile Thr Asp Asp Val Glu Val Asn Ser
                               60                               65                               70

tat ctt tct gtg agt ata ttt agg aac act tca tga atct tccttaattt      413
Tyr Leu Ser Val Ser Ile Phe Arg Asn Thr Ser
                               75                               80

tcatatctag tatctttaat ttacatgtat ctttggtaat atcaacatgc tgggctctgt      473
atgtgaaaat ttggggcagg taaatatata atcttttttaa atgcttctgt ttggttgaat      533
tggttaggaa tgctcttacc agtgggaggt ctgggttttgc ttttttgttg gtggctaaac      593
agcgaaaaaa cctattaggc tggatgcacc gggatcatgcc      633

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<210> 85

<211> 2437

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (184)..(2172)

<400> 85

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aggagtcggg tttgtcttgc caatggaagt tggagtggag ccactcccga ctgtgtgcct      120
gtcagatgtg ccaccccgcc acaactggcc aatgggggtga cggaaggcct ggactatggc      180

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ttc atg aag gaa gta aca ttc cac tgt cat gag ggc tac atc ttg cac	228
Met Lys Glu Val Thr Phe His Cys His Glu Gly Tyr Ile Leu His	
1 5 10 15	
ggt gct cca aaa ctc acc tgt cag tca gat ggc aac tgg gat gca gag	276
Gly Ala Pro Lys Leu Thr Cys Gln Ser Asp Gly Asn Trp Asp Ala Glu	
20 25 30	
att cct ctc tgt aaa cca gtc aac tgt gga cct cct gaa gat ctt gcc	324
Ile Pro Leu Cys Lys Pro Val Asn Cys Gly Pro Pro Glu Asp Leu Ala	
35 40 45	
cat ggt ttc cct aat ggt ttt tcc ttt att cat ggg ggc cat ata cag	372
His Gly Phe Pro Asn Gly Phe Ser Phe Ile His Gly Gly His Ile Gln	
50 55 60	
tat cag tgc ttt cct ggt tat aag ctc cat gga aat tca tca aga agg	420
Tyr Gln Cys Phe Pro Gly Tyr Lys Leu His Gly Asn Ser Ser Arg Arg	
65 70 75	
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Cys Leu Ser Asn Gly Ser Trp Ser Gly Ser Ser Pro Ser Cys Leu Pro	
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Thr Asp Val Gly Ser Arg Leu Ala Gly Arg Asp Ala Leu Ala Pro Pro	1295	1300	1305	
cag gcc aac ggg ggc cct ccc gac ccg ggc ttc ctg cgt ccg cag cga				3987
Gln Ala Asn Gly Gly Pro Pro Asp Pro Gly Phe Leu Arg Pro Gln Arg	1310	1315	1320	
gca gcc ctc tat atc ctt ggg gac aaa gcc cag ctc aag ggt gtg cgg				4035
Ala Ala Leu Tyr Ile Leu Gly Asp Lys Ala Gln Leu Lys Gly Val Arg	1325	1330	1335	
tca gac ccc ctg cag cag tgg gag ctg gtg ccc att gag gta ttc gag				4083
Ser Asp Pro Leu Gln Gln Trp Glu Leu Val Pro Ile Glu Val Phe Glu	1340	1345	1350	1355
gca cgg cag gtg aag gct agc ttc aag aag ctg ctg aaa gca tgt gtc				4131
Ala Arg Gln Val Lys Ala Ser Phe Lys Lys Leu Leu Lys Ala Cys Val	1360	1365	1370	
cca ggc tgc ccc gct gct gag ccc agc cca gcc tcc ttc ctg cgc tca				4179
Pro Gly Cys Pro Ala Ala Glu Pro Ser Pro Ala Ser Phe Leu Arg Ser	1375	1380	1385	
ctg gag gac tca gag tgg ctg atc cag atc cac aag ctg ctg cag gtg				4227
Leu Glu Asp Ser Glu Trp Leu Ile Gln Ile His Lys Leu Leu Gln Val	1390	1395	1400	
tct gtg ctg gtg gtg gag ctc ctg gat tca ggc tcc tcc gtg ctg gtg				4275
Ser Val Leu Val Val Glu Leu Leu Asp Ser Gly Ser Ser Val Leu Val	1405	1410	1415	
ggc ctg gag gat ggc tgg gac atc acc acc cag gtg gta tcc ttg gtg				4323
Gly Leu Glu Asp Gly Trp Asp Ile Thr Thr Gln Val Val Ser Leu Val	1420	1425	1430	1435

cag ctg ctc tca gac ccc ttc tac cgc acg ctg gag ggc ttt cgc ctg Gln Leu Leu Ser Asp Pro Phe Tyr Arg Thr Leu Glu Gly Phe Arg Leu 1440 1445 1450	4371
ctg gtg gag aag gag tgg ctg tcc ttc ggc cat cgc ttc agc cac cgt Leu Val Glu Lys Glu Trp Leu Ser Phe Gly His Arg Phe Ser His Arg 1455 1460 1465	4419
gga gct cac acc ctg gcc ggg cag agc agc ggc ttc aca ccc gtc ttc Gly Ala His Thr Leu Ala Gly Gln Ser Ser Gly Phe Thr Pro Val Phe 1470 1475 1480	4467
ctg cag ttc ctg gac tgc gta cac cag gtc cac ctg cag ttc ccc atg Leu Gln Phe Leu Asp Cys Val His Gln Val His Leu Gln Phe Pro Met 1485 1490 1495	4515
gag ttt gag ttc agc cag ttc tac ctc aag ttc ctc ggc tac cac cat Glu Phe Glu Phe Ser Gln Phe Tyr Leu Lys Phe Leu Gly Tyr His His 1500 1505 1510 1515	4563
gtg tcc cgc cgt ttc cgg acc ttc ctg ctc gac tct gac tat gag cgc Val Ser Arg Arg Phe Arg Thr Phe Leu Leu Asp Ser Asp Tyr Glu Arg 1520 1525 1530	4611
att gag ctg ggg ctg ctg tat gag gag aag ggg gaa cgc agg ggc cag Ile Glu Leu Gly Leu Leu Tyr Glu Glu Lys Gly Glu Arg Arg Gly Gln 1535 1540 1545	4659
gtg ccg tgc agg tct gtg tgg gag tat gtg gac cgg ctg agc aag agg Val Pro Cys Arg Ser Val Trp Glu Tyr Val Asp Arg Leu Ser Lys Arg 1550 1555 1560	4707
acg cct gtg ttc cac aat tac atg tat gcg ccc gag gac gca gag gtc Thr Pro Val Phe His Asn Tyr Met Tyr Ala Pro Glu Asp Ala Glu Val 1565 1570 1575	4755
ctg cgg ccc tac agc aac gtg tcc aac ctg aag gtg tgg gac ttc tac Leu Arg Pro Tyr Ser Asn Val Ser Asn Leu Lys Val Trp Asp Phe Tyr 1580 1585 1590 1595	4803
act gag gag acg ctg gcc gag ggc cct ccc tat gac tgg gaa ctg gcc Thr Glu Glu Thr Leu Ala Glu Gly Pro Pro Tyr Asp Trp Glu Leu Ala 1600 1605 1610	4851
cag ggg ccc cct gaa ccc cca gag gaa gaa cgg tct gat gga ggc gct Gln Gly Pro Pro Glu Pro Pro Glu Glu Glu Arg Ser Asp Gly Gly Ala 1615 1620 1625	4899
ccc cag agc agg cgc cgc gtg gtg tgg ccc tgt tac gac agc tgc ccg Pro Gln Ser Arg Arg Arg Val Val Trp Pro Cys Tyr Asp Ser Cys Pro 1630 1635 1640	4947
cgg gcc cag cct gac gcc atc tca cgc ctg ctg gag gag ctg cag agg Arg Ala Gln Pro Asp Ala Ile Ser Arg Leu Leu Glu Glu Leu Gln Arg 1645 1650 1655	4995
ctg gag aca gag ttg ggc caa ccc gct gag cgc tgg aag gac acc tgg Leu Glu Thr Glu Leu Gly Gln Pro Ala Glu Arg Trp Lys Asp Thr Trp 1660 1665 1670 1675	5043

gac cgg gtg aag gct gca cag cgc ctc gag ggc cgg cca gac ggc cgt	5091
Asp Arg Val Lys Ala Ala Gln Arg Leu Glu Gly Arg Pro Asp Gly Arg	
1680 1685 1690	
ggc acc cct agc tcc ctc ctt gtg tcc acc gca ccc cac cac cgt cgc	5139
Gly Thr Pro Ser Ser Leu Leu Val Ser Thr Ala Pro His His Arg Arg	
1695 1700 1705	
tcg ctg ggt gtg tac ctg cag gag ggg ccc gtg ggc tcc acc ctg agc	5187
Ser Leu Gly Val Tyr Leu Gln Glu Gly Pro Val Gly Ser Thr Leu Ser	
1710 1715 1720	
ctc agc ctg gac agc gac cag agt agt ggc tca acc aca tcc ggc tcc	5235
Leu Ser Leu Asp Ser Asp Gln Ser Ser Gly Ser Thr Thr Ser Gly Ser	
1725 1730 1735	
cgt cag gct gcc cgc cgc agc acc agc acc ctg tac agc cag ttc cag	5283
Arg Gln Ala Ala Arg Arg Ser Thr Ser Thr Leu Tyr Ser Gln Phe Gln	
1740 1745 1750 1755	
aca gca gag agt gag aac agg tcc tac gag ggc act ctg tac aag aag	5331
Thr Ala Glu Ser Glu Asn Arg Ser Tyr Glu Gly Thr Leu Tyr Lys Lys	
1760 1765 1770	
ggg gcc ttc atg aag cct tgg aag gcc cgc tgg ttc gtg ctg gac aag	5379
Gly Ala Phe Met Lys Pro Trp Lys Ala Arg Trp Phe Val Leu Asp Lys	
1775 1780 1785	
acc aag cac cag ctg cgc tac tac gac cac cgt gtg gac aca gag tgc	5427
Thr Lys His Gln Leu Arg Tyr Tyr Asp His Arg Val Asp Thr Glu Cys	
1790 1795 1800	
aag ggt gtc atc gac ttg gcg gag gtg gag gct gtg gca cct ggc acg	5475
Lys Gly Val Ile Asp Leu Ala Glu Val Glu Ala Val Ala Pro Gly Thr	
1805 1810 1815	
ccc act atg ggt gcc cct aag act gtg gac gag aag gcc ttc ttt gac	5523
Pro Thr Met Gly Ala Pro Lys Thr Val Asp Glu Lys Ala Phe Phe Asp	
1820 1825 1830 1835	
gtg aag aca acg cgt cgc gtt tac aac ttc tgt gcc cag gac gtg ccc	5571
Val Lys Thr Thr Arg Arg Val Tyr Asn Phe Cys Ala Gln Asp Val Pro	
1840 1845 1850	
tcg gcc cag cag tgg gtg gac cgg atc cag agc tgc ctg tcg gac gcc	5619
Ser Ala Gln Gln Trp Val Asp Arg Ile Gln Ser Cys Leu Ser Asp Ala	
1855 1860 1865	
tga gcct ccagccctg cccggctgct ctgcttcagg tcgttaccga ccactagggg	5676

<210> 87

<211> 1769

<212> DNA

<213> Homo sapiens

<220>
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 <222> (282)..(1769)

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 ctgcattggc gggccccctg tgctctcttc tggcattctc tgcctctgtc ctcatattct 120
 tgttaggcca ggtgggcttg ctgcagggac acccccagtg cctggattac gggccccctt 180
 tccagcccc tctgcacctt gagttttgct ctgactatga gtccttcggc tgctgtgatc 240
 agcacaagga ccgcccgcac gctgcccggg actgggacat c atg gaa tat ttt 293
 Met Glu Tyr Phe
 1
 gat ctg aag aga cat gag ctg tgt gga gat tac att aaa gac atc ctt 341
 Asp Leu Lys Arg His Glu Leu Cys Gly Asp Tyr Ile Lys Asp Ile Leu
 5 10 15 20
 tgc cag gag tgc tgc ccc tac gca gcc cac ctg tac gac gcc gaa aac 389
 Cys Gln Glu Cys Ser Pro Tyr Ala Ala His Leu Tyr Asp Ala Glu Asn
 25 30 35
 acc cag acg cct ctg cgg aat ctg ccg ggc ctg tgc tct gat tac tgc 437
 Thr Gln Thr Pro Leu Arg Asn Leu Pro Gly Leu Cys Ser Asp Tyr Cys
 40 45 50
 tct gcc ttc cat tct aac tgt cac tca gcc att tcc ctg ctg acc aat 485
 Ser Ala Phe His Ser Asn Cys His Ser Ala Ile Ser Leu Leu Thr Asn
 55 60 65
 gac cgc ggc ctg cag gag tct cat gga agg gac ggt acc cgc ttc tgc 533
 Asp Arg Gly Leu Gln Glu Ser His Gly Arg Asp Gly Thr Arg Phe Cys
 70 75 80
 cac ctg ctg gac ctt cct gac aag gac tat tgc ttc cct aat gtc ctg 581
 His Leu Leu Asp Leu Pro Asp Lys Asp Tyr Cys Phe Pro Asn Val Leu
 85 90 95 100
 agg aac gac tat ctg aac cgc cac ctg ggc atg gtg gcc caa gat cct 629
 Arg Asn Asp Tyr Leu Asn Arg His Leu Gly Met Val Ala Gln Asp Pro
 105 110 115
 cag ggc tgc ctg cag ctg tgc ctg agc gag gtg gcc aac ggg ctg agg 677
 Gln Gly Cys Leu Gln Leu Cys Leu Ser Glu Val Ala Asn Gly Leu Arg
 120 125 130
 aac ccc gtc tcc atg gtc cat gct ggg gac ggc acc cat cgc ttc ttt 725
 Asn Pro Val Ser Met Val His Ala Gly Asp Gly Thr His Arg Phe Phe
 135 140 145
 gtt gcc gag cag gta gga gtg gtg tgg gtc tac ctg cct gat ggg agt 773
 Val Ala Glu Gln Val Gly Val Val Trp Val Tyr Leu Pro Asp Gly Ser
 150 155 160
 cgc ctg gag caa ccc ttc ctg gac ctg aag aac atc gtg ttg acc acc 821
 Arg Leu Glu Gln Pro Phe Leu Asp Leu Lys Asn Ile Val Leu Thr Thr
 165 170 175 180

cca tgg atc ggg gat gag aga ggc ttc ttg ggg ttg gct ttt cac ccc	869
Pro Trp Ile Gly Asp Glu Arg Gly Phe Leu Gly Leu Ala Phe His Pro	
185 190 195	
aaa ttc cgc cac aat cgc aag ttc tat att tat tat tcg tgc ctg gac	917
Lys Phe Arg His Asn Arg Lys Phe Tyr Ile Tyr Tyr Ser Cys Leu Asp	
200 205 210	
aag aag aag gta gaa aag atc cga att agt gag atg aag gtt tct cgg	965
Lys Lys Lys Val Glu Lys Ile Arg Ile Ser Glu Met Lys Val Ser Arg	
215 220 225	
gct gat cct aac aaa gct gac ctg aaa tca gag agg gtc atc ttg gag	1013
Ala Asp Pro Asn Lys Ala Asp Leu Lys Ser Glu Arg Val Ile Leu Glu	
230 235 240	
att gaa gaa cca gcc tca aac cat aat ggc gga caa ctt ctt ttt ggc	1061
Ile Glu Glu Pro Ala Ser Asn His Asn Gly Gly Gln Leu Leu Phe Gly	
245 250 255 260	
ctg gat ggc tat atg tac ata ttc act ggg gac ggg gga cag gct gga	1109
Leu Asp Gly Tyr Met Tyr Ile Phe Thr Gly Asp Gly Gly Gln Ala Gly	
265 270 275	
gat ccc ttt ggc ctg ttt gga aat gct cag aac aaa agt tcc ctg ctg	1157
Asp Pro Phe Gly Leu Phe Gly Asn Ala Gln Asn Lys Ser Ser Leu Leu	
280 285 290	
gga aaa gtt tta agg atc gat gtg aac agg gca ggc tca cat ggc aag	1205
Gly Lys Val Leu Arg Ile Asp Val Asn Arg Ala Gly Ser His Gly Lys	
295 300 305	
cgg tac cga gtc ccc tcg gac aat cca ttt gtt tct gag cca ggg gcc	1253
Arg Tyr Arg Val Pro Ser Asp Asn Pro Phe Val Ser Glu Pro Gly Ala	
310 315 320	
cac ccc gcc atc tat gcc tat ggg atc agg aac atg tgg cgt tgt gct	1301
His Pro Ala Ile Tyr Ala Tyr Gly Ile Arg Asn Met Trp Arg Cys Ala	
325 330 335 340	
gtg gac cga ggg gac ccc atc acg cgc cag ggc cga ggc cgg ata ttc	1349
Val Asp Arg Gly Asp Pro Ile Thr Arg Gln Gly Arg Gly Arg Ile Phe	
345 350 355	
tgt ggg gac gtg ggc cag aac agg ttt gaa gag gtt gac ctc att ttg	1397
Cys Gly Asp Val Gly Gln Asn Arg Phe Glu Glu Val Asp Leu Ile Leu	
360 365 370	
aaa ggt gga aac tat ggc tgg aga gca aag gaa ggg ttt gca tgt tat	1445
Lys Gly Gly Asn Tyr Gly Trp Arg Ala Lys Glu Gly Phe Ala Cys Tyr	
375 380 385	
gac aaa aaa ctt tgt cac aat gcc tct ttg gag gag caa gcc aca gaa	1493
Asp Lys Lys Leu Cys His Asn Ala Ser Leu Glu Glu Gln Ala Thr Glu	
390 395 400	
gat ggc agc cca gaa tcc ctg ggc agg cct gcc tct ggg gtt cca atc	1541
Asp Gly Ser Pro Glu Ser Leu Gly Arg Pro Ala Ser Gly Val Pro Ile	
405 410 415 420	
tct ggg gtg gtg ctg gac aca ggg gtg tcc ggc aga gga gag gct cca	1589

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Ser Gly Val Val Leu Asp Thr Gly Val Ser Gly Arg Gly Glu Ala Pro
      425                      430                      435

cca ccg cct gca gct ttc acc aaa gga gat gat gaa ctt gct atg ggt      1637
Pro Pro Pro Ala Ala Phe Thr Lys Gly Asp Asp Glu Leu Ala Met Gly
      440                      445                      450

gct gat cag ccc tgg gaa ggc aca gga cgt ggt gct gcc cag gca aag      1685
Ala Asp Gln Pro Trp Glu Gly Thr Gly Arg Gly Ala Ala Gln Ala Lys
      455                      460                      465

atc ctg ctt ctt cca ttt ctt gtt ttt tct atc ttc ctg caa agc cat      1733
Ile Leu Leu Leu Pro Phe Leu Val Phe Ser Ile Phe Leu Gln Ser His
      470                      475                      480

aag tcg act aga caa aaa ata aac cct tat gtt tag                        1769
Lys Ser Thr Arg Gln Lys Ile Asn Pro Tyr Val
      485                      490                      495

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<210> 88
 <211> 792
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (92) .. (745)

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cagtctactt gaaaaggatc ctgcctttca g      atg att act att gcc aag gaa      112
                               1      Met Ile Thr Ile Ala Lys Glu
                               5

aca ggc ctt ggc ctg aag gta cta gga gga att aac cgg aat gaa ggc      160
Thr Gly Leu Gly Leu Lys Val Leu Gly Gly Ile Asn Arg Asn Glu Gly
      10                      15                      20

cca ttg gta tat att cag gaa att att cct gga gga gac tgt tat aag      208
Pro Leu Val Tyr Ile Gln Glu Ile Ile Pro Gly Gly Asp Cys Tyr Lys
      25                      30                      35

gat ggt cgt ttg aag cca gga gat caa ctt gtc tca gtc aac aag gaa      256
Asp Gly Arg Leu Lys Pro Gly Asp Gln Leu Val Ser Val Asn Lys Glu
      40                      45                      50                      55

tct atg att ggt gta tca ttt gaa gaa gca aaa agc ata att acc aga      304
Ser Met Ile Gly Val Ser Phe Glu Glu Ala Lys Ser Ile Ile Thr Arg
      60                      65                      70

gcc aag ttg agg tta gaa tct gct tgg gag ata gca ttc ata aga caa      352
Ala Lys Leu Arg Leu Glu Ser Ala Trp Glu Ile Ala Phe Ile Arg Gln
      75                      80                      85

aaa tcc gac aac att cag cca gaa aat ctg tca tgt aca tca ctt ata      400
Lys Ser Asp Asn Ile Gln Pro Glu Asn Leu Ser Cys Thr Ser Leu Ile

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90	95	100	
gaa gct tca gga gaa tat	gga cct caa gcc tca aca tta agt ctt ttt		448
Glu Ala Ser Gly Glu Tyr	Gly Pro Gln Ala Ser Thr Leu Ser Leu Phe		
105	110	115	
tct tct cct cct gaa ata cta atc cca aag acc tca tcc act ccc aaa			496
Ser Ser Pro Pro Glu Ile Leu Ile Pro Lys Thr Ser Ser Thr Pro Lys			
120	125	130	135
aca aat aat gac att tta tct tct tgt gag ata aaa act gga tac aac			544
Thr Asn Asn Asp Ile Leu Ser Ser Cys Glu Ile Lys Thr Gly Tyr Asn			
140	145	150	
aaa aca gta cag att cca att act tca gaa aac agt act gtg ggt ttg			592
Lys Thr Val Gln Ile Pro Ile Thr Ser Glu Asn Ser Thr Val Gly Leu			
155	160	165	
tct aat aca ggc tct aaa tta tct tgg tat tca gcc cac aaa gga aca			640
Ser Asn Thr Gly Ser Lys Leu Ser Trp Tyr Ser Ala His Lys Gly Thr			
170	175	180	
aca cca agc cct gag aca gca agt aca agc aga ctc aaa agg gac agt			688
Thr Pro Ser Pro Glu Thr Ala Ser Thr Ser Arg Leu Lys Arg Asp Ser			
185	190	195	
gtc ttt tgg aga ttt tgt cca ggt tgc cag aaa ctt gtt ttg ctt gca			736
Val Phe Trp Arg Phe Cys Pro Gly Cys Gln Lys Leu Val Leu Leu Ala			
200	205	210	215
gtt gga tga agtaaatt gttggtgcac atgaaatttc caatatatta gattcacagc			792
Val Gly			

<210> 89
 <211> 937
 <212> DNA
 <213> Homo sapiens

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 <222> (107)..(646)

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cggcacctgc tgccgaggga ccccgcggcc cgccccggtg ctcgtg	115
	atg ggg ctg Met Gly Leu 1
atc ttc gcc aaa ctg tgg agc ctc ttc tgt aac caa gaa cac aaa gta	163
Ile Phe Ala Lys Leu Trp Ser Leu Phe Cys Asn Gln Glu His Lys Val	
5	10
att ata gtg gga ctg gat aat gca ggg aaa acc acc att ctt tac caa	211
Ile Ile Val Gly Leu Asp Asn Ala Gly Lys Thr Thr Ile Leu Tyr Gln	
20	25
30	35

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ttc tta atg aat gaa gtg gtt cac act tct cca acc ata gga agc aat      259
Phe Leu Met Asn Glu Val Val His Thr Ser Pro Thr Ile Gly Ser Asn
                               40                               45                               50

gtt gaa gaa ata gtt gtg aag aac act cat ttt ctt atg tgg gat att      307
Val Glu Glu Ile Val Val Lys Asn Thr His Phe Leu Met Trp Asp Ile
                               55                               60                               65

ggg ggt cag gag tct ctg cga tca tcc tgg aac aca tat tac tca aat      355
Gly Gly Gln Glu Ser Leu Arg Ser Ser Trp Asn Thr Tyr Tyr Ser Asn
                               70                               75                               80

aca gag ttc atc att ctt gtt gtt gat agc att gac agg gaa cga cta      403
Thr Glu Phe Ile Ile Leu Val Val Asp Ser Ile Asp Arg Glu Arg Leu
                               85                               90                               95

gct att aca aaa gaa gaa tta tac aga atg ttg gct cat gag gat tta      451
Ala Ile Thr Lys Glu Glu Leu Tyr Arg Met Leu Ala His Glu Asp Leu
100                               105                               110                               115

cgg aag gct gca gtc ctt atc ttt gca aat aaa cag gat atg aaa ggg      499
Arg Lys Ala Ala Val Leu Ile Phe Ala Asn Lys Gln Asp Met Lys Gly
                               120                               125                               130

tgt atg aca gca gct gaa atc tcg aaa tac ctc acc ctt agt tca att      547
Cys Met Thr Ala Ala Glu Ile Ser Lys Tyr Leu Thr Leu Ser Ser Ile
                               135                               140                               145

aag gat cat cca tgg cac att caa tcc tgc tgt gct ctc aca gga gaa      595
Lys Asp His Pro Trp His Ile Gln Ser Cys Cys Ala Leu Thr Gly Glu
                               150                               155                               160

ggg tta tgc caa ggt cta gag tgg atg acc tcc cgg att ggt gtg aga      643
Gly Leu Cys Gln Gly Leu Glu Trp Met Thr Ser Arg Ile Gly Val Arg
165                               170                               175

taa cttt ttgtcttgaa agagactgct ctatttattc tgtgacatga acattttttc      700

ctagtacctt tggctgctaa ggcagcagca tgtttaattt ataacaacac aaacctctga      760

gagcaacact tgaatcaagt gcagctgaac tggaacataa aagatttttt cttaactttt      820

tttttttaac aactaatct tcagttggat gaatgtaatg tataactatg ttttcagcaa      880

caattcttct gtttattcta attaatacgt gactgccttg taagaaaaaa aaaaaaa      937

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<210> 90
 <211> 4397
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (306) .. (4397)

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atccgggatg tctcaatagc tgtggccttg acgtccacct cggaccctcg ccccggaacc      180
agcccagttc ccaatgggcc ctctgcccgg ggagcgggtc taccggcctg gatgtgaaag      240
agagcttggg gaccccagag acctcggaac cttcagcttt ggaagtgacg tcggtggggg      300
tcccc      atg ggg ccg gac gag gcc aca cca ccc gac ctg gtg ctt cct      347
              Met Gly Pro Asp Glu Ala Thr Pro Pro Asp Leu Val Leu Pro
                1              5              10

gcc tgg cgt ctg cgc cac gga gca ttc agg acg ctg gtg acc agg gag      395
Ala Trp Arg Leu Arg His Gly Ala Phe Arg Thr Leu Val Thr Arg Glu
  15              20              25              30

cca gga gcc ccc agg atg ggt gcc ccg agc gcg tgc cgg acg ctg gtg      443
Pro Gly Ala Pro Arg Met Gly Ala Pro Ser Ala Cys Arg Thr Leu Val
              35              40              45

ttg gct ctg gcg gcc atg ctc gtg gtg ccg cag gca gag acc cag ggc      491
Leu Ala Leu Ala Ala Met Leu Val Val Pro Gln Ala Glu Thr Gln Gly
              50              55              60

cct gtg gag ccg agc tgg gag aat gca ggg cac acc atg gat ggc ggt      539
Pro Val Glu Pro Ser Trp Glu Asn Ala Gly His Thr Met Asp Gly Gly
              65              70              75

gcc ccg acg tcc tgc ccc acc cgg cgc gtg agc ttt gtt cca ccc gtc      587
Ala Pro Thr Ser Ser Pro Thr Arg Arg Val Ser Phe Val Pro Pro Val
  80              85              90

act gtc ttc ccc agc ctg agc ccc ctg aac ccg gcg cac aat ggg cgg      635
Thr Val Phe Pro Ser Leu Ser Pro Leu Asn Pro Ala His Asn Gly Arg
  95              100              105              110

gtg tgc agc acc tgg ggt gac ttc cac tac aag acc ttc gac ggc gac      683
Val Cys Ser Thr Trp Gly Asp Phe His Tyr Lys Thr Phe Asp Gly Asp
              115              120              125

gtc ttc cgc ttc cct ggc ctt tgc aac tac gtg ttc tct gag cac tgc      731
Val Phe Arg Phe Pro Gly Leu Cys Asn Tyr Val Phe Ser Glu His Cys
              130              135              140

cgc gcc gcc tac gag gac ttc aac gtc cag cta cgc cga ggc cta gtg      779
Arg Ala Ala Tyr Glu Asp Phe Asn Val Gln Leu Arg Arg Gly Leu Val
              145              150              155

ggc tcc agg cct gtg gtc acc cgt gtt gtc atc aag gcc cag ggg ctg      827
Gly Ser Arg Pro Val Val Thr Arg Val Val Ile Lys Ala Gln Gly Leu
              160              165              170

gtg ctg gag gcg tcc aac ggc tcc gtc ctc atc aat ggg cag cgg gag      875
Val Leu Glu Ala Ser Asn Gly Ser Val Leu Ile Asn Gly Gln Arg Glu
              175              180              185              190

gag ctg cct tac agc cgc act ggc ctc ctg gtg gag cag agc ggg gac      923
Glu Leu Pro Tyr Ser Arg Thr Gly Leu Leu Val Glu Gln Ser Gly Asp

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195										200										205									
tac	atc	aag	gtc	agc	atc	cgg	ctg	gtg	ctg	aca	ttc	ctg	tgg	aac	gga														
Tyr	Ile	Lys	Val	Ser	Ile	Arg	Leu	Val	Leu	Thr	Phe	Leu	Trp	Asn	Gly														971
			210					215					220																
gag	gac	agt	gcc	ctg	ctg	gag	ctg	gat	ccc	aaa	tac	gcc	aac	cag	acc														1019
Glu	Asp	Ser	Ala	Leu	Leu	Glu	Leu	Asp	Pro	Lys	Tyr	Ala	Asn	Gln	Thr														
			225					230					235																
tgt	ggc	ctg	tgt	ggg	gac	ttc	aac	ggc	ctc	ccg	gcc	ttc	aac	gag	ttc														1067
Cys	Gly	Leu	Cys	Gly	Asp	Phe	Asn	Gly	Leu	Pro	Ala	Phe	Asn	Glu	Phe														
			240					245					250																
tat	gcc	cac	agt	gag	tgc	cac	ctg	gac	gcc	agg	ctg	acc	ccg	ctc	cag														1115
Tyr	Ala	His	Ser	Glu	Cys	His	Leu	Asp	Ala	Arg	Leu	Thr	Pro	Leu	Gln														
							260						265																
ttt	ggg	aac	ctg	cag	aag	ttg	gat	ggg	ccc	acg	gag	cag	tgc	ccg	gac														1163
Phe	Gly	Asn	Leu	Gln	Lys	Leu	Asp	Gly	Pro	Thr	Glu	Gln	Cys	Pro	Asp														
							275						280																
ccg	ctg	ccc	ttg	ccg	gcc	ggc	aac	tgc	acg	gac	gag	gag	ggc	atc	tgc														1211
Pro	Leu	Pro	Leu	Pro	Ala	Gly	Asn	Cys	Thr	Asp	Glu	Glu	Gly	Ile	Cys														
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cac	cgc	acc	ctg	ctg	ggg	ccg	gcc	ttt	gcg	gag	tgc	cac	gca	ctg	gtg														1259
His	Arg	Thr	Leu	Leu	Gly	Pro	Ala	Phe	Ala	Glu	Cys	His	Ala	Leu	Val														
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Asp	Ser	Thr	Ala	Tyr	Leu	Ala	Ala	Cys	Ala	Gln	Asp	Leu	Cys	Arg	Cys														
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Pro	Thr	Cys	Pro	Cys	Ala	Thr	Phe	Val	Glu	Tyr	Ser	Arg	Gln	Cys	Ala														
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His	Ala	Gly	Gly	Gln	Pro	Arg	Asn	Trp	Arg	Cys	Pro	Glu	Leu	Cys	Pro														
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cgg	acc	tgc	ccc	ctc	aac	atg	cag	cac	cag	gag	tgt	ggc	tca	ccc	tgc														1451
Arg	Thr	Cys	Pro	Leu	Asn	Met	Gln	His	Gln	Glu	Cys	Gly	Ser	Pro	Cys														
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Cys	Val	Asp	Gly	Cys	Phe	Cys	Pro	Pro	Gly	Thr	Val	Leu	Asp	Asp	Ile														
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Thr	His	Ser	Gly	Cys	Leu	Pro	Leu	Gly	Gln	Cys	Pro	Cys	Thr	His	Gly														
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Gln Asn Gln Ala Asp Asp Phe Thr Ala Leu Ser Gly Val Val Glu Ala	
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Tyr Ile Leu Ala Gln Asp Tyr Cys Gly Asp Asn Thr Thr His Gly Thr	
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Pro Gly Thr Pro Ala Thr Thr Pro Phe Thr Phe Thr Thr Ala Trp Val			
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Gln Asn Thr Glu Thr Ser Ser Leu Val Ser Met Thr Ser Ala Thr Ile
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Pro Ser Val Arg Pro Thr Phe Thr Ser Thr His Asn Thr Leu Thr Ser
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Ser Leu Leu Thr Thr Phe Pro Gly Thr Tyr Ser Phe Ser Ser Ser Met
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Pro Ala Ser Thr Ser Thr Leu His Thr Thr Ala Glu Ser Thr Thr Ala
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His Thr Thr Thr Thr Ser Phe Thr Thr Ser Thr Thr Met Glu Ser Pro
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Phe Ser Glu Glu Thr Leu Thr Thr Ala Met Thr Ser Thr Pro Pro Ile
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Thr Ala Val Thr Pro Thr Pro Val Thr Pro Ser Ser Leu Ser Thr Asp	
705 710 715	

atc ccg acc aca agc cta cga act ctc acc cct tcg tct gtg ggc acc Ile Pro Thr Thr Ser Leu Arg Thr Leu Thr Pro Ser Ser Val Gly Thr 720 725 730	2208
agc act tca ttg act aca acc aca gac ttt ccc tct ata ccc act gat Ser Thr Ser Leu Thr Thr Thr Thr Asp Phe Pro Ser Ile Pro Thr Asp 735 740 745	2256
atc agt acc tta cca act cga aca cac atc att tca tct tct ccc tcc Ile Ser Thr Leu Pro Thr Arg Thr His Ile Ile Ser Ser Ser Pro Ser 750 755 760	2304
atc caa agt aca gaa acc tca tcc ctt gtg ggc acc acc tct ccc acc Ile Gln Ser Thr Glu Thr Ser Ser Leu Val Gly Thr Thr Ser Pro Thr 765 770 775 780	2352
atg tcc act gtg aga atg acc ctc aga att act gag aac acc cca atc Met Ser Thr Val Arg Met Thr Leu Arg Ile Thr Glu Asn Thr Pro Ile 785 790 795	2400
agt tcc ttt agc aca agt att gtt gtt ata cct gaa acc cca aca cag Ser Ser Phe Ser Thr Ser Ile Val Val Ile Pro Glu Thr Pro Thr Gln 800 805 810	2448
acc cct cct gta ctg acg tca gcc act ggg acc caa aca tct cct gca Thr Pro Pro Val Leu Thr Ser Ala Thr Gly Thr Gln Thr Ser Pro Ala 815 820 825	2496
cct act act gtc acc ttt gga agt acg gat tcc tcc acg tcc act ctt Pro Thr Thr Val Thr Phe Gly Ser Thr Asp Ser Ser Thr Ser Thr Leu 830 835 840	2544
cat act ctt act cca tca aca gcc ttg agc acg atc gtg tca aca tca His Thr Leu Thr Pro Ser Thr Ala Leu Ser Thr Ile Val Ser Thr Ser 845 850 855 860	2592
cag gtt cct att cct agc aca cat tcc tcc acc ctt caa aca act cct Gln Val Pro Ile Pro Ser Thr His Ser Ser Thr Leu Gln Thr Thr Pro 865 870 875	2640
tct act ccc tca ttg caa act tca ctc aca tct aca agt gag ttc act Ser Thr Pro Ser Leu Gln Thr Ser Leu Thr Ser Thr Ser Glu Phe Thr 880 885 890	2688
aca gaa tct ttc act agg gga agt acg tct aca aat gca atc ttg act Thr Glu Ser Phe Thr Arg Gly Ser Thr Ser Thr Asn Ala Ile Leu Thr 895 900 905	2736
tct ttt agt acc atc atc tgg tcc tca aca ccc act att atc atg tcc Ser Phe Ser Thr Ile Ile Trp Ser Ser Thr Pro Thr Ile Ile Met Ser 910 915 920	2784
tct tct cca tct tct gcc agc ata act cca gtg ttc tcc act acc att Ser Ser Pro Ser Ser Ala Ser Ile Thr Pro Val Phe Ser Thr Thr Ile 925 930 935 940	2832
cat tct gtt cct tct tca cca tac att ttc agt aca gaa aat gtg ggc His Ser Val Pro Ser Ser Pro Tyr Ile Phe Ser Thr Glu Asn Val Gly 945 950 955	2880
tcc gct tct atc aca ggc ttt cct agt ctc tct tcc tct gca act acc	2928

Ser Ala Ser Ile Thr Gly Phe Pro Ser Leu Ser Ser Ser Ala Thr Thr	
960 965 970	
agc act tct tca acc agc tcc tct ctg acc aca gct ctc act gaa ata	2976
Ser Thr Ser Ser Thr Ser Ser Ser Leu Thr Thr Ala Leu Thr Glu Ile	
975 980 985	
acc ccc ttt tct tat att tcc ctt ccc tcc acc aca ccc tgt cca gga	3024
Thr Pro Phe Ser Tyr Ile Ser Leu Pro Ser Thr Thr Pro Cys Pro Gly	
990 995 1000	
act ata aca att acc ata gtc cct gcc tct ccc act gat cca tgt gtt	3072
Thr Ile Thr Ile Thr Ile Val Pro Ala Ser Pro Thr Asp Pro Cys Val	
1005 1010 1015 1020	
gaa atg gat ccc agc act gaa gct act tct cct ccc acc acc cca tta	3120
Glu Met Asp Pro Ser Thr Glu Ala Thr Ser Pro Pro Thr Thr Pro Leu	
1025 1030 1035	
aca gtc ttt ccc ttt act acc gaa atg gtc acc tgt cct acc tcc atc	3168
Thr Val Phe Pro Phe Thr Thr Glu Met Val Thr Cys Pro Thr Ser Ile	
1040 1045 1050	
agt atc caa act act ctt act aca tat atg gac act tct tcc atg atg	3216
Ser Ile Gln Thr Thr Leu Thr Thr Tyr Met Asp Thr Ser Ser Met Met	
1055 1060 1065	
cca gaa agt gag tcc agc atc tca ccc aat gct tcc agt tcc act ggc	3264
Pro Glu Ser Glu Ser Ser Ile Ser Pro Asn Ala Ser Ser Ser Thr Gly	
1070 1075 1080	
act ggg act gta ccc aca aac aca gtt ttc aca agt act cga ctg ccc	3312
Thr Gly Thr Val Pro Thr Asn Thr Val Phe Thr Ser Thr Arg Leu Pro	
1085 1090 1095 1100	
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Thr Ser Glu Thr Trp Leu Ser Asn Ser Ser Val Ile Pro Leu Pro Leu	
1105 1110 1115	
cct ggc gtc tct acc atc ccg ctc acc atg aaa cca agc agt agc ctc	3408
Pro Gly Val Ser Thr Ile Pro Leu Thr Met Lys Pro Ser Ser Ser Leu	
1120 1125 1130	
ccg acc atc ctg agg act tca agc aag tca aca cac cca tcc cca ccc	3456
Pro Thr Ile Leu Arg Thr Ser Ser Lys Ser Thr His Pro Ser Pro Pro	
1135 1140 1145	
acc act agg act tca gag aca cca gtg gcc act acc cag act cct acc	3504
Thr Thr Arg Thr Ser Glu Thr Pro Val Ala Thr Thr Gln Thr Pro Thr	
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acc ctt aca tca cgc agg aca act cgc atc act tct cag atg acc aca	3552
Thr Leu Thr Ser Arg Arg Thr Thr Arg Ile Thr Ser Gln Met Thr Thr	
1165 1170 1175 1180	
cag tcc acg ttg acc acc act gca ggc acc tgt gac aat ggt ggc acc	3600
Gln Ser Thr Leu Thr Thr Thr Ala Gly Thr Cys Asp Asn Gly Gly Thr	
1185 1190 1195	
tgg gaa cag ggc cag tgt gct tgc ctt ccg ggg ttt tct ggg gac cgc	3648
Trp Glu Gln Gly Gln Cys Ala Cys Leu Pro Gly Phe Ser Gly Asp Arg	

1200	1205	1210	
tgt cag ctc cag acc aga tgc cag aat ggg ggt cag tgg gat ggc ctc Cys Gln Leu Gln Thr Arg Cys Gln Asn Gly Gly Gln Trp Asp Gly Leu 1215 1220 1225			3696
aaa tgc cag tgc ccc agc acc ttc tat ggt tcc agt tgt gag ttt gct Lys Cys Gln Cys Pro Ser Thr Phe Tyr Gly Ser Ser Cys Glu Phe Ala 1230 1235 1240			3744
gtg gaa cag gtg gat cta gat gca gaa gat ttt tgc aga cat gca ggg Val Glu Gln Val Asp Leu Asp Ala Glu Asp Phe Cys Arg His Ala Gly 1245 1250 1255 1260			3792
ctt cac ctt caa ggg tgt gga gat cct gtc cct gag gaa tgg cag cat Leu His Leu Gln Gly Cys Gly Asp Pro Val Pro Glu Glu Trp Gln His 1265 1270 1275			3840
cgt ggt gga cta cct ggt cct gct gga gat gcc ctt cag ccc cca gct Arg Gly Gly Leu Pro Gly Pro Ala Gly Asp Ala Leu Gln Pro Pro Ala 1280 1285 1290			3888
gga gag cga gta tga gcaggtgaag accacgctga aggaggggct gcagaacgcc Gly Glu Arg Val 1295			3943
agccaggatg tgaacagctg ccaggactcc cagaccctgt gttttaagcc tgactccatc			4003
aaggtgaaca acaacagcaa gacagagctg accccggcag ccatctgccg cgcgcgcgtc			4063
ccacgggcta tgaagagttc tacttcccct tgggtggaggc caccgggctc cgctgtgtca			4123
ccaaatgcac gtctgggggtg gacaacgcca tcgactgtca ccaggggccag tgcgttctgg			4183
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cagcgcagag gccggtcctg ggaccaggac aggaaatggt tcgagacctg ggatgaggaa			4423
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gacacaaggg tctgcattgc gtccatttca agaggtgacc ccaggacgcg ggcagcccag			4663
gctcctgctg ttcttgggca agatgagact gttcccccaa atcccatcct tctccttcca			4723
acttggctga aacccacctg gagacgcagt tcacgtccag gctcttcac tgtggaatct			4783
tgggcaagtc agtaacgagc ctcagtttcc tcacctgcaa aacgggtaca gcattcctgt			4843
atgatacgtc acgccgttgt tgtgaaaacc acatagactt ggtcaattct cggtcctact			4903
ctgccctccc gtctcagccc tcgtgttgcc attgcctctc tcggatcctc caatcctcac			4963
gtccttcacc tgggtctctgg ccctgggttct tattttctct caattcccta ctgcctgttt			5023

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cttacttttga acctggagggc agcctgcagc cccatcccat ctcttgccct ctctgatct 5083
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cttcacccat cctgcacccc agtccccag ccctaaatcc tccctcctct cctcacatcc 5203
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cggtcacccct gttgcccagt tcccggtttc tcttgctctc attcctgtat cctttccccc 5323
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ctgagccctt gaaatcctca gtgccttgg cggggaagat tggctttggg gacaggaggt 5683
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<210> 92
<211> 748
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (202) ..(456)

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<400> 92
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ttgttgtggg tcccaggcgg tgccttcgag actggctcag cctccatctt cgatgggtcc 180
tccctggctg cctatgagga c atg ctg gtt gtg atc gtc cag tac cgg ctg 231
Met Leu Val Val Ile Val Gln Tyr Arg Leu
1 5 10
gga ata ttt ggc ttc ttc acc aca tgg gat cag cac gct ccc ggg aac 279
Gly Ile Phe Gly Phe Phe Thr Thr Trp Asp Gln His Ala Pro Gly Asn
15 20 25
tgg gcc ttc aag gac cag gtg gct gct cta tcc tgg gtc cag aag aac 327
Trp Ala Phe Lys Asp Gln Val Ala Ala Leu Ser Trp Val Gln Lys Asn
30 35 40
atc gag ttc ttc ggt ggg gac ccc agc tct gtg acc atc ttt gat tct 375
Ile Glu Phe Phe Gly Gly Asp Pro Ser Ser Val Thr Ile Phe Asp Ser
45 50 55
gtc tcc cat ggc cga agg ctt att cca caa agc cgt cat gga gag tgg 423

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Val	Ser	His	Gly	Arg	Arg	Leu	Ile	Pro	Gln	Ser	Arg	His	Gly	Glu	Trp	
60						65					70					
ggg	ggc	cat	cat	cct	tta	cct	gaa	ggc	cca	tga	ttatgaga	agagt	gagga			474
Gly	Gly	His	His	Pro	Leu	Pro	Glu	Gly	Pro							
75						80										
cgtacgaata	ctgttaacac	cttgccagct	tcctctcctc	agttagggga	gaatgtgttc											534
aggcaccttc	tcaccatgtg	ccatctatcc	cacgatattt	gtcatctgtc	tcttaattat											594
ctactacaga	gtgaggccct	agagaccagg	atctctctgt	ccttcaggcc	cccagcataa											654
taagtgggtat	atatcaggca	gctataaatg	ttctggatga	atgagctaata	gaatgagctg											714
tttcattcaa	tgcatattaa	ttaaaaaaaaa	aaaa													748

<210> 93
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (901)..(1524)

<400> 93	
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ccgggaccac ttcctacccc agaactcccc ccgcccagcc cccactgccc cccaccacc	180
cctccaaccg ccagacttcc cacactcccc gcatcagtgc acggcccccg aggactccac	240
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gggtcccca gatcttcctt ccaggagcac accagggagt caggctactc gtgggggcat	360
gtctgctcag ctaccggcca tctccaatgt ggccaaactc cttcctcact ctggctgggc	420
caacacacag taagtaaggt gtatcgggaa tgggtgggggt atggggagca tegtgggtca	480
cgctgcgggg gccgtgggga caggcgccaa ggaggccagc ctcacaaggg catctctgtc	540
atgggtggaaa gatggaatta ggcttgggac acaccccgcc cacctacggg tgtatcccaa	600
atgccgcccg ccgcacactc aggcgcgacc atctgagccc cctcctctga gaggcagggc	660
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tgcttattgt tttcatctaa ttttgtgggg gtgtgctgtg gtgtgcgcat gtgtgtgtgc	840
aggtgggtgc ttgcgtgtgc aacgtgtgtg ctgcgtgttt gtgtgctgtg agctgtgttc	900
atg tat gtg ctg cgc atg agt gtg tgt gct gtg tgt gca tgt gtg tgc	948

Met	Tyr	Val	Leu	Arg	Met	Ser	Val	Cys	Ala	Val	Cys	Ala	Cys	Val	Cys		
1				5					10					15			
tgt	gtg	ttt	gtg	tgt	gct	gtg	ttc	atg	tgt	gct	gtg	cat	gcg	tgt	gtg	996	
Cys	Val	Phe	Val	Cys	Ala	Val	Phe	Met	Cys	Ala	Val	His	Ala	Cys	Val		
			20					25					30				
ctg	tgt	gca	tgt	gtg	tgc	tgt	gtg	ctg	tgt	tca	tgt	gtg	tgc	tgt	gtg	1044	
Leu	Cys	Ala	Cys	Val	Cys	Cys	Val	Leu	Cys	Ser	Cys	Val	Cys	Cys	Val		
		35					40					45					
tgc	atg	tgc	tgt	gtg	cat	gtg	tgt	gct	gtg	ttt	gtg	tgt	gtg	ctg	tgt	1092	
Cys	Met	Cys	Cys	Val	His	Val	Cys	Ala	Val	Phe	Val	Cys	Val	Leu	Cys		
	50					55					60						
gtg	ctg	tgt	tcg	tgt	gtg	ctg	tgt	tcg	cgt	gtg	tgt	gct	gtg	tgt	gca	1140	
Val	Leu	Cys	Ser	Cys	Val	Leu	Cys	Ser	Arg	Val	Cys	Ala	Val	Cys	Ala		
65					70				75						80		
tgt	gtg	tgc	tgt	gtc	ttt	gtg	tgt	gtg	ctg	tgt	gct	agt	gtg	ctg	tgt	1188	
Cys	Val	Cys	Cys	Val	Phe	Val	Cys	Val	Leu	Cys	Ala	Ser	Val	Leu	Cys		
				85					90					95			
gtg	cat	gtg	tgt	gcg	tgt	gct	gtg	cgt	ttg	tgt	gct	gtg	tgc	tcg	tgt	1236	
Val	His	Val	Cys	Ala	Cys	Ala	Val	Arg	Leu	Cys	Ala	Val	Cys	Ser	Cys		
			100					105					110				
gtg	tgc	tgt	gtg	tgc	gtg	tgt	gct	gtg	cgt	ttg	tgt	gtg	cgt	gtg	cgt	1284	
Val	Cys	Cys	Val	Cys	Val	Cys	Ala	Val	Arg	Leu	Cys	Val	Arg	Val	Arg		
		115					120					125					
ttg	cgt	gtg	tgc	tgt	gtg	tgc	atg	tgt	gtg	cgt	gtg	tgt	gcc	gtg	cgt	1332	
Leu	Arg	Val	Cys	Cys	Val	Cys	Met	Cys	Val	Arg	Val	Cys	Ala	Val	Arg		
	130					135					140						
ttg	tgt	gct	gtg	tgt	gca	tgt	gtg	tgc	gtg	tgt	gtg	ctg	tgc	gtt	tgt	1380	
Leu	Cys	Ala	Val	Cys	Ala	Cys	Val	Cys	Val	Cys	Val	Leu	Cys	Val	Cys		
145					150					155					160		
gtg	tgt	gct	gtg	tgc	tca	tct	gtg	tgc	tgt	gtg	tgc	tgt	gcg	ttt	gtg	1428	
Val	Cys	Ala	Val	Cys	Ser	Ser	Val	Cys	Cys	Val	Cys	Cys	Ala	Phe	Val		
				165					170					175			
tgt	gtg	ctg	tat	gct	cgt	gtg	tgt	gct	gtg	ctc	gtg	tgt	gtg	ctg	tgt	1476	
Cys	Val	Leu	Tyr	Ala	Arg	Val	Cys	Ala	Val	Leu	Val	Cys	Val	Leu	Cys		
			180					185					190				
tca	tgc	gtg	tgc	tgt	gtg	ttg	tgt	gtg	tgt	agc	tgc	ggg	gat	gca	taa	1524	
Ser	Cys	Val	Cys	Cys	Val	Leu	Cys	Val	Cys	Ser	Cys	Gly	Asp	Ala			
		195				200						205					
agt	atg	agt	ctt	ttt	tagga	tg	gga	aattga	gat	gta	aagat	ttg	ggg	ggtga	ggg	tcgtgcc	1584
aatt	acattt	catt	tgcatg	gatt	tttggtt	tt	catgctct	gtcctcccct	cctttggtct								1644
tact	gggtcc	ctct	gactgc	tct	gtgattt	ttag	tgatgg	aaaagg	gagt	gagg	agccag						1704
tct	gggttgt	tgct	atttttc	ggat	ggccag	tttacc	cctga	aaattccc	gt	gaga	agggag						1764
atgg	cggtag	cagc	gacgtg	cccac	cctgtg	atttct	gggg	tccttctttt	ctctttgctg								1824

gttcagggac tcaagtccag gccaatTTga ctcaaagtcc aaggagagaag agaaagaggg 1884
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 tac 1947

<210> 94
 <211> 254
 <212> PRT
 <213> Homo sapiens

<400> 94
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 20 25 30
 Cys Tyr Asn Glu Pro Lys Val Thr Ser Cys Pro Gln Gln Gly Leu
 35 40 45
 Gln Ala Val Pro Val Gly Ile Pro Ala Ala Ser Gln Arg Ile Phe Leu
 50 55 60
 His Gly Asn Arg Ile Ser His Val Pro Ala Ala Ser Phe Arg Ala Cys
 65 70 75 80
 Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Val Leu Ala Arg Ile
 85 90 95
 Asp Ala Ala Ala Phe Thr Gly Leu Ala Leu Leu Glu Gln Leu Asp Leu
 100 105 110
 Ser Asp Asn Ala Gln Leu Arg Ser Val Asp Pro Ala Thr Phe His Gly
 115 120 125
 Leu Gly Arg Leu His Thr Leu His Leu Asp Arg Cys Gly Leu Gln Glu
 130 135 140
 Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr
 145 150 155 160
 Leu Gln Asp Asn Ala Leu Gln Ala Leu Pro Asp Asp Thr Phe Arg Asp
 165 170 175
 Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile Ser Ser
 180 185 190
 Val Pro Glu Arg Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu
 195 200 205
 Leu His Gln Asn Arg Val Ala His Val His Pro His Ala Phe Arg Asp
 210 215 220
 Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Ala
 225 230 235 240
 Leu Pro Thr Glu Ala Leu Ala Pro Cys Val Pro Cys Ser Thr
 245 250

<210> 95
 <211> 353
 <212> PRT
 <213> Homo sapiens

<400> 95
 Met Ala Ala Thr Lys Arg Lys Arg Arg Gly Gly Phe Ala Val Gln Ala
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 Lys Lys Pro Lys Arg Asn Glu Ile Asp Ala Glu Pro Pro Ala Lys Arg
 20 25 30
 His Ala Thr Ala Glu Glu Val Glu Glu Glu Glu Arg Asp Arg Ile Pro

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<210> 96
<211> 410
<212> PRT
<213> Homo sapiens
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<400> 96															
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Cys	Phe	Leu	Leu	Leu	Ala	Leu	Val	Leu	Val	Pro	Ser	Asp	Ala	Ser	Gly
			20					25					30		
Gln	Ser	Ser	Arg	Asn	Asp	Trp	Gln	Val	Leu	Gln	Pro	Glu	Gly	Pro	Met
		35				40					45				
Leu	Val	Ala	Glu	Gly	Glu	Thr	Leu	Leu	Leu	Arg	Cys	Met	Val	Val	Gly
	50					55					60				
Ser	Cys	Thr	Asp	Gly	Met	Ile	Lys	Trp	Val	Lys	Ile	Ala	Leu	Ala	Ser
65					70					75					80

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Phe Tyr Glu Asp Gly Gly Asp Glu Asp Ile Val Thr Ile Ser Gln Ala
      85                      90                      95
Thr Pro Ser Ser Val Ser Arg Gly Thr Ala Pro Ser Asp Asn Arg Val
      100                    105                    110
Thr Ser Phe Arg Asp Leu Ile His Asp Gln Asp Glu Asp Glu Glu
      115                    120                    125
Glu Glu Gly Gln Arg Phe Tyr Ala Gly Gly Ser Glu Arg Ser Gly Gln
      130                    135                    140
Gln Ile Val Gly Pro Pro Arg Lys Lys Ser Pro Asn Glu Leu Val Asp
      145                    150                    155                    160
Asp Leu Phe Lys Gly Ala Lys Glu His Gly Ala Val Ala Val Glu Arg
      165                    170                    175
Val Thr Lys Ser Pro Gly Glu Thr Ser Lys Pro Arg Pro Phe Ala Gly
      180                    185                    190
Gly Gly Tyr Arg Leu Gly Ala Ala Pro Glu Glu Glu Ser Ala Tyr Val
      195                    200                    205
Ala Gly Glu Lys Arg Gln His Ser Ser Gln Asp Val His Val Val Leu
      210                    215                    220
Lys Leu Trp Lys Ser Gly Phe Ser Leu Asp Asn Gly Glu Leu Arg Ser
      225                    230                    235                    240
Tyr Gln Asp Pro Ser Asn Ala Gln Phe Leu Glu Ser Ile Arg Arg Gly
      245                    250                    255
Glu Val Pro Ala Glu Leu Arg Arg Leu Ala His Gly Gly Gln Val Asn
      260                    265                    270
Leu Asp Met Glu Asp His Arg Asp Glu Asp Phe Val Lys Pro Lys Gly
      275                    280                    285
Ala Leu Gln Ala Phe Thr Gly Glu Gly Gln Lys Leu Gly Ser Thr Ala
      290                    295                    300
Pro Gln Val Leu Ser Thr Ser Ser Pro Ala Gln Gln Ala Glu Asn Glu
      305                    310                    315                    320
Ala Lys Ala Ser Ser Ser Ile Leu Ile Asn Glu Ser Glu Pro Thr Thr
      325                    330                    335
Asn Ile Gln Ile Arg Leu Ala Asp Gly Gly Arg Leu Val Gln Lys Phe
      340                    345                    350
Asn His Ser His Arg Ile Ser Asp Ile Arg Leu Phe Ile Val Asp Ala
      355                    360                    365
Arg Pro Ala Met Ala Ala Thr Ser Phe Ile Leu Met Thr Thr Phe Pro
      370                    375                    380
Asn Lys Glu Leu Ala Asp Glu Ser Gln Thr Leu Lys Glu Ala Asn Leu
      385                    390                    395                    400
Leu Asn Ala Val Ile Val Gln Arg Leu Thr
      405                    410

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<210> 97
<211> 379
<212> PRT
<213> Homo sapiens

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<400> 97
Met Cys Ser Thr Met Ser Ala Pro Thr Cys Leu Ala His Leu Pro Pro
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Cys Phe Leu Leu Leu Ala Leu Val Leu Val Pro Ser Asp Ala Ser Gly
      20      25      30
Gln Ser Ser Arg Asn Asp Trp Gln Val Leu Gln Pro Glu Gly Pro Met
      35      40      45
Leu Val Ala Glu Gly Glu Thr Leu Leu Leu Arg Cys Met Val Val Gly
      50      55      60
Ser Cys Thr Asp Gly Met Ile Lys Trp Val Lys Ile Ala Leu Ala Ser

```

65					70					75				80	
Phe	Tyr	Glu	Asp	Gly	Gly	Asp	Glu	Asp	Ile	Val	Thr	Ile	Ser	Gln	Ala
				85					90					95	
Thr	Pro	Ser	Ser	Val	Ser	Arg	Gly	Thr	Ala	Pro	Ser	Asp	Asn	Arg	Val
			100					105					110		
Thr	Ser	Phe	Arg	Asp	Leu	Ile	His	Asp	Gln	Asp	Glu	Asp	Glu	Glu	Glu
		115					120					125			
Glu	Glu	Gly	Gln	Arg	Phe	Tyr	Ala	Gly	Gly	Ser	Glu	Arg	Ser	Gly	Gln
		130					135					140			
Gln	Ile	Val	Gly	Pro	Pro	Arg	Lys	Lys	Ser	Pro	Asn	Glu	Leu	Val	Asp
					150					155					160
Asp	Leu	Phe	Lys	Gly	Ala	Lys	Glu	His	Gly	Ala	Val	Ala	Val	Glu	Arg
				165					170					175	
Val	Thr	Lys	Ser	Pro	Gly	Glu	Thr	Ser	Lys	Pro	Arg	Val	His	Val	Val
			180					185					190		
Leu	Lys	Leu	Trp	Lys	Ser	Gly	Phe	Ser	Leu	Asp	Asn	Gly	Glu	Leu	Arg
		195					200					205			
Ser	Tyr	Gln	Asp	Pro	Ser	Asn	Ala	Gln	Phe	Leu	Glu	Ser	Ile	Arg	Arg
		210				215					220				
Gly	Glu	Val	Pro	Ala	Glu	Leu	Arg	Arg	Leu	Ala	His	Gly	Gly	Gln	Val
					230					235					240
Asn	Leu	Asp	Met	Glu	Asp	His	Arg	Asp	Glu	Asp	Phe	Val	Lys	Pro	Lys
				245					250					255	
Gly	Ala	Phe	Lys	Ala	Phe	Thr	Gly	Glu	Gly	Gln	Lys	Leu	Gly	Ser	Thr
			260					265					270		
Ala	Pro	Gln	Val	Leu	Ser	Thr	Ser	Ser	Pro	Ala	Gln	Gln	Ala	Glu	Asn
			275				280					285			
Glu	Ala	Lys	Ala	Ser	Ser	Ser	Ile	Leu	Ile	Asp	Glu	Ser	Glu	Pro	Thr
		290				295					300				
Thr	Asn	Ile	Gln	Ile	Arg	Leu	Ala	Asp	Gly	Gly	Arg	Leu	Val	Gln	Lys
				310					315						320
Phe	Asn	His	Ser	His	Arg	Ile	Ser	Asp	Ile	Arg	Leu	Phe	Ile	Val	Asp
				325					330					335	
Ala	Arg	Pro	Ala	Met	Ala	Ala	Thr	Ser	Phe	Ile	Leu	Met	Thr	Thr	Phe
			340					345					350		
Pro	Asn	Lys	Glu	Leu	Ala	Asp	Glu	Ser	Gln	Thr	Leu	Lys	Glu	Ala	Asn
		355					360					365			
Leu	Leu	Asn	Ala	Val	Ile	Val	Gln	Arg	Leu	Thr					
		370				375									

<210> 98
 <211> 196
 <212> PRT
 <213> Homo sapiens

<400> 98
 Met Ala Ala Glu Arg Gln Glu Ala Leu Arg Glu Phe Val Ala Val Thr
 1 5 10 15
 Gly Ala Glu Glu Asp Arg Ala Arg Phe Phe Leu Glu Ser Ala Gly Trp
 20 25 30
 Asp Leu Gln Ile Ala Leu Ala Ser Phe Tyr Glu Asp Gly Gly Asp Glu
 35 40 45
 Asp Ile Val Thr Ile Ser Gln Ala Thr Pro Ser Ser Val Ser Arg Gly
 50 55 60
 Thr Ala Pro Ser Asp Asn Arg Val Thr Ser Phe Arg Asp Leu Ile His
 65 70 75 80
 Asp Gln Asp Glu Asp Glu Glu Glu Glu Glu Gly Gln Arg Ser Arg Phe
 85 90 95

```

Tyr Ala Gly Gly Ser Glu Arg Ser Gly Gln Gln Ile Val Gly Pro Pro
      100      105      110
Arg Lys Lys Ser Pro Asn Glu Leu Val Asp Asp Leu Phe Lys Gly Ala
      115      120      125
Lys Glu His Gly Ala Val Ala Val Glu Arg Val Thr Lys Ser Pro Gly
      130      135      140
Glu Thr Ser Lys Pro Arg Pro Phe Ala Gly Gly Gly Tyr Arg Leu Gly
      145      150      155      160
Ala Ser Thr Arg Gly Arg Val Cys Leu Cys Gly Arg Arg Lys Glu Ala
      165      170      175
Ala Phe Gln Pro Arg Cys Ser Cys Ser Ile Glu Thr Leu Glu Glu Trp
      180      185      190
Ile Gln Pro Gly
      195

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<210> 99
<211> 100
<212> PRT
<213> Homo sapiens

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```

<400> 99
Met Phe Ala Pro Arg Leu Leu Asp Leu Gln Lys Thr Lys Tyr Ala Arg
  1      5      10      15
Phe Met Asn His Arg Val Pro Ala His Lys Arg Tyr Gln Pro Thr Glu
      20      25      30
Tyr Glu His Ala Ala Asn Cys Ala Thr His Ala Phe Trp Ile Ile Pro
      35      40      45
Ser Ile Leu Gly Ser Ser Asn Leu Tyr Phe Leu Ser Asp Asp Asp Trp
      50      55      60
Glu Thr Ile Ser Ala Trp Ile Tyr Gly Leu Gly Leu Cys Gly Leu Phe
      65      70      75      80
Val Val Ser Thr Val Phe His Thr Ile Ser Trp Lys Lys Ser His Leu
      85      90      95
Arg Trp Gly Phe
      100

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<210> 100
<211> 580
<212> PRT
<213> Homo sapiens

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<400> 100
Met Arg Pro Trp Leu Arg His Leu Val Leu Gln Ala Leu Arg Asn Ser
  1      5      10      15
Arg Ala Phe Cys Gly Ser His Gly Lys Pro Ala Pro Leu Pro Val Pro
      20      25      30
Gln Lys Ile Val Ala Thr Trp Glu Ala Ile Ser Leu Gly Arg Gln Leu
      35      40      45
Val Pro Glu Tyr Phe Asn Phe Ala His Asp Val Leu Asp Val Trp Ser
      50      55      60
Arg Leu Glu Glu Ala Gly His Arg Pro Pro Asn Pro Ala Phe Trp Trp
      65      70      75      80
Val Asn Gly Thr Gly Ala Glu Ile Lys Trp Ser Phe Glu Glu Leu Gly
      85      90      95
Lys Gln Ser Arg Lys Ala Ala Asn Val Leu Gly Gly Ala Cys Gly Leu

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			100					105					110				
Gln	Pro	Gly	Asp	Arg	Met	Met	Leu	Val	Leu	Pro	Arg	Leu	Pro	Glu	Trp		
		115					120					125					
Trp	Leu	Val	Ser	Val	Ala	Cys	Met	Arg	Thr	Gly	Thr	Val	Met	Ile	Pro		
	130					135					140						
Gly	Val	Thr	Gln	Leu	Thr	Glu	Lys	Asp	Leu	Lys	Tyr	Arg	Leu	Gln	Ala		
145					150					155					160		
Ser	Arg	Ala	Lys	Ser	Ile	Ile	Thr	Ser	Asp	Ser	Leu	Ala	Pro	Arg	Val		
				165					170					175			
Asp	Ala	Ile	Ser	Ala	Glu	Cys	Pro	Ser	Leu	Gln	Thr	Lys	Leu	Leu	Val		
			180					185					190				
Ser	Asp	Ser	Ser	Arg	Pro	Gly	Trp	Leu	Asn	Phe	Arg	Glu	Leu	Leu	Arg		
		195					200					205					
Glu	Ala	Ser	Thr	Glu	His	Asn	Cys	Met	Arg	Thr	Lys	Ser	Arg	Asp	Pro		
		210				215					220						
Leu	Ala	Ile	Tyr	Phe	Thr	Lys	Arg	Glu	Pro	Pro	Gly	Ala	Pro	Lys	Met		
225					230					235					240		
Val	Glu	His	Ser	Gln	Ser	Ser	Tyr	Gly	Leu	Gly	Phe	Val	Ala	Ser	Gly		
				245					250					255			
Arg	Arg	Trp	Val	Ala	Leu	Thr	Glu	Ser	Asp	Ile	Phe	Trp	Asn	Thr	Thr		
			260					265					270				
Asp	Thr	Gly	Trp	Val	Lys	Ala	Ala	Trp	Thr	Leu	Phe	Ser	Ala	Trp	Pro		
		275					280					285					
Asn	Gly	Ser	Cys	Ile	Phe	Val	His	Glu	Leu	Pro	Arg	Val	Asp	Ala	Lys		
	290					295					300						
Val	Ile	Leu	Asn	Thr	Leu	Ser	Lys	Phe	Pro	Ile	Thr	Thr	Leu	Cys	Cys		
305					310					315					320		
Val	Pro	Thr	Ile	Phe	Arg	Leu	Leu	Val	Gln	Glu	Asp	Leu	Thr	Arg	Tyr		
				325					330					335			
Gln	Phe	Gln	Ser	Leu	Arg	His	Cys	Leu	Thr	Gly	Gly	Glu	Ala	Leu	Asn		
			340					345					350				
Pro	Asp	Val	Arg	Glu	Lys	Trp	Lys	His	Gln	Thr	Gly	Val	Glu	Leu	Tyr		
		355					360					365					
Glu	Gly	Tyr	Gly	Gln	Ser	Glu	Thr	Val	Val	Ile	Cys	Ala	Asn	Pro	Lys		
		370				375					380						
Gly	Met	Lys	Ile	Lys	Ser	Gly	Ser	Met	Gly	Lys	Ala	Ser	Pro	Pro	Tyr		
385					390					395					400		
Asp	Val	Gln	Ile	Val	Asp	Asp	Glu	Gly	Asn	Val	Leu	Pro	Pro	Gly	Glu		
				405					410					415			
Glu	Gly	Asn	Val	Ala	Val	Arg	Ile	Arg	Pro	Thr	Arg	Pro	Phe	Cys	Phe		
			420					425					430				
Phe	Asn	Cys	Tyr	Leu	Asp	Asn	Pro	Glu	Lys	Thr	Ala	Ala	Ser	Glu	Gln		
		435					440					445					
Gly	Asp	Phe	Tyr	Ile	Thr	Gly	Asp	Arg	Ala	Arg	Met	Asp	Lys	Asp	Gly		
	450					455					4						

<210> 101
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 101
 Met Asp Leu Pro Arg Gly Leu Val Val Ala Trp Ala Leu Ser Leu Trp
 1 5 10 15
 Pro Gly Phe Thr Asp Thr Phe Asn Met Asp Thr Arg Lys Pro Arg Val
 20 25 30
 Ile Pro Gly Ser Arg Thr Ala Phe Phe Gly Tyr Thr Val Gln Gln His
 35 40 45
 Asp Ile Ser Gly Asn Lys Trp Leu Val Val Gly Ala Pro Leu Glu Thr
 50 55 60
 Asn Gly Tyr Gln Lys Thr Gly Asp Val Tyr Lys Cys Pro Val Ile His
 65 70 75 80
 Gly Asn Cys Thr Lys Leu Asn Leu Gly Asn Val Gly Trp Trp Ser Leu
 85 90 95
 His Asn Glu Ala Ser Gly Cys Leu Thr Gln Gly Arg Leu
 100 105

<210> 102
 <211> 156
 <212> PRT
 <213> Homo sapiens

<400> 102
 Met Gln Lys Leu Glu Leu Gly Arg Tyr Asn Glu Thr His Ala Ile Ala
 1 5 10 15
 Lys Trp Leu Leu Glu Lys Gln Glu Leu Gly Gly Gly Phe Arg Ser Thr
 20 25 30
 Gln Thr Thr Val Val Ala Leu Glu Ala Leu Thr Arg Phe Arg Glu Ala
 35 40 45
 Val Pro Phe Lys Gly Ile Gln Asp Leu His Val Gln Ile Arg Ala Pro
 50 55 60
 Lys Thr Ala Leu Asn Val Asn Trp Tyr Ile Asp His Ser Asn Ala Tyr
 65 70 75 80
 Gln Gln Arg Ser Ala Lys Phe Leu Ala Gln Asp Asp Leu Glu Ile Lys
 85 90 95
 Ala Ser Gly Asn Gly Arg Gly Thr Ile Ser Ile Leu Thr Met Tyr His
 100 105 110
 Lys Ser Pro Glu Ser Arg Glu Asp Asn Cys Asn Leu Tyr His Leu Asn
 115 120 125
 Ala Thr Leu His Ser Ala Leu Glu Glu Asn Lys Lys Gly Gly Glu Thr
 130 135 140
 Phe Arg Leu Arg Met Glu Thr Arg Phe Gln Asn Asn
 145 150 155

<210> 103
 <211> 198
 <212> PRT
 <213> Homo sapiens

<400> 103
 Met Ala Leu Arg His Leu Ala Leu Leu Ala Gly Leu Leu Val Gly Val
 1 5 10 15
 Ala Ser Lys Ser Met Glu Asn Thr Ala Gln Leu Pro Glu Cys Cys Val
 20 25 30
 Asp Val Val Gly Val Asn Ala Ser Cys Pro Gly Ala Ser Leu Cys Gly
 35 40 45
 Pro Gly Cys Tyr Arg Arg Trp Asn Ala Asp Gly Ser Ala Ser Cys Val
 50 55 60
 Arg Cys Gly Asn Gly Thr Leu Pro Ala Tyr Asn Gly Ser Glu Cys Arg
 65 70 75 80
 Ser Phe Ala Gly Pro Gly Ala Pro Phe Pro Met Asn Arg Ser Ser Gly
 85 90 95
 Thr Pro Gly Arg Pro His Pro Gly Ala Pro Arg Val Ala Ala Ser Leu
 100 105 110
 Phe Leu Gly Thr Phe Phe Ile Ser Ser Gly Leu Ile Leu Ser Val Ala
 115 120 125
 Gly Phe Phe Tyr Leu Lys Arg Ser Ser Lys Leu Pro Arg Ala Cys Tyr
 130 135 140
 Arg Arg Asn Lys Ala Pro Ala Leu Gln Pro Gly Glu Ala Ala Ala Met
 145 150 155 160
 Ile Pro Pro Pro Gln Ser Ser Val Arg Lys Pro Arg Tyr Val Arg Arg
 165 170 175
 Glu Arg Pro Leu Asp Arg Ala Thr Asp Pro Ala Ala Phe Pro Gly Glu
 180 185 190
 Ala Arg Ile Ser Asn Val
 195

<210> 104
 <211> 254
 <212> PRT
 <213> Homo sapiens

<400> 104
 Met Gly Leu Ser Ile Phe Leu Leu Leu Cys Val Leu Gly Leu Ser Gln
 1 5 10 15
 Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg Asn Ser
 20 25 30
 Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu Arg Cys Gly
 35 40 45
 Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala Ala His Cys Ser
 50 55 60
 Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His Ser Leu Ser Gln Leu
 65 70 75 80
 Asp Trp Thr Glu Gln Ile Arg His Ser Gly Phe Ser Val Thr His Pro
 85 90 95
 Gly Tyr Leu Gly Ala Ser Thr Ser His Glu His Asp Leu Arg Leu Leu
 100 105 110
 Arg Leu Arg Leu Pro Val Arg Val Thr Ser Ser Val Gln Pro Leu Pro
 115 120 125
 Leu Pro Asn Asp Cys Ala Thr Ala Gly Thr Glu Cys His Val Ser Gly
 130 135 140
 Trp Gly Ile Thr Asn His Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln
 145 150 155 160
 Cys Leu Asn Leu Ser Ile Val Ser His Ala Thr Cys His Gly Val Tyr
 165 170 175

Pro Gly Arg Ile Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly
 180 185 190
 Gln Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly
 195 200 205
 Val Leu Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln
 210 215 220
 Asp Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Ser Ser Thr Leu Val
 225 230 235 240
 Gly Leu Gly Thr Ser Trp Asn Phe Asn Ser Cys Gln Pro Phe
 245 250

<210> 105
 <211> 404
 <212> PRT
 <213> Homo sapiens

<400> 105
 Met Ile Trp Lys Arg Ser Ala Val Leu Arg Phe Tyr Ser Val Cys Gly
 1 5 10 15
 Leu Leu Leu Gln Ala Ala Ala Ser Lys Asn Lys Val Lys Gly Ser Gln
 20 25 30
 Gly Gln Phe Pro Leu Thr Gln Asn Val Thr Val Val Glu Gly Gly Thr
 35 40 45
 Ala Ile Leu Thr Cys Arg Val Asp Gln Asn Asp Asn Thr Ser Leu Gln
 50 55 60
 Trp Ser Asn Pro Ala Gln Gln Thr Leu Tyr Phe Asp Asp Lys Lys Ala
 65 70 75 80
 Leu Arg Asp Asn Arg Ile Glu Leu Val Arg Ala Ser Trp His Glu Leu
 85 90 95
 Ser Ile Ser Val Ser Asp Val Ser Leu Ser Asp Glu Gly Gln Tyr Thr
 100 105 110
 Cys Ser Leu Phe Thr Met Pro Val Lys Thr Ser Lys Ala Tyr Leu Thr
 115 120 125
 Val Leu Gly Val Pro Glu Lys Pro Gln Ile Ser Gly Phe Ser Ser Pro
 130 135 140
 Val Met Glu Gly Asp Leu Met Gln Leu Thr Cys Lys Thr Ser Gly Ser
 145 150 155 160
 Lys Pro Ala Ala Asp Ile Arg Trp Phe Lys Asn Asp Lys Glu Ile Lys
 165 170 175
 Asp Val Lys Tyr Leu Lys Glu Glu Asp Ala Asn Arg Lys Thr Phe Thr
 180 185 190
 Val Ser Ser Thr Leu Asp Phe Arg Val Asp Arg Ser Asp Asp Gly Val
 195 200 205
 Ala Val Ile Cys Arg Val Asp His Glu Ser Leu Asn Ala Thr Pro Gln
 210 215 220
 Val Ala Met Gln Val Leu Glu Ile His Tyr Thr Pro Ser Val Lys Ile
 225 230 235 240
 Ile Pro Ser Thr Pro Phe Pro Gln Glu Gly Gln Pro Leu Ile Leu Thr
 245 250 255
 Cys Glu Ser Lys Gly Lys Pro Leu Pro Glu Pro Val Leu Trp Thr Lys
 260 265 270
 Asp Gly Gly Glu Leu Pro Asp Pro Asp Arg Met Val Val Ser Gly Arg
 275 280 285
 Glu Leu Asn Ile Leu Phe Leu Asn Lys Thr Asp Asn Gly Thr Tyr Arg
 290 295 300
 Cys Glu Ala Thr Asn Thr Ile Gly Gln Ser Ser Ala Glu Tyr Val Leu
 305 310 315 320
 Ile Val His Asp Pro Asn Ala Leu Ala Gly Gln Asn Gly Pro Asp His

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          325          330          335
Ala Leu Ile Gly Gly Ile Val Ala Val Val Val Phe Val Thr Leu Cys
          340          345          350
Ser Ile Phe Leu Leu Gly Arg Tyr Leu Ala Arg His Lys Gly Thr Tyr
          355          360          365
Leu Thr Asn Glu Ala Lys Gly Ala Glu Asp Ala Pro Asp Ala Asp Thr
          370          375          380
Ala Ile Ile Asn Ala Glu Gly Ser Gln Val Asn Ala Glu Glu Lys Lys
          385          390          395          400
Glu Tyr Phe Ile

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<210> 106
<211> 1600
<212> PRT
<213> Homo sapiens

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          <400> 106
Met Thr Leu Glu Gly Leu Tyr Leu Ala Arg Gly Pro Leu Ala Arg Leu
  1          5          10          15
Leu Leu Ala Trp Ser Ala Leu Leu Cys Met Ala Gly Gly Gln Gly Arg
          20          25          30
Trp Asp Gly Ala Leu Glu Ala Ala Gly Pro Gly Arg Val Arg Arg Arg
          35          40          45
Gly Ser Pro Gly Ile Leu Gln Gly Cys Val Val Pro Gly Met Leu Gly
          50          55          60
Asp Pro Phe Gly Val Asp Trp Ala Val Leu Gly Pro Ala Glu Tyr Pro
          65          70          75          80
Gly Gly Cys Pro His Gly Gln Gly Leu Thr Arg Pro Ile Ser Leu Ser
          85          90          95
Pro Lys Ala Glu Cys Val Arg Leu Pro Val Pro Cys Leu Leu Leu Ser
          100          105          110
Arg Leu Glu Asp Ile Pro Trp Gln Glu Pro Val Cys Arg Thr Arg Ala
          115          120          125
Cys Gly Glu Gly Phe Cys Ser Gln Pro Asn Leu Cys Thr Cys Ala Asp
          130          135          140
Gly Thr Leu Ala Pro Ser Cys Gly Val Ser Arg Gly Ser Gly Cys Ser
          145          150          155          160
Val Ser Cys Met Asn Gly Gly Thr Cys Arg Gly Ala Ser Cys Leu Cys
          165          170          175
Gln Lys Gly Tyr Thr Gly Thr Val Cys Gly Gln Pro Ile Cys Asp Arg
          180          185          190
Gly Cys His Asn Gly Gly Arg Cys Ile Gly Pro Asn Arg Cys Ala Cys
          195          200          205
Val Tyr Gly Phe Met Gly Pro Gln Cys Glu Arg Asp Tyr Arg Thr Gly
          210          215          220
Pro Cys Phe Gly Gln Val Gly Pro Glu Gly Cys Gln His Gln Leu Thr
          225          230          235          240
Gly Leu Val Cys Thr Lys Ala Leu Cys Cys Ala Thr Val Gly Arg Ala
          245          250          255
Trp Gly Leu Pro Cys Glu Leu Cys Pro Ala Gln Pro His Pro Cys Arg
          260          265          270
Arg Gly Phe Ile Pro Asn Ile His Thr Gly Ala Cys Gln Asp Val Asp
          275          280          285
Glu Cys Gln Ala Val Pro Gly Leu Cys Gln Gly Gly Ser Cys Val Asn
          290          295          300
Met Val Gly Ser Phe His Cys Arg Cys Pro Val Gly His Arg Leu Ser
          305          310          315          320

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Asp Ser Ser Ala Ala Cys Glu Asp Tyr Arg Ala Gly Ala Cys Phe Ser
          325                      330                      335
Val Leu Phe Gly Gly Arg Cys Ala Gly Asp Leu Ala Gly His Tyr Thr
          340                      345                      350
Arg Arg Gln Cys Cys Cys Asp Arg Gly Gln Val Leu Gly Ser Val Ala
          355                      360                      365
Arg Ser Leu Ser Cys Val Leu Leu Gly Ala Pro Val Asn Glu Phe Gln
          370                      375                      380
Gln Leu Cys Ala Gln Arg Leu Pro Leu Leu Pro Gly His Pro Gly Leu
          385                      390                      395                      400
Phe Pro Gly Leu Leu Gly Phe Gly Ser Asn Gly Met Gly Pro Pro Leu
          405                      410                      415
Gly Pro Ala Arg Leu Asn Pro His Gly Ser Asp Ala Arg Gly Ile Pro
          420                      425                      430
Ser Leu Gly Pro Gly Asn Ser Asn Ile Gly Thr Ala Thr Leu Asn Gln
          435                      440                      445
Thr Ile Asp Ile Cys Arg His Phe Thr Asn Leu Cys Leu Asn Gly Arg
          450                      455                      460
Cys Leu Pro Thr Pro Ser Ser Tyr Arg Cys Glu Cys Asn Val Gly Tyr
          465                      470                      475                      480
Thr Gln Asp Val Arg Gly Glu Cys Ile Asp Val Asp Glu Cys Thr Ser
          485                      490                      495
Ser Pro Cys His His Gly Asp Cys Val Asn Ile Pro Gly Thr Tyr His
          500                      505                      510
Cys Arg Cys Tyr Pro Gly Phe Gln Ala Thr Pro Thr Arg Gln Ala Cys
          515                      520                      525
Val Asp Val Asp Glu Cys Ile Val Ser Gly Gly Leu Cys His Leu Gly
          530                      535                      540
Arg Cys Val Asn Thr Glu Gly Ser Phe Gln Cys Val Cys Asn Ala Gly
          545                      550                      555                      560
Phe Glu Leu Ser Pro Asp Gly Lys Asn Cys Val Ala Ala Ala Pro Gly
          565                      570                      575
Arg Gln Thr His Leu Arg Leu Gly Glu Ala Glu Gly Phe Lys Asp Asn
          580                      585                      590
Ser Thr Val Gln Glu Pro Tyr Pro His Ile Thr Asp Pro Gly Arg Pro
          595                      600                      605
Ser Gly Val Thr Leu Ala Ser Ala Leu Arg Cys Leu Arg Pro Cys Leu
          610                      615                      620
Ser Ser Asp Trp Ser Arg Trp Glu His Ser Pro Ile Trp Ser Pro Leu
          625                      630                      635                      640
Leu Pro Glu Met Leu Trp Leu Cys Ser Ser Val His Thr Pro Thr Leu
          645                      650                      655
Pro Gly Arg Pro Glu Pro Leu Gly Arg Ala Val Gly Trp Cys Thr Gly
          660                      665                      670
Glu Ala Gln Ile Ser Pro Gly Leu Ser Gly His Pro Gly Tyr Pro Glu
          675                      680                      685
Ser Gly Ala Leu Leu Glu Gly Gln Ser Arg Gly Ser Pro Glu Ala Arg
          690                      695                      700
Ala Gly Ala Asn Arg Gly Asp His Asn Glu Cys Ala Thr Ser Thr Met
          705                      710                      715                      720
Cys Val Asn Gly Val Cys Leu Asn Glu Asp Trp Gln Leu Leu Leu Pro
          725                      730                      735
Leu Gln Thr Arg Ala Ser Cys Trp Arg Leu Ala Ala Ile Thr Ala Leu
          740                      745                      750
Asp Ala Arg His Leu Arg Glu Arg His Cys Thr Asn Thr Glu Gly Ser
          755                      760                      765
Phe Arg Cys Gln Cys Leu Gly Gly Leu Ala Val Gly Thr Asp Gly Arg
          770                      775                      780
Val Cys Val Asp Thr His Val Arg Ser Thr Cys Tyr Gly Ala Ile Glu
          785                      790                      795                      800
Lys Gly Ser Cys Ala Arg Pro Phe Pro Gly Thr Val Thr Lys Ser Glu

```

				805					810					815		
Cys	Cys	Cys	Ala	Asn	Pro	Asp	His	Gly	Phe	Gly	Glu	Pro	Cys	Gln	Leu	
			820					825					830			
Cys	Pro	Ala	Lys	Asp	Ser	Ala	Glu	Phe	Gln	Ala	Leu	Cys	Ser	Ser	Gly	
		835					840					845				
Leu	Gly	Ile	Thr	Thr	Asp	Gly	Arg	Asp	Ile	Asn	Glu	Cys	Ala	Leu	Asp	
	850					855					860					
Pro	Glu	Val	Cys	Ala	Asn	Gly	Val	Cys	Glu	Asn	Leu	Arg	Gly	Ser	Tyr	
865					870					875					880	
Arg	Cys	Val	Cys	Asn	Leu	Gly	Tyr	Glu	Ala	Gly	Ala	Ser	Gly	Lys	Asp	
			885						890					895		
Cys	Thr	Asp	Val	Asp	Glu	Cys	Ala	Leu	Asn	Ser	Leu	Leu	Cys	Asp	Asn	
		900						905					910			
Gly	Trp	Cys	Gln	Asn	Ser	Pro	Gly	Ser	Tyr	Ser	Cys	Ser	Cys	Pro	Pro	
	915						920					925				
Gly	Phe	His	Phe	Trp	Gln	Asp	Thr	Glu	Ile	Cys	Lys	Asp	Val	Asp	Glu	
	930					935					940					
Cys	Leu	Ser	Ser	Pro	Cys	Val	Ser	Gly	Val	Cys	Arg	Asn	Leu	Ala	Gly	
945					950					955					960	
Ser	Tyr	Thr	Cys	Lys	Cys	Gly	Pro	Gly	Ser	Arg	Leu	Asp	Pro	Ser	Gly	
			965						970					975		
Thr	Phe	Cys	Leu	Asp	Ser	Thr	Lys	Gly	Thr	Cys	Trp	Leu	Lys	Ile	Gln	
		980						985					990			
Glu	Ser	Arg	Cys	Glu	Val	Asn	Leu	Gln	Gly	Ala	Ser	Leu	Arg	Ser	Glu	
	995					1000						1005				
Cys	Cys	Ala	Thr	Leu	Gly	Ala	Ala	Trp	Gly	Ser	Pro	Cys	Glu	Arg	Cys	
	1010					1015					1020					
Glu	Ile	Gly	Ser	Ile	Leu	Leu	Glu	Ala	Ser	Gln	Ala	Pro	Met	Gly	Lys	
1025				1030						1035				1040		
Ala	Leu	His	Gly	Ala	Gly	Pro	Pro	Leu	Gly	Trp	His	Glu	Lys	Met	Thr	
		1045						1050					1055			
Pro	Leu	Phe	Thr	Leu	Val	Leu	Pro	Val	Ala	Asp	Ser	Thr	Pro	Glu	Val	
		1060						1065				1070				
Thr	Val	Arg	Asn	Ser	Arg	Val	Asp	Glu	Cys	Leu	Ser	Ser	Pro	Cys	Val	
	1075					1080						1085				
Ser	Gly	Val	Cys	Arg	Asn	Leu	Ala	Gly	Ser	Tyr	Thr	Cys	Lys	Cys	Gly	
	1090				1095					1100						
Pro	Gly	Ser	Arg	Leu	Asp	Pro	Ser	Gly	Thr	Phe	Cys	Leu	Asp	Ser	Thr	
1105				1110					1115					1120		
Lys	Gly	Thr	Cys	Trp	Leu	Lys	Ile	Gln	Glu	Ser	Arg	Cys	Glu	Val	Asn	
			1125					1								

Lys Asp Val Asn Glu Cys Lys Val Phe Pro Gly Leu Cys Thr His Gly
 1300 1305 1310
 Thr Cys Arg Asn Thr Val Gly Ser Phe His Cys Ala Cys Ala Gly Gly
 1315 1320 1325
 Phe Ala Leu Asp Ala Gln Glu Arg Asn Cys Thr Asp Ile Asp Glu Cys
 1330 1335 1340
 Arg Ile Ser Pro Asp Leu Cys Gly Gln Gly Thr Cys Val Asn Thr Pro
 1345 1350 1355 1360
 Gly Ser Phe Glu Cys Glu Cys Phe Pro Gly Tyr Glu Ser Gly Phe Met
 1365 1370 1375
 Leu Met Lys Asn Cys Met Asp Val Asp Glu Cys Ala Arg Asp Pro Leu
 1380 1385 1390
 Leu Cys Arg Gly Gly Thr Cys Thr Asn Thr Asp Gly Ser Tyr Lys Cys
 1395 1400 1405
 Gln Cys Pro Pro Gly His Glu Leu Thr Ala Lys Gly Thr Ala Cys Glu
 1410 1415 1420
 Asp Ile Asp Glu Cys Ser Leu Ser Asp Gly Leu Cys Pro His Gly Gln
 1425 1430 1435 1440
 Cys Val Asn Val Ile Gly Ala Phe Gln Cys Ser Cys His Ala Gly Phe
 1445 1450 1455
 Gln Ser Thr Pro Asp Arg Gln Gly Cys Val Asp Ile Asn Glu Cys Arg
 1460 1465 1470
 Val Gln Asn Gly Gly Cys Asp Val His Cys Ile Asn Thr Glu Gly Ser
 1475 1480 1485
 Tyr Arg Cys Ser Cys Gly Gln Gly Tyr Ser Leu Met Pro Asp Gly Arg
 1490 1495 1500
 Ala Cys Ala Asp Val Asp Glu Cys Glu Glu Asn Pro Arg Val Cys Asp
 1505 1510 1515 1520
 Gln Gly His Cys Thr Asn Met Pro Gly Gly His Arg Cys Leu Cys Tyr
 1525 1530 1535
 Asp Gly Phe Met Ala Thr Pro Asp Met Arg Thr Cys Val Asp Val Ala
 1540 1545 1550
 Leu Leu Pro Pro Ala Leu Tyr Pro Gly Pro Gly His Leu Pro His Cys
 1555 1560 1565
 Leu Pro Gly Thr Gly Gln Ala Leu Gln Val Ser Pro Gly Leu Asp Ala
 1570 1575 1580
 Val Leu Trp Gly Thr Glu Pro Ala Pro Gln Leu Gly Ile Pro Gly Arg
 1585 1590 1595 1600

<210> 107

<211> 180

<212> PRT

<213> Homo sapiens

<400> 107

Met Asp Ser Tyr Gly Thr Ser Asn Asn Cys Trp Leu Ser Leu Ala Ser
 1 5 10 15
 Gly Ala Ile Trp Ala Phe Val Ala Pro Ala Leu Phe Val Ile Val Val
 20 25 30
 Asn Ile Gly Ile Leu Ile Ala Val Thr Arg Val Ile Ser Gln Ile Ser
 35 40 45
 Ala Asp Asn Tyr Lys Ile His Gly Asp Pro Ser Ala Phe Lys Leu Thr
 50 55 60
 Ala Lys Ala Val Ala Val Leu Leu Pro Ile Leu Gly Thr Ser Trp Val
 65 70 75 80
 Phe Gly Val Leu Ala Val Asn Gly Cys Ala Val Val Phe Gln Tyr Met

				85					90				95				
Phe	Ala	Thr	Leu	Asn	Ser	Leu	Gln	Gly	Leu	Phe	Ile	Phe	Leu	Phe	His		
			100					105					110				
Cys	Leu	Leu	Asn	Ser	Glu	Val	Arg	Ala	Ala	Phe	Lys	His	Lys	Thr	Lys		
		115					120					125					
Val	Trp	Ser	Leu	Thr	Ser	Ser	Ser	Ala	Arg	Thr	Ser	Asn	Ala	Lys	Pro		
	130				135						140						
Phe	His	Ser	Asp	Leu	Met	Asn	Gly	Thr	Arg	Pro	Gly	Met	Ala	Ser	Thr		
145				150						155					160		
Lys	Leu	Ser	Pro	Trp	Asp	Lys	Ser	Ser	His	Ser	Ala	His	Arg	Val	Asp		
				165					170					175			
Leu	Ser	Ala	Val														
			180														

<210> 108
 <211> 374
 <212> PRT
 <213> Homo sapiens

<400> 108

Met	Met	Pro	Gly	Thr	Ala	Leu	Glu	Gly	Val	Leu	Leu	Ala	Val	Leu	Leu		
1				5					10					15			
Val	Gly	Leu	Gln	Thr	Ala	Thr	Gly	Arg	Leu	Leu	Ser	Gly	Gln	Pro	Val		
			20				25						30				
Cys	Arg	Gly	Gly	Thr	Gln	Arg	Pro	Cys	Tyr	Lys	Val	Ile	Tyr	Phe	His		
	35					40					45						
Asp	Thr	Ser	Arg	Arg	Leu	Asn	Phe	Glu	Glu	Ala	Lys	Glu	Ala	Cys	Arg		
	50				55					60							
Arg	Asp	Gly	Gly	Gln	Leu	Val	Ser	Ile	Glu	Ser	Glu	Asp	Glu	Gln	Lys		
65				70					75					80			
Leu	Ile	Glu	Lys	Phe	Ile	Glu	Asn	Leu	Leu	Pro	Ser	Asp	Gly	Asp	Phe		
			85					90					95				
Trp	Ile	Gly	Leu	Arg	Arg	Arg	Glu	Glu	Lys	Gln	Ser	Asn	Ser	Thr	Ala		
		100					105						110				
Cys	Gln	Asp	Leu	Tyr	Ala	Trp	Thr	Asp	Gly	Ser	Ile	Ser	Gln	Phe	Arg		
	115					120						125					
Asn	Trp	Tyr	Val	Asp	Glu	Pro	Ser	Cys	Gly	Ser	Glu	Val	Cys	Val	Val		
	130				135					140							
Met	Tyr	His	Gln	Pro	Ser	Ala	Pro	Ala	Gly	Ile	Gly	Gly	Pro	Tyr	Met		
145				150						155					160		
Phe	Gln	Trp	Asn	Asp	Arg	Cys	Asn	Met	Lys	Asn	Asn	Phe	Ile	Cys			
			165					170					175				
Lys	Tyr	Ser	Asp	Glu	Lys	Pro	Ala	Val	Pro	Ser	Arg	Glu	Ala	Glu	Gly		
		180					185					190					
Glu	Glu	Thr	Glu	Leu	Thr	Thr	Pro	Val	Leu	Pro	Glu	Glu	Thr	Gln	Glu		
	195						200					205					
Glu	Asp	Ala	Lys	Lys	Thr	Phe	Lys	Glu	Ser	Arg	Glu	Ala	Ala	Leu	Asn		
	210				215					220							
Leu	Ala	Tyr	Ile	Leu	Ile	Pro	Ser	Ile	Pro	Leu	Leu	Leu	Leu	Leu	Val		
225				230						235					240		
Val	Thr	Thr	Val	Val	Cys	Trp	Val	Trp	Ile	Cys	Arg	Lys	Arg	Lys	Arg		
			245					250						255			
Glu	Gln	Pro	Asp	Pro	Ser	Thr	Lys	Lys	Gln	His	Thr	Ile	Trp	Pro	Ser		
		260					265					270					
Pro	His	Gln	Gly	Asn	Ser	Pro	Asp	Leu	Glu	Val	Tyr	Asn	Val	Ile	Arg		
	275			280								285					
Lys	Gln	Ser	Glu	Ala	Asp	Leu	Ala	Glu	Thr	Arg	Pro	Asp	Leu	Lys	Asn		
	290					295					300						

Ile Ser Phe Arg Val Cys Ser Gly Glu Ala Thr Pro Asp Asp Met Ser
 305 310 315 320
 Cys Asp Tyr Asp Asn Met Ala Val Asn Pro Ser Glu Ser Gly Phe Val
 325 330 335
 Thr Leu Val Ser Val Glu Ser Gly Phe Val Thr Asn Asp Ile Tyr Glu
 340 345 350
 Phe Ser Pro Asp Gln Met Gly Arg Ser Lys Glu Ser Gly Trp Val Glu
 355 360 365
 Asn Glu Ile Tyr Gly Tyr
 370

<210> 109
 <211> 503
 <212> PRT
 <213> Homo sapiens

<400> 109
 Met Tyr Leu Val Ala Gly Asp Arg Gly Leu Ala Gly Cys Gly His Leu
 1 5 10 15
 Leu Val Ser Leu Leu Gly Leu Leu Leu Leu Leu Ala Arg Ser Gly Thr
 20 25 30
 Arg Ala Leu Val Cys Leu Pro Cys Asp Glu Ser Lys Cys Glu Glu Pro
 35 40 45
 Arg Asn Cys Pro Gly Ser Ile Val Gln Gly Val Cys Gly Cys Cys Tyr
 50 55 60
 Thr Cys Ala Ser Gln Arg Asn Glu Ser Cys Gly Gly Thr Phe Gly Ile
 65 70 75 80
 Tyr Gly Thr Cys Asp Arg Gly Leu Arg Cys Val Ile Arg Pro Pro Leu
 85 90 95
 Asn Gly Asp Ser Leu Thr Glu Tyr Glu Ala Gly Val Cys Glu Asp Glu
 100 105 110
 Asn Trp Thr Asp Asp Gln Leu Leu Gly Phe Lys Pro Cys Asn Glu Asn
 115 120 125
 Leu Ile Ala Gly Cys Asn Ile Asn Gly Lys Cys Glu Cys Asn Thr
 130 135 140
 Ile Arg Thr Cys Ser Asn Pro Phe Glu Phe Pro Ser Gln Asp Met Cys
 145 150 155 160
 Leu Ser Ala Leu Lys Arg Ile Glu Glu Glu Lys Pro Asp Cys Ser Lys
 165 170 175
 Ala Arg Cys Glu Val Gln Phe Ser Pro Arg Cys Pro Glu Asp Ser Val
 180 185 190
 Leu Ile Glu Gly Tyr Ala Pro Pro Gly Glu Cys Cys Pro Leu Pro Ser
 195 200 205
 Arg Cys Val Cys Asn Pro Ala Gly Cys Leu Arg Lys Val Cys Gln Pro
 210 215 220
 Gly Asn Leu Asn Ile Leu Val Ser Lys Ala Ser Gly Lys Pro Gly Glu
 225 230 235 240
 Cys Cys Asp Leu Tyr Glu Cys Lys Pro Val Phe Gly Val Asp Cys Arg
 245 250 255
 Thr Val Glu Cys Pro Pro Val Gln Gln Thr Ala Arg Cys Pro Pro Asp
 260 265 270
 Ser Tyr Glu Thr Gln Val Arg Leu Thr Ala Asp Gly Cys Cys Pro Leu
 275 280 285
 Pro Pro Arg Cys Glu Cys Leu Ser Gly Leu Cys Gly Phe Pro Val Cys
 290 295 300
 Glu Val Gly Ser Thr Pro Arg Ile Val Ser Arg Gly Asp Gly Thr Pro
 305 310 315 320
 Gly Lys Cys Cys Asp Val Phe Glu Cys Val Asn Asp Thr Lys Pro Ala

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          325          330          335
Cys Val Phe Asn Asn Val Glu Tyr Tyr Asp Gly Asp Met Phe Arg Met
          340          345          350
Asp Asn Cys Arg Phe Cys Arg Cys Gln Gly Gly Val Ala Ile Cys Phe
          355          360          365
Thr Ala Gln Cys Gly Glu Ile Asn Cys Glu Arg Tyr Tyr Val Pro Glu
          370          375          380
Gly Glu Cys Cys Pro Val Cys Glu Asp Pro Val Tyr Pro Phe Asn Asn
          385          390          395          400
Pro Ala Gly Cys Tyr Ala Asn Gly Leu Ile Leu Ala His Gly Asp Arg
          405          410          415
Trp Arg Glu Asp Asp Cys Thr Phe Cys Gln Cys Val Asn Gly Glu Arg
          420          425          430
His Cys Val Ala Thr Val Cys Gly Gln Thr Cys Thr Asn Pro Val Lys
          435          440          445
Val Pro Gly Glu Cys Cys Pro Val Cys Glu Glu Pro Thr Ile Ile Thr
          450          455          460
Val Asp Pro Pro Ala Cys Gly Glu Leu Ser Asn Cys Thr Leu Thr Gly
          465          470          475          480
Lys Asp Cys Ile Asn Gly Phe Lys Arg Asp His Asn Gly Cys Arg Thr
          485          490          495
Cys Gln Cys Ile Asn Ser Glu
          500

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<210> 110
<211> 123
<212> PRT
<213> Homo sapiens

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          <400> 110
Met Trp Leu Pro Pro Ala Leu Leu Leu Leu Ser Leu Ser Gly Cys Phe
  1          5          10          15
Ser Ile Gln Gly Pro Glu Ser Val Arg Ala Pro Glu Gln Gly Ser Leu
          20          25          30
Thr Val Gln Cys His Tyr Lys Gln Gly Trp Glu Thr Tyr Ile Lys Trp
          35          40          45
Trp Cys Arg Gly Val Arg Trp Asp Thr Cys Lys Ile Leu Ile Glu Thr
          50          55          60
Arg Gly Ser Glu Gln Gly Glu Lys Ser Asp Arg Val Ser Ile Lys Asp
          65          70          75          80
Asn Gln Lys Asp Arg Thr Phe Thr Val Thr Met Glu Gly Leu Arg Arg
          85          90          95
Asp Asp Ala Asp Val Tyr Trp Cys Gly Ile Glu Arg Arg Gly Pro Asp
          100          105          110
Leu Gly Thr Gln Val Lys Val Ile Val Asp Pro
          115          120

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<210> 111
<211> 120
<212> PRT
<213> Homo sapiens

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          <400> 111
Met Ser Cys Ile Leu Gly Phe Cys Phe Pro Gly Cys Phe Ser Ile Gln
  1          5          10          15

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Gly Pro Glu Ser Val Arg Ala Pro Glu Gln Gly Ser Leu Thr Val Gln
 20 25 30
 Cys His Tyr Lys Gln Gly Trp Glu Thr Tyr Ile Lys Trp Trp Cys Arg
 35 40 45
 Gly Val Arg Trp Asp Thr Cys Lys Ile Leu Ile Glu Thr Arg Gly Ser
 50 55 60
 Glu Gln Gly Glu Lys Ser Asp Arg Val Ser Ile Lys Asp Asn Gln Lys
 65 70 75 80
 Asp Arg Thr Phe Thr Val Thr Met Glu Gly Leu Arg Arg Asp Asp Ala
 85 90 95
 Asp Val Tyr Trp Cys Gly Ile Glu Arg Arg Gly Pro Asp Leu Gly Thr
 100 105 110
 Gln Val Lys Val Ile Val Asp Pro
 115 120

<210> 112
 <211> 346
 <212> PRT
 <213> Homo sapiens

<400> 112
 Met Glu Arg Lys Phe Met Ser Leu Gln Pro Ser Ile Ser Val Ser Glu
 1 5 10 15
 Met Glu Pro Asn Gly Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys Thr
 20 25 30
 Ile Glu Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile
 35 40 45
 Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu
 50 55 60
 Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu
 65 70 75 80
 Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp
 85 90 95
 Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg
 100 105 110
 Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe
 115 120 125
 Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe
 130 135 140
 Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly
 145 150 155 160
 Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser
 165 170 175
 Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu
 180 185 190
 Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val
 195 200 205
 Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile
 210 215 220
 Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val
 225 230 235 240
 Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe
 245 250 255
 Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr
 260 265 270
 Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val
 275 280 285
 Ile Thr Leu Ala Leu Ala Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu

290		295		300
Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu				
305		310		315
Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val				320
		325		330
Ser Val Trp Leu Arg Lys Glu Thr Arg Val				335
		340		345

<210> 113
 <211> 403
 <212> PRT
 <213> Homo sapiens

<400> 113

Met Glu Thr Tyr Ala Glu Val Gly Lys Glu Gly Lys Pro Ser Cys Ala	
1 5 10 15	
Ser Val Asp Leu Gln Gly Asp Ser Ser Leu Gln Val Glu Ile Ser Asp	
20 25 30	
Ala Val Ser Glu Arg Asp Lys Val Lys Phe Thr Val Gln Thr Lys Ser	
35 40 45	
Cys Leu Pro His Phe Ala Gln Thr Glu Phe Ser Val Val Arg Gln His	
50 55 60	
Glu Glu Phe Ile Trp Leu His Asp Ala Tyr Val Glu Asn Glu Glu Tyr	
65 70 75 80	
Ala Gly Leu Ile Ile Pro Pro Ala Pro Pro Arg Pro Asp Phe Glu Ala	
85 90 95	
Ser Arg Glu Lys Leu Gln Lys Leu Gly Glu Gly Asp Ser Ser Val Thr	
100 105 110	
Arg Glu Glu Phe Ala Lys Met Lys Gln Glu Leu Glu Ala Glu Tyr Leu	
115 120 125	
Ala Ile Phe Lys Lys Thr Val Ala Met His Glu Val Phe Leu Gln Arg	
130 135 140	
Leu Ala Ala His Pro Thr Leu Arg Arg Asp His Asn Phe Phe Val Phe	
145 150 155 160	
Leu Glu Tyr Gly Gln Asp Leu Ser Val Arg Gly Lys Asn Arg Lys Glu	
165 170 175	
Leu Leu Gly Gly Phe Leu Arg Asn Ile Val Lys Ser Ala Asp Glu Ala	
180 185 190	
Leu Ile Thr Gly Met Ser Gly Leu Lys Glu Val Asp Asp Phe Phe Glu	
195 200 205	
His Glu Arg Thr Phe Leu Leu Glu Tyr His Thr Arg Ile Arg Asp Ala	
210 215 220	
Cys Leu Arg Ala Asp Arg Val Met Arg Ala His Lys Cys Leu Ala Asp	
225 230 235 240	
Asp Tyr Ile Pro Ile Ser Ala Ala Leu Ser Ser Leu Gly Thr Gln Glu	
245 250 255	
Val Asn Gln Leu Arg Thr Ser Phe Leu Lys Leu Ala Glu Leu Phe Glu	
260 265 270	
Arg Leu Arg Lys Leu Glu Gly Arg Val Ala Ser Asp Glu Asp Leu Lys	
275 280 285	
Leu Ser Asp Met Leu Arg Tyr Tyr Met Arg Asp Ser Gln Ala Ala Lys	
290 295 300	
Asp Leu Leu Tyr Arg Arg Leu Arg Ala Leu Ala Asp Tyr Glu Asn Ala	
305 310 315 320	
Asn Lys Ala Leu Asp Lys Ala Arg Thr Arg Asn Arg Glu Val Arg Pro	
325 330 335	
Ala Glu Ser His Gln Gln Leu Cys Cys Gln Arg Phe Glu Arg Leu Ser	
340 345 350	

Asp Ser Ala Lys Gln Glu Leu Met Asp Phe Lys Ser Arg Arg Val Ser
 355 360 365
 Ser Phe Arg Lys Asn Leu Ile Glu Leu Ala Glu Leu Glu Leu Lys His
 370 375 380
 Ala Lys Ala Ser Thr Leu Ile Leu Arg Asn Thr Leu Val Ala Leu Lys
 385 390 395 400
 Gly Glu Pro

<210> 114
 <211> 806
 <212> PRT
 <213> Homo sapiens

<400> 114
 Met Ala Val Arg Ala Leu Lys Leu Leu Thr Thr Leu Leu Ala Val Val
 1 5 10 15
 Ala Ala Ala Ser Gln Ala Glu Val Glu Ser Glu Ala Gly Trp Gly Met
 20 25 30
 Val Thr Pro Asp Leu Leu Phe Ala Glu Gly Thr Ala Ala Tyr Ala Arg
 35 40 45
 Gly Asp Trp Pro Gly Val Val Leu Ser Met Glu Arg Ala Leu Arg Ser
 50 55 60
 Arg Ala Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Gln Cys Ala
 65 70 75 80
 Ala Asp Phe Pro Trp Glu Leu Asp Pro Asp Trp Ser Pro Ser Pro Ala
 85 90 95
 Gln Ala Ser Gly Ala Ala Ala Leu Arg Asp Leu Ser Phe Phe Gly Gly
 100 105 110
 Leu Leu Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro Pro Ala
 115 120 125
 Ala His Ser Leu Ser Glu Glu Met Glu Leu Glu Phe Arg Lys Arg Ser
 130 135 140
 Pro Tyr Asn Tyr Leu Gln Val Ala Tyr Phe Lys Val Gln Thr Cys Leu
 145 150 155 160
 Glu Pro Gly Gly Arg Gly Pro Ser Gly Glu Arg Ser Val Ala Gly Asp
 165 170 175
 Leu Arg Ser Leu Gly Asp Arg Gly Ser Val Arg Arg Glu Gly Lys Val
 180 185 190
 Ala Ser Trp Leu Gly Ser Ser Pro Arg Ser Arg Gly Glu Leu Leu Pro
 195 200 205
 Gly Arg Arg Pro Ser Ser Pro Ser Ser His Gly Gln Met Leu Thr Pro
 210 215 220
 Lys Ile Asn Lys Leu Glu Lys Ala Val Ala Ala Ala His Thr Phe Phe
 225 230 235 240
 Val Gly Asn Pro Glu His Met Glu Met Gln Gln Asn Leu Asp Tyr Tyr
 245 250 255
 Gln Thr Met Ser Gly Val Lys Glu Ala Asp Phe Lys Asp Leu Glu Thr
 260 265 270
 Gln Pro His Met Gln Glu Phe Arg Leu Gly Val Arg Leu Tyr Ser Glu
 275 280 285
 Glu Gln Pro Gln Glu Ala Val Pro His Leu Glu Ala Ala Leu Gln Glu
 290 295 300
 Tyr Phe Val Ala Tyr Glu Glu Cys Arg Ala Leu Cys Glu Gly Pro Tyr
 305 310 315 320
 Asp Tyr Asp Gly Tyr Asn Tyr Leu Glu Tyr Asn Ala Asp Leu Phe Gln
 325 330 335
 Ala Ile Thr Asp His Tyr Ile Gln Val Leu Asn Cys Lys Gln Asn Cys

			340					345				350			
Val	Thr	Glu	Leu	Ala	Ser	His	Pro	Ser	Arg	Glu	Lys	Pro	Phe	Glu	Asp
		355					360					365			
Phe	Leu	Pro	Ser	His	Tyr	Asn	Tyr	Leu	Gln	Phe	Ala	Tyr	Tyr	Asn	Ile
	370					375						380			
Gly	Asn	Tyr	Thr	Gln	Ala	Val	Glu	Cys	Ala	Lys	Thr	Tyr	Leu	Leu	Phe
385					390					395				400	
Phe	Pro	Asn	Asp	Glu	Val	Met	Asn	Gln	Asn	Leu	Ala	Tyr	Tyr	Ala	Ala
				405					410					415	
Met	Leu	Gly	Glu	Glu	His	Thr	Arg	Ser	Ile	Gly	Pro	Arg	Glu	Ser	Ala
			420					425					430		
Lys	Glu	Tyr	Arg	Gln	Arg	Ser	Leu	Leu	Glu	Lys	Glu	Leu	Leu	Phe	Phe
		435					440					445			
Ala	Tyr	Asp	Val	Phe	Gly	Ile	Pro	Phe	Val	Asp	Pro	Asp	Ser	Trp	Thr
	450					455					460				
Pro	Glu	Glu	Val	Ile	Pro	Lys	Arg	Leu	Gln	Glu	Lys	Gln	Lys	Ser	Glu
465					470					475				480	
Arg	Glu	Thr	Ala	Val	Arg	Ile	Ser	Gln	Glu	Ile	Gly	Asn	Leu	Met	Lys
				485					490					495	
Glu	Ile	Glu	Thr	Leu	Val	Glu	Glu	Lys	Thr	Lys	Glu	Ser	Leu	Asp	Val
			500					505					510		
Ser	Arg	Leu	Thr	Arg	Glu	Gly	Gly	Pro	Leu	Leu	Tyr	Glu	Gly	Ile	Ser
	515						520					525			
Leu	Thr	Met	Asn	Ser	Lys	Leu	Leu	Asn	Gly	Ser	Gln	Arg	Val	Val	Met
	530					535					540				
Asp	Gly	Val	Ile	Ser	Asp	His	Glu	Cys	Gln	Glu	Leu	Gln	Arg	Leu	Thr
545					550					555				560	
Asn	Val	Ala	Ala	Thr	Ser	Gly	Asp	Gly	Tyr	Arg	Gly	Gln	Thr	Ser	Pro
				565					570					575	
His	Thr	Pro	Asn	Glu	Lys	Phe	Tyr	Gly	Val	Thr	Val	Phe	Lys	Ala	Leu
			580					585					590		
Lys	Leu	Gly	Gln	Glu	Gly	Lys	Val	Pro	Leu	Gln	Ser	Ala	His	Leu	Tyr
	595						600					605			
Tyr	Asn	Val	Thr	Glu	Lys	Val	Arg	Arg	Ile	Met	Glu	Ser	Tyr	Phe	Arg
	610					615					620				
Leu	Asp	Thr	Pro	Leu	Tyr	Phe	Ser	Tyr	Ser	His	Leu	Val	Cys	Arg	Thr
625					630					635				640	
Ala	Ile	Glu	Glu	Val	Gln	Ala	Glu	Arg	Lys	Asp	Asp	Ser	His	Pro	Val
				645					650					655	
His	Val	Asp	Asn	Cys	Ile	Leu	Asn	Ala	Glu	Thr	Leu	Val	Cys	Val	Lys
			660					665					670		
Glu	Pro	Pro	Ala	Tyr	Thr	Phe	Arg	Asp	Tyr	Ser	Ala	Ile	Leu	Tyr	Leu
	675						680					685			
Asn	Gly	Asp	Phe	Asp	Gly	Gly	Asn	Phe	Tyr	Phe	Thr	Glu	Leu	Asp	Ala
	690				695						700				
Lys	Thr	Val	Thr	Ala	Glu	Val	Gln	Pro	Gln	Cys	Gly	Arg	Ala	Val	Gly
705					710					715				720	
Phe	Ser	Ser	Gly	Thr	Glu	Asn	Pro	His	Gly	Val	Lys	Ala	Val	Thr	Arg
				725					730					735	
Gly	Gln	Arg	Cys	Ala	Ile	Ala	Leu	Trp	Phe	Thr	Leu	Asp	Pro	Arg	His
			740					745					750		
Ser	Glu	Arg	Asp	Arg	Val	Gln	Ala	Asp	Asp	Leu	Val	Lys	Met	Leu	Phe
	755						760					765			
Ser	Pro	Glu	Glu	Met	Asp	Leu	Ser	Gln	Glu	Gln	Pro	Leu	Asp	Ala	Gln
	770					775					780				
Gln	Gly	Pro	Pro	Glu	Pro	Ala	Gln	Glu	Ser	Leu	Ser	Gly	Ser	Glu	Ser
785					790					795				800	
Lys	Pro	Lys	Asp	Glu	Leu										
					805										

<210> 115
 <211> 906
 <212> PRT
 <213> Homo sapiens

<400> 115
 Met Ala Leu Glu Gln Ala Leu Gln Ala Ala Arg Gln Gly Glu Leu Asp
 1 5 10 15
 Val Leu Arg Ser Leu His Ala Ala Gly Leu Leu Gly Pro Ser Leu Arg
 20 25 30
 Asp Pro Leu Asp Ala Leu Pro Val His His Ala Ala Arg Ala Gly Lys
 35 40 45
 Leu His Cys Leu Arg Phe Leu Val Glu Glu Ala Ala Leu Pro Ala Ala
 50 55 60
 Ala Arg Ala Arg Asn Gly Ala Thr Pro Ala His Asp Ala Ser Ala Thr
 65 70 75 80
 Gly His Leu Ala Cys Leu Gln Trp Leu Leu Ser Gln Gly Gly Cys Arg
 85 90 95
 Val Gln Ala Phe Pro Glu Ser Leu Gly Val Arg Ala Val Ala Leu Gly
 100 105 110
 Leu Val Pro Val Ser Cys Arg Asp Asn Gln Asp Lys Asp Asn Ser Gly
 115 120 125
 Ala Thr Val Leu His Leu Ala Ala Arg Phe Gly His Pro Glu Val Val
 130 135 140
 Asn Trp Leu Leu His His Gly Gly Gly Asp Pro Thr Ala Ala Thr Asp
 145 150 155 160
 Met Gly Ala Leu Pro Ile His Tyr Ala Ala Ala Lys Gly Asp Phe Pro
 165 170 175
 Ser Leu Arg Leu Leu Val Glu His Tyr Pro Glu Gly Val Asn Ala Gln
 180 185 190
 Thr Lys Asn Gly Ala Thr Pro Leu Tyr Leu Ala Cys Gln Gly His
 195 200 205
 Leu Glu Val Thr Gln Tyr Leu Val Gln Glu Cys Gly Ala Asp Pro His
 210 215 220
 Ala Arg Ala His Asp Gly Met Thr Pro Leu His Ala Ala Ala Gln Met
 225 230 235 240
 Gly His Ser Pro Val Ile Val Trp Leu Val Ser Cys Thr Asp Val Ser
 245 250 255
 Leu Ser Glu Gln Asp Lys Asp Gly Ala Thr Ala Met His Phe Ala Ala
 260 265 270
 Ser Arg Gly His Thr Lys Val Leu Ser Trp Leu Leu Leu His Gly Gly
 275 280 285
 Glu Ile Ser Ala Asp Leu Trp Gly Gly Thr Pro Leu His Asp Ala Ala
 290 295 300
 Glu Asn Gly Glu Leu Glu Cys Cys Gln Ile Leu Val Val Asn Gly Ala
 305 310 315 320
 Glu Leu Asp Val Arg Asp Arg Asp Gly Tyr Thr Ala Ala Asp Leu Ser
 325 330 335
 Asp Phe Asn Gly His Ser His Cys Thr Arg Tyr Leu Arg Thr Val Glu
 340 345 350
 Asn Leu His Arg Gly Met Val Leu Ala Leu Gly Ala Ala Glu His Ser
 355 360 365
 Lys Ala Gln Arg Pro Glu Ala Ala Gly Gly Pro Glu Asp Glu Leu Pro
 370 375 380
 Pro Ala Lys Glu Ser Leu Glu Glu Asn Glu Trp Pro Ser Arg Gly Gln
 385 390 395 400
 Gly Leu Val Pro Ser Ala Pro Thr Ala Val Gly Gln Ser Val Glu His
 405 410 415
 Arg Val Leu Ser Arg Asp Pro Ser Ala Glu Leu Glu Ala Lys Gln Pro

			420					425				430			
Asp	Ser	Gly	Met	Ser	Ser	Pro	Asn	Thr	Thr	Val	Ser	Val	Gln	Pro	Leu
		435					440					445			
Asn	Phe	Asp	Leu	Ser	Ser	Pro	Thr	Ser	Thr	Leu	Ser	Asn	Tyr	Asp	Ser
		450				455					460				
Cys	Ser	Ser	Ser	His	Ser	Ser	Ile	Lys	Gly	Gln	His	Pro	Pro	Cys	Gly
465					470					475				480	
Leu	Ser	Ser	Ala	Arg	Ala	Ala	Asp	Ile	Gln	Ser	Tyr	Met	Asp	Met	Leu
			485						490				495		
Asn	Pro	Glu	Leu	Gly	Leu	Pro	Arg	Gly	Thr	Ile	Gly	Lys	Pro	Thr	Pro
		500						505					510		
Pro	Pro	Pro	Pro	Pro	Ser	Phe	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Gly	Thr
		515					520					525			
Gln	Leu	Pro	Pro	Pro	Pro	Pro	Gly	Tyr	Pro	Ala	Pro	Lys	Pro	Pro	Val
		530				535					540				
Gly	Pro	Gln	Ala	Ala	Asp	Ile	Tyr	Met	Gln	Thr	Lys	Asn	Lys	Leu	Arg
545					550				555					560	
His	Val	Glu	Thr	Glu	Ala	Leu	Lys	Lys	Glu	Leu	Ser	Ser	Cys	Asp	Gly
			565						570					575	
His	Asp	Gly	Leu	Arg	Arg	Gln	Asp	Ser	Ser	Arg	Lys	Pro	Arg	Ala	Phe
		580						585					590		
Ser	Lys	Gln	Pro	Ser	Thr	Gly	Asp	Tyr	Tyr	Arg	Gln	Leu	Gly	Arg	Cys
		595					600					605			
Pro	Gly	Glu	Thr	Leu	Ala	Ala	Arg	Pro	Gly	Met	Ala	His	Ser	Glu	Glu
		610				615					620				
Ala	Ala	Leu	Leu	Pro	Gly	Asn	His	Val	Pro	Asn	Gly	Cys	Ala	Ala	Asp
625					630				635					640	
Pro	Lys	Ala	Ser	Arg	Glu	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
			645					650					655		
Pro	Leu	Pro	Glu	Ala	Ala	Ser	Ser	Pro	Pro	Pro	Ala	Pro	Pro	Leu	Pro
		660						665					670		
Leu	Glu	Ser	Ala	Gly	Pro	Gly	Cys	Gly	Gln	Arg	Arg	Ser	Ser	Ser	Ser
		675					680					685			
Thr	Gly	Ser	Thr	Lys	Ser	Phe	Asn	Met	Met	Ser	Pro	Thr	Gly	Asp	Asn
		690				695					700				
Ser	Glu	Leu	Leu	Ala	Glu	Ile	Lys	Ala	Gly	Lys	Ser	Leu	Lys	Pro	Thr
705					710					715				720	
Pro	Gln	Ser	Lys	Gly	Leu	Thr	Thr	Val	Phe	Ser	Gly	Ile	Gly	Gln	Pro
			725					730						735	
Ala	Phe	Gln	Pro	Asp	Ser	Pro	Leu	Pro	Ser	Val	Ser	Pro	Ala	Leu	Ser
		740						745					750		
Pro	Val	Arg	Ser	Pro	Thr	Pro	Pro	Ala	Ala	Gly	Phe	Gln	Pro	Leu	Leu
		755					760					765			
Asn	Gly	Ser	Leu	Val	Pro	Val	Pro	Pro	Thr	Thr	Pro	Ala	Pro	Gly	Val
		770				775					780				
Gln	Leu	Asp	Val	Glu	Ala	Leu	Ile	Pro	Thr	His	Asp	Glu	Gln	Gly	Arg
785					790					795				800	
Pro	Ile	Pro	Glu	Trp	Lys	Arg	Gln	Val	Met	Val	Arg	Lys	Met	Gln	Leu
			805					810					815		
Lys	Met	Gln	Glu	Glu	Glu	Glu	Gln	Arg	Arg	Lys	Glu	Glu	Glu	Glu	Glu
			820					825					830		
Ala	Arg	Leu	Ala	Ser	Met	Pro	Ala	Trp	Arg	Arg	Asp	Leu	Leu	Arg	Lys
		835					840					845			
Lys	Leu	Glu	Glu	Glu	Arg	Glu	Gln	Lys	Arg	Lys	Glu	Glu	Glu	Arg	Gln
		850				855					860				
Lys	Gln	Glu	Glu	Leu	Arg	Arg	Glu	Lys	Glu	Gln	Ser	Glu	Lys	Leu	Arg
865					870					875				880	
Thr	Leu	Gly	Tyr	Asp	Glu	Ser	Lys	Leu	Ala	Pro	Trp	Gln	Arg	Gln	Val
			885						890					895	
Ile	Leu	Lys	Lys	Gly	Asp	Ile	Ala	Lys	Tyr						
			900					905							

<210> 116
 <211> 848
 <212> PRT
 <213> Homo sapiens

<400> 116
 Met Ala Leu Glu Gln Ala Leu Gln Ala Ala Arg Gln Gly Glu Leu Asp
 1 5 10 15
 Val Leu Arg Ser Leu His Ala Ala Gly Leu Leu Gly Pro Ser Leu Arg
 20 25 30
 Asp Pro Leu Asp Ala Leu Pro Val His His Ala Ala Arg Ala Gly Lys
 35 40 45
 Leu His Cys Leu Arg Phe Leu Val Glu Glu Ala Ala Leu Pro Ala Ala
 50 55 60
 Ala Arg Ala Arg Asn Gly Ala Thr Pro Ala His Asp Ala Ser Ala Thr
 65 70 75 80
 Gly His Leu Ala Cys Leu Gln Trp Leu Leu Ser Gln Gly Gly Cys Arg
 85 90 95
 Val Gln Ala Phe Pro Glu Ser Leu Gly Val Arg Ala Val Ala Leu Gly
 100 105 110
 Leu Val Pro Val Ser Cys Arg Asp Asn Gln Asp Lys Asp Asn Ser Gly
 115 120 125
 Ala Thr Val Leu His Leu Ala Ala Arg Phe Gly His Pro Glu Val Val
 130 135 140
 Asn Trp Leu Leu His His Gly Gly Gly Asp Pro Thr Ala Ala Thr Asp
 145 150 155 160
 Met Gly Ala Leu Pro Ile His Tyr Ala Ala Lys Gly Asp Phe Pro
 165 170 175
 Ser Leu Arg Leu Leu Val Glu His Tyr Pro Glu Gly Val Asn Ala Gln
 180 185 190
 Thr Lys Asn Gly Ala Thr Pro Leu Tyr Leu Ala Cys Gln Glu Gly His
 195 200 205
 Leu Glu Val Thr Gln Tyr Leu Val Gln Glu Cys Gly Ala Asp Pro His
 210 215 220
 Ala Arg Ala His Asp Gly Met Thr Pro Leu His Ala Ala Ala Gln Met
 225 230 235 240
 Gly His Ser Pro Val Ile Val Trp Leu Val Ser Cys Thr Asp Val Ser
 245 250 255
 Leu Ser Glu Gln Asp Lys Asp Gly Ala Thr Ala Met His Phe Ala Ala
 260 265 270
 Ser Arg Gly His Thr Lys Val Leu Ser Trp Leu Leu Leu His Gly Gly
 275 280 285
 Glu Ile Ser Ala Asp Leu Trp Gly Gly Thr Pro Leu His Asp Ala Ala
 290 295 300
 Glu Asn Gly Glu Leu Glu Cys Cys Gln Ile Leu Val Val Asn Gly Ala
 305 310 315 320
 Glu Leu Asp Val Arg Asp Arg Asp Gly Tyr Thr Ala Ala Asp Leu Ser
 325 330 335
 Asp Phe Asn Gly His Ser His Cys Thr Arg Tyr Leu Arg Thr Val Glu
 340 345 350
 Asn Leu Ser Val Glu His Arg Val Leu Ser Arg Asp Pro Ser Ala Glu
 355 360 365
 Leu Glu Ala Lys Gln Pro Asp Ser Gly Met Ser Ser Pro Asn Thr Thr
 370 375 380
 Val Ser Val Gln Pro Leu Asn Phe Asp Leu Ser Ser Pro Thr Ser Thr
 385 390 395 400
 Leu Ser Asn Tyr Asp Ser Cys Ser Ser Ser His Ser Ser Ile Lys Gly

<210> 117

<211> 588
 <212> PRT
 <213> Homo sapiens

<400> 117
 Met Leu Arg Leu Gln Ala Pro Gly Pro Ala Gly Arg Pro Arg Cys Phe
 1 5 10 15
 Pro Leu Arg Ala Arg Leu Phe Thr Arg Phe Ala Glu Ala Gly Arg
 20 25 30
 Ser Thr Leu Arg Leu Pro Ala His Asp Thr Pro Gly Ala Gly Ala Val
 35 40 45
 Gln Leu Leu Leu Ser Asp Cys Pro Pro Asp Arg Leu Arg Arg Phe Leu
 50 55 60
 Arg Thr Leu Arg Leu Lys Leu Ala Ala Ala Pro Gly Pro Gly Pro Ala
 65 70 75 80
 Ser Ala Arg Ala Gln Leu Leu Gly Pro Arg Pro Arg Asp Phe Val Thr
 85 90 95
 Ile Ser Pro Val Gln Pro Glu Glu Arg Arg Leu Arg Ala Ala Thr Arg
 100 105 110
 Val Pro Asp Thr Thr Leu Val Lys Arg Pro Val Glu Pro Gln Ala Gly
 115 120 125
 Ala Glu Pro Ser Thr Glu Ala Pro Arg Trp Pro Leu Pro Val Lys Arg
 130 135 140
 Leu Ser Leu Pro Ser Thr Lys Pro Gln Leu Ser Glu Glu Gln Ala Ala
 145 150 155 160
 Val Leu Arg Ala Ala Leu Lys Gly Gln Ser Ile Phe Phe Thr Gly Ser
 165 170 175
 Ala Gly Thr Gly Lys Ser Tyr Leu Leu Lys Arg Ile Leu Gly Ser Leu
 180 185 190
 Pro Pro Thr Gly Thr Glu Ala Thr Ala Ser Thr Gly Val Ala Ala Cys
 195 200 205
 His Ile Gly Gly Thr Thr Leu His Ala Phe Ala Gly Ile Gly Ser Gly
 210 215 220
 Gln Ala Pro Leu Ala Gln Cys Val Ala Leu Ala Gln Arg Pro Gly Val
 225 230 235 240
 Arg Gln Gly Trp Leu Asn Cys Gln Arg Leu Val Ile Asp Glu Ile Ser
 245 250 255
 Met Val Glu Ala Asp Leu Phe Asp Lys Leu Glu Ala Val Ala Arg Ala
 260 265 270
 Val Arg Gln Gln Asn Lys Pro Phe Gly Gly Ile Gln Leu Ile Ile Cys
 275 280 285
 Gly Asp Phe Leu Gln Leu Pro Pro Val Thr Lys Gly Ser Gln Pro Pro
 290 295 300
 Arg Phe Cys Phe Gln Ser Lys Ser Trp Lys Arg Gly Val Pro Val Thr
 305 310 315 320
 Leu Glu Leu Thr Lys Gly Gly Arg Gln Ala Asn Gln Thr Phe Phe Phe
 325 330 335
 Leu Leu Gln Ala Val Arg Leu Gly Arg Cys Ser Asp Glu Val Thr Arg
 340 345 350
 Gln Leu Gln Ala Thr Ala Ser His Lys Val Gly Arg Asp Gly Ile Val
 355 360 365
 Ala Thr Arg Leu Cys Thr His Gln Asp Asp Val Ala Leu Thr Asn Glu
 370 375 380
 Arg Arg Leu Gln Glu Leu Pro Gly Lys Val His Arg Phe Glu Ala Met
 385 390 395 400
 Asp Ser Asn Pro Glu Leu Ala Ser Thr Leu Asp Ala Gln Cys Pro Val
 405 410 415
 Ser Gln Leu Leu Gln Leu Lys Leu Gly Ala Gln Val Met Leu Val Lys
 420 425 430
 Asn Leu Ser Val Ser Arg Gly Leu Val Asn Gly Ala Arg Gly Val Val

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      435      440      445
Val Gly Phe Glu Ala Glu Gly Arg Gly Leu Pro Gln Val Arg Phe Leu
      450      455      460
Cys Gly Val Thr Glu Val Ile His Ala Asp Arg Trp Thr Val Gln Ala
465      470      475      480
Thr Gly Gly Gln Leu Ser Arg Gln Gln Leu Pro Leu Gln Leu Ala
      485      490      495
Trp Ala Met Ser Ile His Lys Ser Gln Gly Met Thr Leu Asp Cys Val
      500      505      510
Glu Ile Ser Leu Gly Arg Val Phe Ala Ser Gly Gln Ala Tyr Val Ala
      515      520      525
Leu Ser Arg Ala Arg Ser Leu Gln Gly Leu Arg Val Leu Asp Phe Asp
      530      535      540
Pro Met Ala Val Arg Cys Asp Pro Arg Val Leu His Phe Tyr Ala Thr
545      550      555      560
Leu Arg Arg Gly Arg Ser Leu Ser Leu Glu Ser Pro Asp Asp Asp Glu
      565      570      575
Ala Ala Ser Asp Gln Glu Asn Met Asp Pro Ile Leu
      580      585

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<210> 118
<211> 526
<212> PRT
<213> Homo sapiens

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      <400> 118
Met Leu Arg Leu Gln Ala Pro Gly Pro Ala Gly Arg Pro Arg Cys Phe
 1      5      10      15
Pro Leu Arg Ala Ala Arg Leu Phe Thr Arg Phe Ala Glu Ala Gly Arg
      20      25      30
Ser Thr Leu Arg Leu Pro Ala His Asp Thr Pro Gly Ala Gly Ala Val
      35      40      45
Gln Leu Leu Leu Ser Asp Cys Pro Pro Asp Arg Leu Arg Arg Phe Leu
      50      55      60
Arg Thr Leu Arg Leu Lys Leu Ala Ala Ala Pro Gly Pro Gly Pro Ala
      65      70      75      80
Ser Ala Arg Ala Gln Leu Leu Gly Pro Arg Pro Arg Asp Phe Val Thr
      85      90      95
Ile Ser Pro Val Gln Pro Glu Glu Arg Arg Leu Arg Ala Ala Thr Arg
      100      105      110
Val Pro Asp Thr Thr Leu Val Lys Arg Pro Val Glu Pro Gln Ala Gly
      115      120      125
Ala Glu Pro Ser Thr Glu Ala Pro Arg Trp Pro Leu Pro Val Lys Arg
      130      135      140
Leu Ser Leu Pro Ser Thr Lys Pro Gln Leu Ser Glu Glu Gln Ala Ala
145      150      155      160
Val Leu Arg Ala Ala Leu Lys Gly Gln Ser Ile Phe Phe Thr Gly Ser
      165      170      175
Ala Gly Thr Gly Lys Ser Tyr Leu Leu Lys Arg Ile Leu Gly Ser Leu
      180      185      190
Pro Pro Thr Gly Thr Glu Ala Thr Ala Ser Thr Gly Val Ala Ala Cys
      195      200      205
His Ile Gly Gly Thr Thr Leu His Ala Phe Ala Gly Ile Gly Ser Gly
      210      215      220
Gln Ala Pro Leu Ala Gln Cys Val Ala Leu Ala Gln Arg Pro Gly Val
225      230      235      240
Arg Gln Gly Trp Leu Asn Cys Gln Arg Leu Val Ile Asp Glu Ile Ser
      245      250      255

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Met Val Glu Ala Asp Leu Phe Asp Lys Leu Glu Ala Val Ala Arg Ala
      260      265      270
Val Arg Gln Gln Asn Lys Pro Phe Gly Gly Ile Gln Leu Ile Ile Cys
      275      280      285
Gly Asp Phe Leu Gln Leu Pro Pro Val Thr Lys Gly Ser Gln Pro Pro
      290      295      300
Arg Phe Cys Phe Gln Ser Ser Pro Asn Arg Cys Ser Asp Glu Val Thr
      305      310      315      320
Arg Gln Leu Gln Ala Thr Ala Ser His Lys Val Gly Arg Asp Gly Ile
      325      330      335
Val Ala Thr Arg Leu Cys Thr His Gln Asp Asp Val Ala Leu Thr Asn
      340      345      350
Glu Arg Arg Leu Gln Glu Leu Pro Gly Lys Val His Arg Phe Glu Ala
      355      360      365
Met Asp Ser Asn Pro Glu Leu Ala Ser Thr Leu Asp Ala Gln Cys Pro
      370      375      380
Val Ser Gln Leu Leu Gln Leu Lys Leu Gly Ala Gln Val Met Leu Val
      385      390      395      400
Lys Asn Leu Ser Val Ser Arg Gly Leu Val Asn Gly Ala Arg Gly Val
      405      410      415
Val Val Gly Phe Glu Ala Glu Gly Arg Gly Leu Pro Gln Val Arg Phe
      420      425      430
Leu Cys Gly Val Thr Glu Val Ile His Ala Asp Arg Trp Thr Val Gln
      435      440      445
Ala Thr Gly Gly Gln Leu Leu Ser Arg Gln Gln Leu Pro Leu Gln Leu
      450      455      460
Ala Trp Ala Met Ser Ile His Lys Ser Gln Gly Leu Arg Val Leu Asp
      465      470      475      480
Phe Asp Pro Met Ala Val Arg Cys Asp Pro Arg Val Leu His Phe Tyr
      485      490      495
Ala Thr Leu Arg Arg Gly Arg Ser Leu Ser Leu Glu Ser Pro Asp Asp
      500      505      510
Asp Glu Ala Ala Ser Asp Gln Glu Asn Met Asp Pro Ile Leu
      515      520      525

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<210> 119
<211> 674
<212> PRT
<213> Homo sapiens

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<400> 119
Met Gln Thr Ser Ser Ser Arg Ser Val His Leu Ser Glu Trp Gln Lys
  1      5      10      15
Asn Tyr Phe Ala Ile Thr Ser Gly Ile Cys Thr Gly Pro Lys Ala Asp
      20      25      30
Ala Tyr Arg Ala Gln Ile Leu Arg Ile Gln Tyr Ala Trp Ala Asn Ser
      35      40      45
Glu Ile Ser Gln Val Cys Ala Thr Lys Leu Phe Lys Lys Tyr Ala Glu
      50      55      60
Lys Tyr Ser Ala Ile Ile Asp Ser Asp Asn Val Glu Ser Gly Leu Asn
      65      70      75      80
Asn Tyr Ala Glu Asn Ile Leu Thr Leu Ala Gly Ser Gln Gln Thr Asp
      85      90      95
Ser Asp Lys Trp Gln Ser Gly Leu Ser Ile Asn Asn Val Phe Lys Met
      100      105      110
Ser Ser Val Gln Lys Met Met Gln Ala Gly Lys Lys Phe Lys Asp Ser
      115      120      125
Leu Leu Glu Pro Ala Leu Ala Ser Val Val Ile His Lys Glu Ala Thr

```

130	135	140
Val Phe Asp Leu Pro Lys Phe Ser Val Cys Gly Ser Ser Gln Glu Ser		
145	150	155
Asp Ser Leu Pro Asn Ser Ala His Asp Arg Asp Arg Thr Gln Asp Phe		160
	165	170
Pro Glu Ser Asn Arg Leu Lys Leu Leu Gln Asn Ala Gln Pro Pro Met		175
	180	185
Val Thr Asn Thr Ala Arg Thr Cys Pro Thr Phe Ser Ala Pro Val Gly		190
	195	200
Glu Ser Ala Thr Ala Lys Phe His Val Thr Pro Leu Phe Gly Asn Val		205
	210	215
Lys Lys Glu Asn His Ser Ser Ala Lys Glu Asn Ile Gly Leu Asn Val		220
225	230	235
Phe Leu Ser Asn Gln Ser Cys Phe Pro Ala Ala Cys Glu Asn Pro Gln		240
	245	250
Arg Lys Ser Phe Tyr Gly Ser Gly Thr Ile Asp Ala Leu Ser Asn Pro		255
	260	265
Ile Leu Asn Lys Ala Cys Ser Lys Thr Glu Asp Asn Gly Pro Lys Glu		270
	275	280
Asp Ser Ser Leu Pro Thr Phe Lys Thr Ala Lys Glu Gln Leu Trp Val		285
	290	295
Asp Gln Gln Lys Lys Tyr His Gln Pro Gln Arg Ala Ser Gly Ser Ser		300
305	310	315
Tyr Gly Gly Val Lys Lys Ser Leu Gly Ala Ser Arg Ser Arg Gly Ile		320
	325	330
Leu Gly Lys Phe Val Pro Pro Ile Pro Lys Gln Asp Gly Gly Glu Gln		335
	340	345
Asn Gly Gly Met Gln Cys Lys Pro Tyr Gly Ala Gly Pro Thr Glu Pro		350
	355	360
Ala His Pro Val Asp Glu Arg Leu Lys Asn Leu Glu Pro Lys Met Ile		365
	370	375
Glu Leu Ile Met Asn Glu Ile Met Asp His Gly Pro Pro Val Asn Trp		380
385	390	395
Glu Asp Ile Ala Gly Val Glu Phe Ala Lys Ala Thr Ile Lys Glu Ile		400
	405	410
Val Val Trp Pro Met Leu Arg Pro Asp Ile Phe Thr Gly Leu Arg Gly		415
	420	425
Pro Pro Lys Gly Ile Leu Leu Phe Gly Pro Pro Gly Thr Gly Lys Thr		430
	435	440
Leu Ile Gly Lys Cys Ile Ala Ser Gln Ser Gly Ala Thr Phe Phe Ser		445
	450	455
Ile Ser Ala Ser Ser Leu Thr Ser Lys Trp Val Gly Glu Gly Glu Lys		460
465	470	475
Met Val Arg Ala Leu Phe Ala Val Ala Arg Cys Gln Gln Pro Ala Val		480
	485	490
Ile Phe Ile Asp Glu Ile Asp Ser Leu Leu Ser Gln Arg Gly Asp Gly		495
	500	505
Glu His Glu Ser Ser Arg Arg Ile Lys Thr Glu Phe Leu Val Gln Leu		510
	515	520
Asp Gly Ala Thr Thr Ser Ser Glu Asp Arg Ile Leu Val Val Gly Ala		525
	530	535
Thr Asn Arg Pro Gln Glu Ile Asp Glu Ala Ala Arg Arg Arg Leu Val		540
545	550	555
Lys Arg Leu Tyr Ile Pro Leu Pro Glu Ala Ser Ala Arg Lys Gln Ile		560
	565	570
Val Ile Asn Leu Met Ser Lys Glu Gln Cys Cys Leu Ser Glu Glu Glu		575
	580	585
Ile Glu Gln Ile Val Gln Gln Ser Asp Ala Phe Ser Gly Ala Asp Met		590
	595	600
Thr Gln Leu Cys Arg Glu Ala Ser Leu Gly Pro Ile Arg Ser Leu Gln		605
	610	615
		620

Thr Ala Asp Ile Ala Thr Ile Thr Pro Asp Gln Val Arg Pro Ile Ala
 625 630 635 640
 Tyr Ile Asp Phe Glu Asn Ala Phe Arg Thr Val Arg Pro Ser Val Ser
 645 650 655
 Pro Lys Asp Leu Glu Leu Tyr Glu Asn Trp Asn Lys Thr Phe Gly Cys
 660 665 670
 Gly Lys

<210> 120
 <211> 333
 <212> PRT
 <213> Homo sapiens

<400> 120
 Met Asn Leu Ser Leu Val Leu Ala Ala Phe Cys Leu Gly Ile Ala Ser
 1 5 10 15
 Ala Val Pro Lys Phe Asp Gln Asn Leu Asp Thr Lys Trp Tyr Gln Trp
 20 25 30
 Lys Ala Thr His Arg Arg Leu Tyr Gly Ala Asn Glu Glu Gly Trp Arg
 35 40 45
 Arg Ala Val Trp Glu Lys Asn Met Lys Met Ile Glu Leu His Asn Gly
 50 55 60
 Glu Tyr Ser Gln Gly Lys His Ser Phe Thr Met Ala Met Asn Ala Phe
 65 70 75 80
 Gly Asp Met Thr Asn Glu Glu Phe Arg Gln Val Met Asn Gly Phe Gln
 85 90 95
 Tyr Gln Lys His Arg Lys Gly Lys Gln Phe Gln Glu Arg Leu Leu Leu
 100 105 110
 Glu Ile Pro Thr Ser Val Asp Trp Arg Glu Lys Gly Tyr Met Thr Pro
 115 120 125
 Val Lys Asp Gln Gly Gln Cys Gly Ser Cys Trp Ala Phe Ser Ala Thr
 130 135 140
 Gly Ala Leu Glu Gly Gln Met Phe Trp Lys Thr Gly Lys Leu Ile Ser
 145 150 155 160
 Leu Asn Glu Gln Asn Leu Val Asp Cys Ser Gly Pro Gln Gly Asn Glu
 165 170 175
 Gly Cys Asn Gly Asp Phe Met Asp Asn Pro Phe Arg Tyr Val Gln Glu
 180 185 190
 Asn Gly Gly Leu Asp Ser Glu Glu Ser Tyr Pro Tyr Glu Ala Thr Glu
 195 200 205
 Glu Ser Cys Lys Tyr Asn Pro Lys Tyr Ser Val Ala Asn Asp Thr Gly
 210 215 220
 Phe Val Asp Ile Pro Lys Gln Glu Lys Ala Leu Met Lys Ala Val Ala
 225 230 235 240
 Thr Val Gly Pro Ile Ser Val Ala Ile Asp Ala Gly His Glu Ser Phe
 245 250 255
 Leu Phe Tyr Lys Glu Gly Ile Tyr Phe Glu Pro Asp Cys Ser Ser Glu
 260 265 270
 Asp Met Asp His Gly Val Leu Val Val Gly Tyr Gly Phe Glu Ser Thr
 275 280 285
 Glu Ser Asp Asn Asn Lys Tyr Trp Leu Val Lys Asn Ser Trp Gly Glu
 290 295 300
 Glu Trp Gly Met Gly Gly Tyr Val Lys Met Ala Lys Asp Arg Arg Asn
 305 310 315 320
 His Cys Gly Ile Ala Ser Ala Ala Ser Tyr Pro Thr Val
 325 330

<210> 121
 <211> 794
 <212> PRT
 <213> Homo sapiens

<400> 121
 Met Leu Cys Gly Arg Trp Arg Arg Cys Arg Arg Pro Pro Glu Glu Pro
 1 5 10 15
 Pro Val Ala Ala Gln Val Ala Ala Gln Val Ala Ala Pro Val Ala Leu
 20 25 30
 Pro Ser Pro Pro Thr Pro Ser Asp Gly Gly Thr Lys Arg Pro Gly Leu
 35 40 45
 Arg Ala Leu Lys Lys Met Gly Leu Thr Glu Asp Glu Asp Val Arg Ala
 50 55 60
 Met Leu Arg Gly Ser Arg Leu Arg Lys Ile Arg Ser Arg Thr Trp His
 65 70 75 80
 Lys Glu Arg Leu Tyr Arg Leu Gln Glu Asp Gly Leu Ser Val Trp Phe
 85 90 95
 Gln Arg Arg Ile Pro Arg Ala Pro Ser Gln His Ile Phe Phe Val Gln
 100 105 110
 His Ile Glu Ala Val Arg Glu Gly His Gln Ser Glu Gly Leu Arg Arg
 115 120 125
 Phe Gly Gly Ala Phe Ala Pro Ala Arg Cys Leu Thr Ile Ala Phe Lys
 130 135 140
 Gly Arg Arg Lys Asn Leu Asp Leu Ala Ala Pro Thr Ala Glu Glu Ala
 145 150 155 160
 Gln Arg Trp Val Arg Gly Leu Thr Lys Leu Arg Ala Arg Leu Asp Ala
 165 170 175
 Met Ser Gln Arg Glu Arg Leu Asp His Trp Ile His Ser Tyr Leu His
 180 185 190
 Arg Ala Asp Ser Asn Gln Asp Ser Lys Met Ser Phe Lys Glu Ile Lys
 195 200 205
 Ser Leu Leu Arg Met Val Asn Val Asp Met Asn Asp Met Tyr Ala Tyr
 210 215 220
 Leu Leu Phe Lys Glu Cys Asp His Ser Asn Asn Asp Arg Leu Glu Gly
 225 230 235 240
 Ala Glu Ile Glu Glu Phe Leu Arg Arg Leu Leu Lys Arg Pro Glu Leu
 245 250 255
 Glu Glu Ile Phe His Gln Tyr Ser Gly Glu Asp Arg Val Leu Ser Ala
 260 265 270
 Pro Glu Leu Leu Glu Phe Leu Glu Asp Gln Gly Glu Glu Gly Ala Thr
 275 280 285
 Leu Ala Arg Ala Gln Gln Leu Ile Gln Thr Tyr Glu Leu Asn Glu Thr
 290 295 300
 Ala Lys Gln His Glu Leu Met Thr Leu Asp Gly Phe Met Met Tyr Leu
 305 310 315 320
 Leu Ser Pro Glu Gly Ala Ala Leu Asp Asn Thr His Thr Cys Val Phe
 325 330 335
 Gln Asp Met Asn Gln Pro Leu Ala His Tyr Phe Ile Ser Ser Ser His
 340 345 350
 Asn Thr Tyr Leu Thr Asp Ser Gln Ile Gly Gly Pro Ser Ser Thr Glu
 355 360 365
 Ala Tyr Val Arg Tyr Cys Ser Arg Gly Ala Phe Ala Gln Gly Cys Arg
 370 375 380
 Cys Val Glu Leu Asp Cys Trp Glu Gly Pro Gly Gly Glu Pro Val Ile
 385 390 395 400
 Tyr His Gly His Thr Leu Thr Ser Lys Ile Leu Phe Arg Asp Val Val
 405 410 415

Gln Ala Val Arg Asp His Ala Phe Thr Leu Ser Pro Tyr Pro Val Ile
 420 425 430
 Leu Ser Leu Glu Asn His Cys Gly Leu Glu Gln Gln Ala Ala Met Ala
 435 440 445
 Arg His Leu Cys Thr Ile Leu Gly Asp Met Leu Val Thr Gln Ala Leu
 450 455 460
 Asp Ser Pro Asn Pro Glu Glu Leu Pro Ser Pro Glu Gln Leu Lys Gly
 465 470 475 480
 Arg Val Leu Val Lys Gly Lys Lys Leu Pro Ala Ala Arg Ser Glu Asp
 485 490 495
 Gly Arg Ala Leu Ser Asp Arg Glu Glu Glu Glu Asp Asp Glu Glu
 500 505 510
 Glu Glu Glu Glu Val Glu Ala Ala Ala Gln Arg Arg Leu Ala Lys Gln
 515 520 525
 Ile Ser Pro Glu Leu Ser Ala Leu Ala Val Tyr Cys His Ala Thr Arg
 530 535 540
 Leu Arg Thr Leu His Pro Ala Pro Asn Ala Pro Gln Pro Cys Gln Val
 545 550 555 560
 Ser Ser Leu Ser Glu Arg Lys Ala Lys Lys Leu Ile Arg Glu Ala Gly
 565 570 575
 Asn Ser Phe Val Arg His Asn Ala Arg Gln Leu Thr Arg Val Tyr Pro
 580 585 590
 Leu Gly Leu Arg Met Asn Ser Ala Asn Tyr Ser Pro Gln Glu Met Trp
 595 600 605
 Asn Ser Gly Cys Gln Leu Val Ala Leu Asn Phe Gln Thr Pro Gly Tyr
 610 615 620
 Glu Met Asp Leu Asn Ala Gly Arg Phe Leu Val Asn Gly Gln Cys Gly
 625 630 635 640
 Tyr Val Leu Lys Pro Ala Cys Leu Arg Gln Pro Asp Ser Thr Phe Asp
 645 650 655
 Pro Glu Tyr Pro Gly Pro Pro Arg Thr Thr Leu Ser Ile Gln Val Leu
 660 665 670
 Thr Ala Gln Gln Leu Pro Lys Leu Asn Ala Glu Lys Pro His Ser Ile
 675 680 685
 Val Asp Pro Leu Val Arg Ile Glu Ile His Gly Val Pro Ala Asp Cys
 690 695 700
 Ala Arg Gln Glu Thr Asp Tyr Val Leu Asn Asn Gly Phe Asn Pro Arg
 705 710 715 720
 Trp Gly Gln Thr Leu Gln Phe Gln Leu Arg Ala Pro Glu Leu Ala Leu
 725 730 735
 Val Arg Phe Val Val Glu Asp Tyr Asp Ala Thr Ser Pro Asn Asp Phe
 740 745 750
 Val Gly Gln Phe Thr Leu Pro Leu Ser Ser Leu Lys Gln Gly Tyr Arg
 755 760 765
 His Ile His Leu Leu Ser Lys Asp Gly Ala Ser Leu Ser Pro Ala Thr
 770 775 780
 Leu Phe Ile Gln Ile Arg Ile Gln Arg Ser
 785 790

<210> 122
 <211> 286
 <212> PRT
 <213> Homo sapiens

<400> 122
 Met Val Asp Leu Ser Val Ser Pro Asp Ser Leu Lys Pro Val Ser Leu
 1 5 10 15
 Thr Ser Ser Leu Val Phe Leu Met His Leu Leu Leu Leu Gln Pro Gly

				20				25					30			
Glu	Pro	Ser	Ser	Glu	Val	Lys	Val	Leu	Gly	Pro	Glu	Tyr	Pro	Ile	Leu	
		35					40					45				
Ala	Leu	Val	Gly	Glu	Glu	Val	Glu	Phe	Pro	Cys	His	Leu	Trp	Pro	Gln	
	50					55					60					
Leu	Asp	Ala	Gln	Gln	Met	Glu	Ile	Arg	Trp	Phe	Arg	Ser	Gln	Thr	Phe	
	65				70					75					80	
Asn	Val	Val	His	Leu	Tyr	Gln	Glu	Gln	Gln	Glu	Leu	Pro	Gly	Arg	Gln	
				85				90						95		
Met	Pro	Ala	Phe	Arg	Asn	Arg	Thr	Lys	Leu	Val	Lys	Asp	Asp	Ile	Ala	
		100						105				110				
Tyr	Gly	Ser	Val	Val	Leu	Gln	Leu	His	Ser	Ile	Ile	Pro	Ser	Asp	Lys	
		115				120						125				
Gly	Thr	Tyr	Gly	Cys	Arg	Phe	His	Ser	Asp	Asn	Phe	Ser	Gly	Glu	Ala	
	130					135					140					
Leu	Trp	Glu	Leu	Glu	Val	Ala	Gly	Leu	Gly	Ser	Asp	Pro	His	Leu	Ser	
145					150					155					160	
Leu	Glu	Gly	Phe	Lys	Glu	Gly	Gly	Ile	Gln	Leu	Arg	Leu	Arg	Ser	Ser	
				165				170						175		
Gly	Trp	Tyr	Pro	Lys	Pro	Lys	Val	Gln	Trp	Arg	Asp	His	Gln	Gly	Gln	
			180					185					190			
Cys	Leu	Pro	Pro	Glu	Phe	Glu	Ala	Ile	Val	Trp	Asp	Ala	Gln	Asp	Leu	
		195					200					205				
Phe	Ser	Leu	Glu	Thr	Ser	Val	Val	Val	Arg	Ala	Gly	Ala	Leu	Ser	Asn	
	210					215					220					
Val	Ser	Val	Ser	Ile	Gln	Asn	Leu	Leu	Leu	Ser	Gln	Lys	Lys	Glu	Leu	
225					230					235					240	
Val	Val	Gln	Ile	Ala	Gly	Gln	Trp	Leu	Leu	Ala	His	Thr	His	Leu	Pro	
				245				250						255		
Ser	Pro	His	Val	Tyr	Ile	His	Ile	Gly	Pro	Lys	Ala	Val	Tyr	Lys	Glu	
			260					265					270			
Thr	Met	Val	Leu	Arg	Leu	Ser	Ala	Tyr	Arg	Val	Cys	Trp	Pro			
		275					280					285				

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<210> 123
<211> 551
<212> PRT
<213> Homo sapiens
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<400> 123															
Met	Thr	Ser	Pro	Gln	Ala	Asp	Phe	Cys	Leu	Gly	Thr	Ala	Leu	His	Ser
1				5					10					15	
Trp	Gly	Leu	Trp	Phe	Thr	Glu	Glu	Gly	Ser	Pro	Ser	Thr	Met	Leu	Thr
			20					25					30		
Gly	Ile	Ala	Val	Gly	Ala	Leu	Leu	Ala	Leu	Ala	Leu	Val	Gly	Val	Leu
		35					40					45			
Ile	Leu	Phe	Met	Phe	Arg	Arg	Leu	Arg	Gln	Phe	Arg	Gln	Ala	Gln	Pro
	50					55					60				
Thr	Pro	Gln	Tyr	Arg	Phe	Arg	Lys	Arg	Asp	Lys	Val	Met	Phe	Tyr	Gly
65					70				75					80	
Arg	Lys	Ile	Met	Arg	Lys	Val	Thr	Thr	Leu	Pro	Asn	Thr	Leu	Val	Glu
				85					90					95	
Asn	Thr	Ala	Leu	Pro	Arg	Gln	Arg	Ala	Arg	Lys	Arg	Thr	Lys	Val	Leu
		100						105					110		
Ser	Leu	Ala	Lys	Arg	Ile	Leu	Arg	Phe	Lys	Lys	Glu	Tyr	Pro	Ala	Leu
		115					120					125			
Gln	Pro	Lys	Glu	Pro	Pro	Pro	Ser	Leu	Leu	Glu	Ala	Asp	Leu	Thr	Glu
	130					135					140				

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Phe Asp Val Lys Asn Ser His Leu Pro Ser Glu Val Leu Tyr Met Leu
145                               150                               155                               160
Lys Asn Val Arg Val Leu Gly His Phe Glu Lys Pro Leu Phe Leu Glu
                               165                               170                               175
Leu Cys Lys His Ile Val Phe Val Gln Leu Gln Glu Gly Glu His Val
                               180                               185                               190
Phe Gln Pro Arg Glu Pro Asp Pro Ser Ile Cys Val Val Gln Asp Gly
                               195                               200                               205
Arg Leu Glu Val Cys Ile Gln Asp Thr Asp Gly Thr Glu Val Val Val
210                               215                               220
Lys Glu Val Leu Ala Gly Asp Ser Val His Ser Leu Leu Ser Ile Leu
225                               230                               235                               240
Asp Ile Ile Thr Gly His Ala Ala Pro Tyr Lys Thr Val Ser Val Arg
                               245                               250                               255
Ala Ala Ile Pro Ser Thr Ile Leu Arg Leu Pro Ala Ala Ala Phe His
260                               265                               270
Gly Val Phe Glu Lys Tyr Pro Glu Thr Leu Val Arg Val Val Gln Ile
275                               280                               285
Ile Met Val Arg Leu Gln Arg Val Thr Phe Leu Ala Leu His Asn Tyr
290                               295                               300
Leu Gly Leu Thr Thr Glu Leu Phe Asn Ala Glu Ser Gln Ala Ile Pro
305                               310                               315                               320
Leu Val Ser Val Ala Ser Val Ala Ala Gly Lys Ala Lys Lys Gln Val
                               325                               330                               335
Phe Tyr Gly Glu Glu Arg Leu Lys Lys Pro Pro Arg Leu Gln Glu
340                               345                               350
Ser Cys Asp Ser Gly Thr Val Leu His Gln Gly Gly Gln Cys Pro Ala
355                               360                               365
Pro Glu Ser Gly Gly Ser Cys Ser His Cys Leu Arg Ser Pro Gln Val
370                               375                               380
Ile Leu His Met Pro Glu Ala Thr Thr His Ile Pro Gly Ser Pro His
385                               390                               395                               400
Thr Ala Gln Val Thr Leu Gln Val Pro Gln Val Thr Ser His Ala Pro
405                               410                               415
Gln Val Tyr Ser His Ala Pro Gln Val Pro Ser Arg Ala Ser Gly Pro
420                               425                               430
Leu Thr Arg Ala Pro Gly His Leu Thr Cys Pro Pro Gly Leu Ile Arg
435                               440                               445
Trp Pro Pro Arg Ser Pro His Val Ser Pro Ser Pro His Met Arg Ala
450                               455                               460
Gly Cys Pro Gln Thr Ser Pro Gly Leu Ile Arg Cys Ala His Leu Leu
465                               470                               475                               480
Thr Cys Gly Leu Asp Val Leu Lys Pro Pro Thr Val Ser Leu Arg Val
485                               490                               495
Pro Val Ser Ser His Glu Ala Arg Met Ser Ser Asp Arg Pro Arg Thr
500                               505                               510
Leu His Pro Pro Phe Phe Ser Cys Ser Gln Asn Ser Pro Leu Gly Gln
515                               520                               525
Val Pro Gly Gly Glu Trp Ala Ser Arg Asp Gly Leu Ser Pro Ala Val
530                               535                               540
Leu Ser Ala Asn Arg Gly Ala
545                               550

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<210> 124
<211> 328
<212> PRT
<213> Homo sapiens

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<400> 124
 Met Ala Leu Pro Ala Leu Gly Leu Asp Pro Trp Ser Leu Leu Gly Leu
 1 5 10 15
 Phe Leu Phe Gln Leu Leu Gln Leu Leu Leu Pro Thr Thr Thr Ala Gly
 20 25 30
 Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr Ala Gly Asp
 35 40 45
 Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly Leu Gln Asp Phe
 50 55 60
 Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr Leu Tyr Val Gly Ala
 65 70 75 80
 Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln Asp Pro Gly Val Pro Arg
 85 90 95
 Leu Lys Asn Met Ile Pro Trp Pro Ala Ser Asp Arg Lys Lys Ser Glu
 100 105 110
 Cys Ala Phe Lys Lys Lys Ser Asn Glu Thr Gln Cys Phe Asn Phe Ile
 115 120 125
 Arg Val Leu Val Ser Tyr Asn Val Thr His Leu Tyr Thr Cys Gly Thr
 130 135 140
 Phe Ala Phe Ser Pro Ala Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr
 145 150 155 160
 Leu Leu Pro Ile Ser Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser
 165 170 175
 Pro Phe Asp Pro Ala His Lys His Thr Ala Val Leu Val Asp Gly Met
 180 185 190
 Leu Tyr Ser Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu
 195 200 205
 Met Arg Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu
 210 215 220
 Arg Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr
 225 230 235 240
 Gln Val Val Tyr Phe Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp Phe
 245 250 255
 Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys Asn Asp
 260 265 270
 Val Gly Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr Phe Leu Lys
 275 280 285
 Ala Gln Leu Leu Cys Thr Gln Pro Gly Gln Leu Pro Phe Asn Val Ile
 290 295 300
 Arg His Ala Val Leu Leu Pro Ala Asp Ser Pro Thr Ala Pro His Ile
 305 310 315 320
 Tyr Ala Val Phe Thr Ser Gln Trp
 325

<210> 125
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 125
 Met Met Glu Thr Met Gln Leu Lys Val Asn Arg His Pro Phe Cys Phe
 1 5 10 15
 Ser Val Lys Gly Gln Val Lys Met Leu Gln Leu Met Arg Leu Gly Leu
 20 25 30
 Arg Val Arg Gly Val Val Glu Ser Ala Cys Gly Arg Glu Met Trp Leu
 35 40 45
 Cys Gly Tyr Lys Gly
 50

<210> 126
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 126
 Met Ala Cys Val Ser Val Asp His Tyr Pro Ala Val Val Cys Ala His
 1 5 10 15
 Trp Gly Pro Cys Leu Arg Thr Ala Gly Arg Ala Arg Leu Val Cys Val
 20 25 30
 Ala Ile Trp Thr Leu Val Leu Leu Gln Thr Met Pro Leu Leu Leu Met
 35 40 45
 Pro Met Thr Lys Pro Leu Val Gly Lys Leu Ala Cys Met Glu Tyr Ser
 50 55 60
 Ser Met Glu Ser Val Leu Gly Leu Pro Leu Met Val Leu Val Ala Phe
 65 70 75 80
 Ala Ile Gly Phe Cys Gly Pro Val Gly Ile Ile Leu Ser Cys Tyr Met
 85 90 95
 Lys Ile Thr Trp Lys Leu Cys Ser Thr Ala Gly Arg Thr Gln
 100 105 110

<210> 127
 <211> 212
 <212> PRT
 <213> Homo sapiens

<400> 127
 Met Leu Ser Ser Val Val Phe Trp Gly Leu Ile Ala Leu Ile Gly Thr
 1 5 10 15
 Ser Arg Gly Ser Tyr Pro Phe Ser His Ser Met Lys Pro His Leu His
 20 25 30
 Pro Arg Leu Tyr His Gly Cys Tyr Gly Asp Ile Met Thr Met Lys Thr
 35 40 45
 Ser Gly Ala Thr Cys Asp Ala Asn Ser Val Met Asn Cys Gly Ile Arg
 50 55 60
 Gly Ser Glu Met Phe Ala Glu Met Asp Leu Arg Ala Ile Lys Pro Tyr
 65 70 75 80
 Gln Thr Leu Ile Lys Glu Val Gly Gln Arg His Cys Val Asp Pro Ala
 85 90 95
 Val Ile Ala Ala Ile Ile Ser Arg Glu Ser His Gly Gly Ser Val Leu
 100 105 110
 Gln Asp Gly Trp Asp His Arg Gly Leu Lys Phe Gly Leu Met Gln Leu
 115 120 125
 Asp Lys Gln Thr Tyr His Pro Val Gly Ala Trp Asp Ser Lys Glu His
 130 135 140
 Leu Ser Gln Ala Thr Gly Ile Leu Thr Glu Arg Ile Lys Ala Ile Gln
 145 150 155 160
 Lys Lys Phe Pro Thr Trp Ser Val Ala Gln His Leu Lys Gly Gly Leu
 165 170 175
 Ser Ala Phe Lys Ser Gly Ile Glu Ala Ile Ala Thr Pro Ser Asp Ile
 180 185 190
 Asp Asn Asp Phe Val Asn Asp Ile Ile Ala Arg Ala Lys Phe Tyr Lys
 195 200 205
 Arg Gln Ser Phe

210

<210> 128
 <211> 267
 <212> PRT
 <213> Homo sapiens

<400> 128
 Met Ile Gly Asn Asn Met Ile Thr Cys Ile Asn Gly Ile Trp Thr Glu
 1 5 10 15
 Leu Pro Met Cys Val Ala Thr His Gln Leu Lys Arg Cys Lys Ile Ala
 20 25 30
 Gly Val Asn Ile Lys Thr Leu Leu Lys Leu Ser Gly Lys Glu Phe Asn
 35 40 45
 His Asn Ser Arg Ile Arg Tyr Arg Cys Ser Asp Ile Phe Arg Tyr Arg
 50 55 60
 His Ser Val Cys Ile Asn Gly Lys Trp Asn Pro Glu Val Asp Cys Thr
 65 70 75 80
 Glu Lys Arg Glu Gln Phe Cys Pro Pro Pro Gln Ile Pro Asn Ala
 85 90 95
 Gln Asn Met Thr Thr Thr Val Asn Tyr Gln Asp Gly Glu Lys Val Ala
 100 105 110
 Val Leu Cys Lys Glu Asn Tyr Leu Leu Pro Glu Ala Lys Glu Ile Val
 115 120 125
 Cys Lys Asp Gly Arg Trp Gln Ser Leu Pro Arg Cys Val Glu Ser Thr
 130 135 140
 Ala Tyr Cys Gly Pro Pro Pro Ser Ile Asn Asn Gly Asp Thr Thr Ser
 145 150 155 160
 Phe Pro Leu Ser Val Tyr Pro Pro Gly Ser Thr Val Thr Tyr Arg Cys
 165 170 175
 Gln Ser Phe Tyr Lys Leu Gln Gly Ser Val Thr Val Thr Cys Arg Asn
 180 185 190
 Lys Gln Trp Ser Glu Pro Pro Arg Cys Leu Asp Pro Cys Val Val Ser
 195 200 205
 Glu Glu Asn Met Asn Lys Asn Asn Ile Gln Leu Lys Trp Arg Asn Asp
 210 215 220
 Gly Lys Leu Tyr Ala Lys Thr Gly Asp Ala Val Glu Phe Gln Cys Lys
 225 230 235 240
 Phe Pro His Lys Ala Met Ile Ser Ser Pro Pro Phe Arg Ala Ile Cys
 245 250 255
 Gln Glu Gly Lys Phe Glu Tyr Pro Ile Cys Glu
 260 265

<210> 129
 <211> 1364
 <212> PRT
 <213> Homo sapiens

<400> 129
 Met Gly Pro Asp Glu Ala Thr Pro Pro Asp Leu Val Leu Pro Ala Trp
 1 5 10 15
 Arg Leu Arg His Gly Ala Phe Arg Thr Leu Val Thr Arg Glu Pro Gly
 20 25 30
 Ala Pro Arg Met Gly Ala Pro Ser Ala Cys Arg Thr Leu Val Leu Ala
 35 40 45

272

Leu Ala Ala Met Leu Val Val Pro Gln Ala Glu Thr Gln Gly Pro Val
 50 55 60
 Glu Pro Ser Trp Glu Asn Ala Gly His Thr Met Asp Gly Gly Ala Pro
 65 70 75 80
 Thr Ser Ser Pro Thr Arg Arg Val Ser Phe Val Pro Pro Val Thr Val
 85 90 95
 Phe Pro Ser Leu Ser Pro Leu Asn Pro Ala His Asn Gly Arg Val Cys
 100 105 110
 Ser Thr Trp Gly Asp Phe His Tyr Lys Thr Phe Asp Gly Asp Val Phe
 115 120 125
 Arg Phe Pro Gly Leu Cys Asn Tyr Val Phe Ser Glu His Cys Arg Ala
 130 135 140
 Ala Tyr Glu Asp Phe Asn Val Gln Leu Arg Arg Gly Leu Val Gly Ser
 145 150 155 160
 Arg Pro Val Val Thr Arg Val Val Ile Lys Ala Gln Gly Leu Val Leu
 165 170 175
 Glu Ala Ser Asn Gly Ser Val Leu Ile Asn Gly Gln Arg Glu Glu Leu
 180 185 190
 Pro Tyr Ser Arg Thr Gly Leu Leu Val Glu Gln Ser Gly Asp Tyr Ile
 195 200 205
 Lys Val Ser Ile Arg Leu Val Leu Thr Phe Leu Trp Asn Gly Glu Asp
 210 215 220
 Ser Ala Leu Leu Glu Leu Asp Pro Lys Tyr Ala Asn Gln Thr Cys Gly
 225 230 235 240
 Leu Cys Gly Asp Phe Asn Gly Leu Pro Ala Phe Asn Glu Phe Tyr Ala
 245 250 255
 His Ser Glu Cys His Leu Asp Ala Arg Leu Thr Pro Leu Gln Phe Gly
 260 265 270
 Asn Leu Gln Lys Leu Asp Gly Pro Thr Glu Gln Cys Pro Asp Pro Leu
 275 280 285
 Pro Leu Pro Ala Gly Asn Cys Thr Asp Glu Glu Gly Ile Cys His Arg
 290 295 300
 Thr Leu Leu Gly Pro Ala Phe Ala Glu Cys His Ala Leu Val Asp Ser
 305 310 315 320
 Thr Ala Tyr Leu Ala Ala Cys Ala Gln Asp Leu Cys Arg Cys Pro Thr
 325 330 335
 Cys Pro Cys Ala Thr Phe Val Glu Tyr Ser Arg Gln Cys Ala His Ala
 340 345 350
 Gly Gly Gln Pro Arg Asn Trp Arg Cys Pro Glu Leu Cys Pro Arg Thr
 355 360 365
 Cys Pro Leu Asn Met Gln His Gln Glu Cys Gly Ser Pro Cys Thr Asp
 370 375 380
 Thr Cys Ser Asn Pro Gln Arg Ala Gln Leu Cys Glu Asp His Cys Val
 385 390 395 400
 Asp Gly Cys Phe Cys Pro Pro Gly Thr Val Leu Asp Asp Ile Thr His
 405 410 415
 Ser Gly Cys Leu Pro Leu Gly Gln Cys Pro Cys Thr His Gly Gly Arg
 420 425 430
 Thr Tyr Ser Pro Gly Thr Ser Phe Asn Thr Thr Cys Ser Ser Cys Thr
 435 440 445
 Cys Ser Gly Gly Leu Trp Gln Cys Gln Asp Leu Pro Cys Pro Gly Thr
 450 455 460
 Cys Ser Val Gln Gly Gly Ala His Ile Ser Thr Tyr Asp Glu Lys Leu
 465 470 475 480
 Tyr Asp Leu His Gly Asp Cys Ser Tyr Val Leu Ser Lys Lys Cys Ala
 485 490 495
 Asp Ser Ser Phe Thr Val Leu Ala Glu Leu Arg Lys Cys Gly Leu Thr
 500 505 510
 Asp Asn Glu Asn Cys Leu Lys Ala Val Thr Leu Ser Leu Asp Gly Gly
 515 520 525
 Asp Thr Ala Ile Arg Val Gln Ala Asp Gly Gly Val Phe Leu Asn Ser

530	535	540
Ile Tyr Thr Gln Leu Pro	Leu Ser Ala Ala Asn	Ile Thr Leu Phe Thr
545	550	555
Pro Ser Ser Phe Phe Ile	Val Val Gln Thr Gly	Leu Gly Leu Gln Leu
565	570	575
Leu Val Gln Leu Val Pro	Leu Met Gln Val Phe	Val Arg Leu Asp Pro
580	585	590
Ala His Gln Gly Gln Met	Cys Gly Leu Cys Gly	Asn Phe Asn Gln Asn
595	600	605
Gln Ala Asp Asp Phe Thr	Ala Leu Ser Gly Val	Val Glu Ala Thr Gly
610	615	620
Ala Ala Phe Ala Asn Thr	Trp Lys Ala Gln Ala	Ala Cys Ala Asn Ala
625	630	635
Arg Asn Ser Phe Glu Asp	Pro Cys Ser Leu Ser	Val Glu Asn Glu Asn
645	650	655
Tyr Ala Arg His Trp Cys	Ser Arg Leu Thr Asp	Pro Asn Ser Ala Phe
660	665	670
Ser Arg Cys His Ser Ile	Ile Asn Pro Lys Pro	Phe His Ser Asn Cys
675	680	685
Met Phe Asp Thr Cys Asn	Cys Glu Arg Ser Glu	Asp Cys Leu Cys Ala
690	695	700
Ala Leu Ser Ser Tyr Val	His Ala Cys Ala Ala	Lys Gly Val Gln Leu
705	710	715
Ser Asp Trp Arg Asp Gly	Val Cys Thr Lys Tyr	Met Gln Asn Cys Pro
725	730	735
Lys Ser Gln Arg Tyr Ala	Tyr Val Val Asp Ala	Cys Gln Pro Thr Cys
740	745	750
Arg Gly Leu Ser Glu Ala	Asp Val Thr Cys Ser	Val Ser Phe Val Pro
755	760	765
Val Asp Gly Cys Thr Cys	Pro Ala Gly Thr Phe	Leu Asn Asp Ala Gly
770	775	780
Ala Cys Val Pro Ala Gln	Lys Cys Pro Cys Tyr	Ala His Gly Thr Val
785	790	795
Leu Ala Pro Gly Glu Val	Val His Asp Glu Gly	Ala Val Cys Ser Cys
805	810	815
Thr Gly Gly Lys Leu Ser	Cys Leu Gly Ala Ser	Leu Gln Lys Ser Thr
820	825	830
Gly Cys Ala Ala Pro Met	Val Tyr Leu Asp Cys	Ser Asn Ser Ser Ala
835	840	845
Gly Thr Pro Gly Ala Glu	Cys Leu Arg Ser Cys	His Thr Leu Asp Val
850	855	860
Gly Cys Phe Ser Thr His	Cys Val Ser Gly Cys	Val Cys Pro Pro Gly
865	870	875
Leu Val Ser Asp Gly Ser	Gly Gly Cys Ile Ala	Glu Glu Asp Cys Pro
885	890	895
Cys Val His Asn Glu Ala	Thr Tyr Lys Pro Gly	Glu Thr Ile Arg Val
900	905	910
Asp Cys Asn Thr Cys Thr	Cys Arg Asn Arg Arg	Trp Glu Cys Ser His
915	920	925
Arg Leu Cys Leu Gly Thr	Cys Val Ala Tyr Gly	Asp Gly His Phe Ile
930	935	940
Thr Phe Asp Gly Asp Arg	Tyr Ser Phe Glu Gly	Ser Cys Glu Tyr Ile
945	950	955
Leu Ala Gln Asp Tyr Cys	Gly Asp Asn Thr Thr	His Gly Thr Phe Arg
965	970	975
Ile Val Thr Glu Asn Ile	Pro Cys Gly Thr Thr	Gly Thr Thr Cys Ser
980	985	990
Lys Ala Ile Lys Leu Phe	Val Glu Ser Tyr Glu	Leu Ile Leu Gln Glu
995	1000	1005
Gly Thr Phe Lys Ala Val	Ala Arg Gly Pro Gly	Gly Asp Pro Pro Tyr
1010	1015	1020

Lys Ile Arg Tyr Met Gly Ile Phe Leu Val Ile Glu Thr His Gly Met
 1025 1030 1035 1040
 Ala Val Ser Trp Asp Arg Lys Thr Ser Val Phe Ile Arg Leu His Gln
 1045 1050 1055
 Asp Tyr Lys Gly Arg Val Cys Gly Leu Cys Gly Asn Phe Asp Asp Asn
 1060 1065 1070
 Ala Ile Asn Asp Phe Ala Thr Arg Ser Arg Ser Val Val Gly Asp Ala
 1075 1080 1085
 Leu Glu Phe Gly Asn Ser Trp Lys Leu Ser Pro Ser Cys Pro Asp Ala
 1090 1095 1100
 Leu Ala Pro Lys Asp Pro Cys Thr Ala Asn Pro Phe Arg Lys Ser Trp
 1105 1110 1115 1120
 Ala Gln Lys Gln Cys Ser Ile Leu His Gly Pro Thr Phe Ala Ala Cys
 1125 1130 1135
 Arg Ser Gln Val Asp Ser Thr Lys Tyr Tyr Glu Ala Cys Val Asn Asp
 1140 1145 1150
 Ala Cys Ala Cys Asp Ser Gly Gly Asp Cys Glu Cys Phe Cys Thr Ala
 1155 1160 1165
 Val Ala Ala Tyr Ala Gln Ala Cys His Asp Ala Gly Leu Cys Val Ser
 1170 1175 1180
 Trp Arg Thr Pro Asp Thr Cys Pro Leu Phe Cys Asp Phe Tyr Asn Pro
 1185 1190 1195 1200
 His Gly Gly Cys Glu Trp His Tyr Gln Pro Cys Gly Ala Pro Cys Leu
 1205 1210 1215
 Lys Thr Cys Arg Asn Pro Ser Gly His Cys Leu Val Asp Leu Pro Gly
 1220 1225 1230
 Leu Glu Gly Cys Tyr Pro Lys Cys Pro Pro Ser Gln Pro Phe Phe Asn
 1235 1240 1245
 Glu Asp Gln Met Lys Cys Val Ala Gln Cys Gly Cys Tyr Asp Lys Asp
 1250 1255 1260
 Gly Asn Tyr Tyr Asp Val Gly Ala Arg Val Pro Thr Ala Glu Asn Cys
 1265 1270 1275 1280
 Gln Ser Cys Asn Cys Thr Pro Ser Gly Ile Gln Cys Ala His Ser Leu
 1285 1290 1295
 Glu Ala Cys Thr Cys Thr Tyr Glu Asp Arg Thr Tyr Ser Tyr Gln Asp
 1300 1305 1310
 Val Ile Tyr Asn Thr Thr Asp Gly Leu Gly Ala Cys Leu Ile Ala Ile
 1315 1320 1325
 Cys Gly Ser Asn Gly Thr Ile Ile Arg Lys Ala Val Ala Cys Pro Gly
 1330 1335 1340
 Thr Pro Ala Thr Thr Pro Phe Thr Phe Thr Thr Ala Trp Val Pro His
 1345 1350 1355 1360
 Ser Thr Thr Ser

<210> 130
 <211> 1296
 <212> PRT
 <213> Homo sapiens

<400> 130
 Met Ser Thr Ser Asp Ile Pro Ser Ser Pro Ser Ile Gln Asn Thr Glu
 1 5 10 15
 Thr Ser Ser Leu Val Ser Met Thr Ser Ala Thr Ile Pro Ser Val Arg
 20 25 30
 Pro Thr Phe Thr Ser Thr His Asn Thr Leu Thr Ser Ser Leu Leu Thr
 35 40 45
 Thr Phe Pro Gly Thr Tyr Ser Phe Ser Ser Ser Met Ser Ala Ser Ser

50	55	60													
Asp Gly Thr Thr His Thr Glu Thr Ile Thr Ser Leu Pro Ala Ser Thr															
65	70	75													80
Ser Thr Leu His Thr Thr Ala Glu Ser Thr Thr Ala His Thr Thr Thr															
	85	90													95
Thr Ser Phe Thr Thr Ser Thr Thr Met Glu Ser Pro Ser Ser Ser Val															
	100	105													110
Ala Thr Thr Ser Thr Gly Gln Thr Thr Phe Ser Ser Ser Thr Ala Thr															
	115	120													125
Phe Thr Glu Thr Thr Thr Leu Thr Pro Thr Thr Asp Phe Ser Glu Glu															
	130	135													140
Thr Leu Thr Thr Ala Met Thr Ser Thr Pro Pro Ile Thr Ser Ser Ile															
	145	150													155
Thr Pro Thr Asn Thr Val Thr Ser Met Thr Thr Met Thr Ser Trp Pro															
	165	170													175
Thr Ala Thr Asn Thr Leu Ser Ser Leu Thr Thr Asn Ile Leu Ser Ser															
	180	185													190
Thr Pro Val Pro Ser Thr Glu Arg Thr Thr Ser His Thr Thr Asn Ile															
	195	200													205
Asn Pro Val Ser Thr Leu Val Thr Thr Leu Pro Thr Thr Ile Thr Arg															
	210	215													220
Ser Thr Pro Thr Ser Glu Thr Thr Tyr Pro Ile Ser Ser Thr Ser Thr															
	225	230													235
Val Thr Glu Ser Thr Thr Glu Ile Thr Tyr Ser Thr Thr Met Thr Glu															
	245	250													255
Thr Ser Ser Ser Ala Thr Ser Leu Pro Leu Thr Ser Pro Leu Val Ser															
	260	265													270
Thr Thr Glu Thr Ala Lys Thr Pro Thr Thr Ile Leu Val Thr Thr Thr															
	275	280													285
Thr Lys Thr Thr Ser His Ser Thr Thr Ser Phe Thr Ser Ser Thr Val															
	290	295													300
Tyr Ser Thr Ala Ser Thr His Thr Thr Ala Ile Thr Ser Val Pro Thr															
	305	310													315
Thr Leu Gly Thr Met Val Thr Ser Thr Ser Arg Ile Pro Ser Thr Val															
	325	330													335
Ser Thr Ser Ile Pro Thr Ser Gln Pro Lys Thr Val Asn Ser Ser Ser															
	340	345													350
Gly Gly Ile Thr Gly Ser Leu Pro Met Met Thr Asp Leu Thr Ser Gly															
	355	360													365
Tyr Thr Val Ser Ser Met Ser Ala Ile Pro Thr Thr Val Ile Pro Thr															
	370	375													380
Ser Leu Thr Val Gln Asn Thr Glu Thr Ser Ile Phe Val Ser Met Thr															
	385	390													395
Ser Ala Thr Thr Pro Ser Gly Arg Pro Thr Phe Thr Ser Thr Val Asn															
	405	410													415
Thr Pro Thr Arg Ser Leu Leu Thr Ser Phe Pro Thr Thr His Leu Phe															
	420	425													430
Ser Ser Ser Met Ser Glu Ser Ser Ala Gly Thr Thr His Thr Glu Ser															
	435	440													445
Ile Ser Ser Pro Pro Ala Thr Thr Ser Thr Leu His Thr Thr Ala Glu															
	450	455													460
Ser Thr Pro Ser Cys Thr Thr Thr Thr Ser Phe Ile Thr Ser Thr Thr															
	465	470													475
Met Glu Pro Leu Ser Thr Ile Val Ala Thr Thr Gly Thr Val Lys Thr															
	485	490													495
Thr Val Thr Ser Thr Ala Thr Phe Arg Glu Thr Thr Thr Thr Thr Thr															
	500	505													510
Ser Thr Thr Asp Ile Ser Thr Glu Ser Leu Met Thr Ala Met Thr Ser															
	515	520													525
Thr Thr Arg Leu Thr Ser Ala Ile Thr Ser Lys Thr Thr Leu Thr Ser															
	530	535													540

Leu	Lys	Thr	Thr	Ala	Ser	Arg	Pro	Thr	Ala	Asn	Ser	Thr	Leu	Ser	Ser
545					550					555					560
Leu	Thr	Ser	Ser	Ile	Leu	Ser	Ser	Thr	Leu	Val	Pro	Ser	Thr	Asp	Met
				565					570						575
Ile	Thr	Ser	His	Thr	Thr	Asn	Leu	Thr	Arg	Ser	Ser	Pro	Leu	Leu	Ala
			580					585					590		
Thr	Leu	Pro	Thr	Thr	Ile	Thr	Arg	Ser	Thr	Pro	Thr	Ser	Glu	Thr	Thr
		595					600					605			
Tyr	Pro	Thr	Ser	Pro	Thr	Ser	Thr	Val	Lys	Gly	Ser	Thr	Thr	Ser	Ile
	610					615					620				
Arg	Tyr	Ser	Thr	Ser	Met	Thr	Gly	Thr	Leu	Ser	Met	Glu	Thr	Ser	Leu
	625				630					635					640
Pro	Pro	Thr	Ser	Ser	Ser	Leu	Pro	Thr	Thr	Glu	Thr	Ala	Thr	Met	Thr
				645					650					655	
Pro	Thr	Thr	Thr	Leu	Ile	Thr	Thr	Thr	Pro	Asn	Thr	Thr	Ser	His	Ser
				660				665					670		
Thr	Pro	Ser	Phe	Thr	Ser	Ser	Thr	Ile	Tyr	Ser	Thr	Val	Ser	Thr	Ser
		675					680					685			
Thr	Thr	Ala	Ile	Thr	Ser	His	Phe	Thr	Thr	Ser	Glu	Thr	Ala	Val	Thr
	690					695					700				
Pro	Thr	Pro	Val	Thr	Pro	Ser	Ser	Leu	Ser	Thr	Asp	Ile	Pro	Thr	Thr
	705				710					715					720
Ser	Leu	Arg	Thr	Leu	Thr	Pro	Ser	Ser	Val	Gly	Thr	Ser	Thr	Ser	Leu
				725					730					735	
Thr	Thr	Thr	Thr	Asp	Phe	Pro	Ser	Ile	Pro	Thr	Asp	Ile	Ser	Thr	Leu
			740					745					750		
Pro	Thr	Arg	Thr	His	Ile	Ile	Ser	Ser	Ser	Pro	Ser	Ile	Gln	Ser	Thr
		755					760					765			
Glu	Thr	Ser	Ser	Leu	Val	Gly	Thr	Thr	Ser	Pro	Thr	Met	Ser	Thr	Val
	770					775					780				
Arg	Met	Thr	Leu	Arg	Ile	Thr	Glu	Asn	Thr	Pro	Ile	Ser	Ser	Phe	Ser
	785				790					795					800
Thr	Ser	Ile	Val	Val	Ile	Pro	Glu	Thr	Pro	Thr	Gln	Thr	Pro	Pro	Val
			805						810					815	
Leu	Thr	Ser	Ala	Thr	Gly	Thr	Gln	Thr	Ser	Pro	Ala	Pro	Thr	Thr	Val
			820					825					830		
Thr	Phe	Gly	Ser	Thr	Asp	Ser	Ser	Thr	Ser	Thr	Leu	His	Thr	Leu	Thr
		835					840					845			
Pro	Ser	Thr	Ala	Leu	Ser	Thr	Ile	Val	Ser	Thr	Ser	Gln	Val	Pro	Ile
	850					855					860				
Pro	Ser	Thr	His	Ser	Ser	Thr	Leu	Gln	Thr	Thr	Pro	Ser	Thr	Pro	Ser
	865				870					875					880
Leu	Gln	Thr	Ser	Leu	Thr	Ser	Thr	Ser	Glu	Phe	Thr	Thr	Glu	Ser	Phe
				885					890				895		
Thr	Arg	Gly	Ser	Thr	Ser	Thr	Asn	Ala	Ile	Leu	Thr	Ser	Phe	Ser	Thr
			900				905						910		
Ile	Ile	Trp	Ser	Ser	Thr	Pro	Thr	Ile	Ile	Met	Ser	Ser	Ser	Pro	Ser
		915					920					925			
Ser	Ala	Ser	Ile	Thr	Pro	Val	Phe	Ser	Thr	Thr	Ile	His	Ser	Val	Pro
	930					935					940				
Ser	Ser	Pro	Tyr	Ile	Phe	Ser	Thr	Glu	Asn	Val	Gly	Ser	Ala	Ser	Ile
	945				950					955					960
Thr	Gly	Phe	Pro	Ser	Leu	Ser	Ser	Ser	Ala	Thr	Thr	Ser	Thr	Ser	Ser
				965					970					975	
Thr	Ser	Ser	Ser	Leu	Thr	Thr	Ala	Leu	Thr	Glu	Ile	Thr	Pro	Phe	Ser
			980					985					990		
Tyr	Ile	Ser	Leu	Pro	Ser	Thr	Thr	Pro	Cys	Pro	Gly	Thr	Ile	Thr	Ile
		995					1000					1005			
Thr	Ile	Val	Pro	Ala	Ser	Pro	Thr	Asp	Pro	Cys	Val	Glu	Met	Asp	Pro
	1010					1015					1020				
Ser	Thr	Glu	Ala	Thr	Ser	Pro	Pro	Thr	Thr	Pro	Leu	Thr	Val	Phe	Pro

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1025          1030          1035          1040
Phe Thr Thr Glu Met Val Thr Cys Pro Thr Ser Ile Ser Ile Gln Thr
          1045          1050          1055
Thr Leu Thr Thr Tyr Met Asp Thr Ser Ser Met Met Pro Glu Ser Glu
          1060          1065          1070
Ser Ser Ile Ser Pro Asn Ala Ser Ser Ser Thr Gly Thr Gly Thr Val
          1075          1080          1085
Pro Thr Asn Thr Val Phe Thr Ser Thr Arg Leu Pro Thr Ser Glu Thr
          1090          1095          1100
Trp Leu Ser Asn Ser Ser Val Ile Pro Leu Pro Leu Pro Gly Val Ser
1105          1110          1115          1120
Thr Ile Pro Leu Thr Met Lys Pro Ser Ser Ser Leu Pro Thr Ile Leu
          1125          1130          1135
Arg Thr Ser Ser Lys Ser Thr His Pro Ser Pro Pro Thr Thr Arg Thr
          1140          1145          1150
Ser Glu Thr Pro Val Ala Thr Thr Gln Thr Pro Thr Thr Leu Thr Ser
          1155          1160          1165
Arg Arg Thr Thr Arg Ile Thr Ser Gln Met Thr Thr Gln Ser Thr Leu
          1170          1175          1180
Thr Thr Thr Ala Gly Thr Cys Asp Asn Gly Gly Thr Trp Glu Gln Gly
1185          1190          1195          1200
Gln Cys Ala Cys Leu Pro Gly Phe Ser Gly Asp Arg Cys Gln Leu Gln
          1205          1210          1215
Thr Arg Cys Gln Asn Gly Gly Gln Trp Asp Gly Leu Lys Cys Gln Cys
          1220          1225          1230
Pro Ser Thr Phe Tyr Gly Ser Ser Cys Glu Phe Ala Val Glu Gln Val
          1235          1240          1245
Asp Leu Asp Ala Glu Asp Phe Cys Arg His Ala Gly Leu His Leu Gln
          1250          1255          1260
Gly Cys Gly Asp Pro Val Pro Glu Glu Trp Gln His Arg Gly Gly Leu
1265          1270          1275          1280
Pro Gly Pro Ala Gly Asp Ala Leu Gln Pro Pro Ala Gly Glu Arg Val
          1285          1290          1295

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<210> 131
 <211> 319
 <212> PRT
 <213> Homo sapiens

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          <400> 131
Met Thr Arg Thr Tyr Glu Asn Phe Gln Tyr Leu Glu Asn Lys Val Lys
  1          5          10          15
Val Gln Gly Phe Lys Asn Gly Pro Leu Pro Leu Gln Ser Leu Leu Gln
          20          25          30
Arg Leu Cys Ser Gly Pro Cys His Leu Leu Ser Leu Gly Leu Gly
          35          40          45
Leu Leu Leu Leu Val Ile Ile Cys Val Val Gly Phe Gln Asn Ser Lys
          50          55          60
Phe Gln Arg Asp Leu Val Thr Leu Arg Thr Asp Phe Ser Asn Phe Thr
          65          70          75          80
Ser Asn Thr Val Ala Glu Ile Gln Ala Leu Thr Ser Gln Gly Ser Ser
          85          90          95
Leu Glu Glu Thr Ile Ala Ser Leu Lys Ala Glu Val Glu Gly Phe Lys
          100          105          110
Gln Glu Arg Gln Ala Gly Val Ser Glu Leu Gln Glu His Thr Thr Gln
          115          120          125

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Lys Ala His Leu Gly His Cys Pro His Cys Pro Ser Val Cys Val Pro
 130 135 140
 Val His Ser Glu Met Leu Leu Arg Val Gln Gln Leu Val Gln Asp Leu
 145 150 155 160
 Lys Lys Leu Thr Cys Gln Val Ala Thr Leu Asn Asn Asn Gly Glu Glu
 165 170 175
 Ala Ser Thr Glu Gly Thr Cys Cys Pro Val Asn Trp Val Glu His Gln
 180 185 190
 Asp Ser Cys Tyr Trp Phe Ser His Ser Gly Met Ser Trp Ala Glu Ala
 195 200 205
 Glu Lys Tyr Cys Gln Leu Lys Asn Ala His Leu Val Val Ile Asn Ser
 210 215 220
 Arg Glu Glu Gln Asn Phe Val Gln Lys Tyr Leu Gly Ser Ala Tyr Thr
 225 230 235 240
 Trp Met Gly Leu Ser Asp Pro Glu Gly Ala Trp Lys Trp Val Asp Gly
 245 250 255
 Thr Asp Tyr Ala Thr Gly Phe Gln Asn Trp Lys Pro Gly Gln Pro Asp
 260 265 270
 Asp Trp Gln Gly His Gly Leu Gly Gly Glu Asp Cys Ala His Phe
 275 280 285
 His Pro Asp Gly Arg Trp Asn Asp Asp Val Cys Gln Arg Pro Tyr His
 290 295 300
 Trp Val Cys Glu Ala Gly Leu Gly Gln Thr Ser Gln Glu Ser His
 305 310 315

<210> 132
 <211> 590
 <212> PRT
 <213> Homo sapiens

<400> 132
 Met Lys Glu Val Thr Phe His Cys His Glu Gly Tyr Ile Leu His Gly
 1 5 10 15
 Ala Pro Lys Leu Thr Cys Gln Ser Asp Gly Asn Trp Asp Ala Glu Ile
 20 25 30
 Pro Leu Cys Lys Pro Val Asn Cys Gly Pro Pro Glu Asp Leu Ala His
 35 40 45
 Gly Phe Pro Asn Gly Phe Ser Phe Ile His Gly Gly His Ile Gln Tyr
 50 55 60
 Gln Cys Phe Pro Gly Tyr Lys Leu His Gly Asn Ser Ser Arg Arg Cys
 65 70 75 80
 Leu Ser Asn Gly Ser Trp Ser Gly Ser Ser Pro Ser Cys Leu Pro Cys
 85 90 95
 Arg Cys Ser Thr Pro Val Ile Glu Tyr Gly Thr Val Asn Gly Thr Asp
 100 105 110
 Phe Asp Cys Gly Lys Ala Ala Arg Ile Gln Cys Phe Lys Gly Phe Lys
 115 120 125
 Leu Leu Gly Leu Ser Glu Ile Thr Cys Glu Ala Asp Gly Gln Trp Ser
 130 135 140
 Ser Gly Phe His His Phe Glu His Thr Ser Cys Gly Ser Leu Pro Met
 145 150 155 160
 Ile Pro Asn Ala Phe Ile Ser Glu Thr Ser Ser Trp Lys Glu Asn Val
 165 170 175
 Ile Thr Tyr Ser Cys Arg Ser Gly Tyr Val Ile Gln Gly Ser Ser Asp
 180 185 190
 Leu Ile Cys Thr Glu Lys Gly Val Trp Ser Gln Pro Tyr Pro Val Cys
 195 200 205
 Glu Pro Leu Ser Cys Gly Ser Pro Pro Ser Val Ala Asn Ala Val Ala

210	215	220
Thr Gly Glu Ala His	Thr Tyr Glu Ser Glu Val Lys Leu Arg Cys Leu	
225	230	235
Glu Gly Tyr Thr Met Asp Thr Asp Thr Arg Ser Ile Thr Cys Gln Lys		240
	245	250
Asp Gly Arg Trp Phe Pro Glu Arg Ile Ser Cys Ser Pro Lys Lys Cys		255
	260	265
Pro Leu Pro Glu Asn Ile Thr His Ile Leu Val His Gly Asp Asp Phe		270
	275	280
Ser Val Asn Arg Gln Val Ser Val Ser Cys Ala Glu Gly Tyr Thr Phe		285
	290	295
Glu Gly Val Asn Ile Ser Val Cys Gln Leu Asp Gly Thr Trp Glu Pro		300
305	310	315
Pro Phe Ser Asp Glu Ser Cys Ser Pro Val Ser Cys Gly Lys Pro Glu		320
	325	330
Ser Pro Glu His Gly Phe Val Val Gly Ser Lys Tyr Thr Phe Glu Ser		335
	340	345
Thr Ile Ile Tyr Gln Cys Glu Pro Gly Tyr Glu Leu Glu Gly Asn Arg		350
	355	360
Glu Arg Val Cys Gln Glu Asn Arg Gln Trp Ser Gly Gly Val Ala Ile		365
	370	375
Cys Lys Glu Thr Arg Cys Glu Thr Pro Leu Glu Phe Leu Asn Gly Lys		380
385	390	395
Ala Asp Ile Glu Asn Arg Thr Thr Gly Pro Asn Val Val Tyr Ser Cys		400
	405	410
Asn Arg Gly Tyr Ser Leu Glu Gly Pro Ser Glu Ala His Cys Thr Glu		415
	420	425
Asn Gly Thr Trp Ser His Pro Val Pro Leu Cys Lys Pro Asn Pro Cys		430
	435	440
Pro Val Pro Phe Val Ile Pro Glu Asn Ala Leu Leu Ser Glu Lys Glu		445
	450	455
Phe Tyr Val Asp Gln Asn Val Ser Ile Lys Cys Arg Glu Gly Phe Leu		460
465	470	475
Leu Gln Gly His Gly Ile Ile Thr Cys Asn Pro Asp Glu Thr Trp Thr		480
	485	490
Gln Thr Ser Ala Lys Cys Glu Lys Ile Ser Cys Gly Pro Pro Ala His		495
	500	505
Val Glu Asn Ala Ile Ala Arg Gly Val His Tyr Gln Tyr Gly Asp Met		510
	515	520
Ile Thr Tyr Ser Cys Tyr Ser Gly Tyr Met Leu Glu Gly Phe Leu Arg		525
	530	535
Ser Val Cys Leu Glu Asn Gly Thr Trp Thr Ser Pro Pro Ile Cys Arg		540
545	550	555
Ala Val Cys Arg Phe Pro Cys Gln Asn Gly Gly Ile Cys Gln Arg Pro		560
	565	570
Asn Ala Cys Ser Cys Pro Glu Gly Trp Asp Gly Ala Pro Leu		575
	580	585
		590

<210> 133

<211> 1544

<212> PRT

<213> Homo sapiens

<400> 133

Met Ser Gly Thr Gln Ser Thr Ile Thr Asp Arg Phe Pro Leu Lys Lys	
1	5
Pro Ile Arg His Gly Ser Ile Leu Asn Arg Glu Ser Pro Thr Asp Lys	
	20
	25
	30

Lys	Gln	Lys	Val	Glu	Arg	Ile	Ala	Ser	His	Asp	Phe	Asp	Pro	Thr	Asp	
		35					40					45				
Ser	Ser	Ser	Lys	Lys	Thr	Lys	Ser	Ser	Ser	Glu	Glu	Ser	Arg	Ser	Glu	
	50					55					60					
Ile	Tyr	Gly	Leu	Val	Gln	Arg	Cys	Val	Ile	Ile	Gln	Lys	Asp	Asp	Asn	
65					70					75					80	
Gly	Phe	Gly	Leu	Thr	Val	Ser	Gly	Asp	Asn	Pro	Val	Phe	Val	Gln	Ser	
				85					90					95		
Val	Lys	Glu	Asp	Gly	Ala	Ala	Met	Arg	Ala	Gly	Val	Gln	Thr	Gly	Asp	
			100					105					110			
Arg	Ile	Ile	Lys	Val	Asn	Gly	Thr	Leu	Val	Thr	His	Ser	Asn	His	Leu	
	115						120					125				
Glu	Val	Val	Lys	Leu	Ile	Lys	Ser	Gly	Ser	Tyr	Val	Ala	Leu	Thr	Val	
130						135					140					
Gln	Gly	Arg	Pro	Pro	Gly	Ser	Pro	Gln	Ile	Pro	Leu	Ala	Asp	Ser	Glu	
145					150					155					160	
Val	Glu	Pro	Ser	Val	Ile	Gly	His	Met	Ser	Pro	Ile	Met	Thr	Ser	Pro	
				165					170					175		
His	Ser	Pro	Gly	Ala	Ser	Gly	Asn	Met	Glu	Arg	Ile	Thr	Ser	Pro	Val	
			180				185						190			
Leu	Met	Gly	Glu	Glu	Asn	Asn	Val	Val	His	Asn	Gln	Lys	Val	Glu	Ile	
	195						200					205				
Leu	Arg	Lys	Met	Leu	Gln	Lys	Glu	Gln	Glu	Arg	Leu	Gln	Leu	Leu	Gln	
210						215					220					
Glu	Asp	Tyr	Asn	Arg	Thr	Pro	Ala	Gln	Arg	Leu	Leu	Lys	Glu	Ile	Gln	
225					230					235					240	
Glu	Ala	Lys	Lys	His	Ile	Pro	Gln	Leu	Gln	Glu	Gln	Leu	Ser	Lys	Ala	
				245					250					255		
Thr	Gly	Ser	Ala	Gln	Asp	Gly	Ala	Val	Val	Thr	Pro	Ser	Arg	Pro	Leu	
			260					265					270			
Gly	Asp	Thr	Leu	Thr	Val	Ser	Glu	Ala	Glu	Thr	Asp	Pro	Gly	Asp	Val	
	275						280					285				
Leu	Gly	Arg	Thr	Asp	Cys	Ser	Ser	Gly	Asp	Ala	Ser	Arg	Pro	Ser	Ser	
290						295					300					
Asp	Asn	Ala	Asp	Ser	Pro	Lys	Ser	Gly	Pro	Lys	Glu	Arg	Ile	Tyr	Leu	
305					310					315					320	
Glu	Glu	Asn	Pro	Glu	Lys	Ser	Glu	Thr	Ile	Gln	Asp	Thr	Asp	Thr	Gln	
				325					330					335		
Ser	Leu	Val	Gly	Ser	Pro	Ser	Thr	Arg	Ile	Ala	Pro	His	Ile	Ile	Gly	
			340					345					350			
Ala	Glu	Asp	Asp	Asp	Phe	Gly	Thr	Glu	His	Glu	Gln	Ile	Asn	Gly	Gln	
		355				360						365				
Cys	Ser	Cys	Phe	Gln	Ser	Ile	Glu	Leu	Leu	Lys	Ser	Arg	Pro	Ala	His	
370						375					380					
Leu	Ala	Val	Phe	Leu	His	His	Val	Val	Ser	Gln	Phe	Asp	Pro	Ala	Thr	
385					390					395					400	
Leu	Leu	Cys	Tyr	Leu	Tyr	Ser	Asp	Leu	Tyr	Lys	His	Thr	Asn	Ser	Lys	
			405						410					415		
Glu	Thr	Arg	Arg	Ile	Phe	Leu	Glu	Phe	His	Gln	Phe	Phe	Leu	Asp	Arg	
			420					425					430			
Ser	Ala	His	Leu	Lys	Val	Ser	Val	Pro	Asp	Glu	Met	Ser	Ala	Asp	Leu	
		435					440					445				
Glu	Lys	Arg	Arg	Pro	Glu	Leu	Ile	Pro	Glu	Asp	Leu	His	Arg	His	Tyr	
	450					455					460					
Ile	Gln	Thr	Met	Gln	Glu	Arg	Val	His	Pro	Glu	Val	Gln	Arg	His	Leu	
465					470					475					480	
Lys	Asp	Phe	Arg	Gln	Lys	Arg	Ser	Met	Gly	Leu	Thr	Leu	Ala	Glu	Ser	
			485						490					495		
Glu	Leu	Thr	Lys	Leu	Asp	Ala	Glu	Arg	Asp	Lys	Asp	Arg	Leu	Thr	Leu	
			500					505					510			
Glu	Lys	Glu	Arg	Thr	Cys	Ala	Glu	Gln	Ile	Val	Ala	Lys	Ile	Glu	Glu	

	515		520		525
Val	Leu Met Thr Ala Gln	Ala Val Glu Glu Asp Lys	Ser Ser Thr Met		
	530	535	540		
Gln	Tyr Val Ile Leu Met Tyr Met Lys His Leu Gly	Val Lys Val Lys			
545		550	555		560
Glu	Pro Arg Asn Leu Glu His Lys Arg Gly Arg Ile Gly Phe Leu Pro				
	565	570			575
Lys	Ile Lys Gln Ser Met Lys Lys Asp Lys Glu Gly Glu Glu Lys Gly				
	580	585			590
Lys	Arg Arg Gly Phe Pro Ser Ile Leu Gly Pro Pro Arg Arg Pro Ser				
	595	600			605
Arg	His Asp Asn Ser Ala Ile Gly Arg Ala Met Glu Leu Gln Lys Ala				
	610	615			620
Arg	His Pro Lys His Leu Ser Thr Pro Ser Ser Val Ser Pro Glu Pro				
625		630			635
Gln	Asp Ser Ala Lys Leu Arg Gln Ser Gly Leu Ala Asn Glu Gly Thr				
	645	650			655
Asp	Ala Gly Tyr Leu Pro Ala Asn Ser Met Ser Ser Val Ala Ser Gly				
	660	665			670
Ala	Ser Phe Ser Gln Glu Gly Gly Lys Glu Asn Asp Thr Gly Ser Lys				
	675	680			685
Gln	Val Gly Glu Thr Ser Ala Pro Gly Asp Thr Leu Asp Gly Thr Pro				
	690	695			700
Arg	Thr Leu Asn Thr Val Phe Val Phe Pro Pro Pro Leu Asp Gln				
705		710			715
Val	Gln Glu Glu Glu Cys Glu Val Glu Arg Val Thr Glu His Gly Thr				
	725	730			735
Pro	Lys Pro Phe Arg Lys Phe Asp Ser Val Ala Phe Gly Glu Ser Gln				
	740	745			750
Ser	Glu Asp Glu Gln Phe Glu Asn Asp Leu Glu Thr Asp Pro Pro Asn				
	755	760			765
Trp	Gln Gln Leu Val Ser Arg Glu Val Leu Leu Gly Leu Lys Pro Cys				
	770	775			780
Glu	Ile Lys Arg Gln Glu Val Ile Asn Glu Leu Phe Tyr Thr Glu Arg				
785		790			795
Ala	His Val Arg Thr Leu Lys Val Leu Asp Gln Val Phe Tyr Gln Arg				
	805	810			815
Val	Ser Arg Glu Gly Ile Leu Ser Pro Ser Glu Leu Trp Lys Ile Phe				
	820	825			830
Ser	Asn Leu Glu Asp Ile Leu Gln Leu His Ile Gly Leu Asn Glu Gln				
	835	840			845
Met	Lys Ala Val Arg Lys Arg Asn Glu Thr Ser Val Ile Asp Gln Ile				
	850	855			860
Gly	Glu Asp Leu Leu Thr Trp Phe Ser Gly Pro Gly Glu Glu Lys Leu				
865		870			875
Lys	His Ala Ala Ala Thr Phe Cys Ser Asn Gln Pro Phe Ala Leu Glu				
	885	890			895
Met	Ile Lys Ser Arg Gln Lys Lys Asp Ser Arg Phe Gln Thr Phe Val				
	900	905			910
Gln	Asp Ala Glu Ser Asn Pro Leu Cys Arg Arg Leu Gln Leu Lys Asp				
	915	920			925
Ile	Ile Pro Thr Gln Met Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu				
	930	935			940
Asp	Asn Ile Ala Lys Tyr Thr Glu Trp Pro Thr Glu Arg Glu Lys Val				
945		950			955
Lys	Lys Ala Ala Asp His Cys Arg Gln Ile Leu Asn Tyr Val Asn Gln				
	965	970			975
Ala	Val Lys Glu Ala Glu Asn Lys Gln Arg Leu Glu Asp Tyr Gln Arg				
	980	985			990
Arg	Leu Asp Thr Ser Ser Leu Lys Leu Ser Glu Tyr Pro Asn Val Glu				
	995	1000			1005

Glu Leu Arg Asn Leu Asp Leu Thr Lys Arg Lys Met Ile His Glu Gly
 1010 1015 1020
 Pro Leu Val Trp Lys Val Asn Arg Asp Lys Thr Ile Asp Leu Tyr Thr
 1025 1030 1035 1040
 Leu Leu Leu Glu Asp Ile Leu Val Leu Leu Gln Lys Gln Asp Asp Arg
 1045 1050 1055
 Leu Val Leu Arg Cys His Ser Lys Ile Leu Ala Ser Thr Ala Asp Ser
 1060 1065 1070
 Lys His Thr Phe Ser Pro Val Ile Lys Leu Ser Thr Val Leu Val Arg
 1075 1080 1085
 Gln Gly Ala Thr Asp Asn Lys Ala Leu Phe Val Ile Ser Met Ser Asp
 1090 1095 1100
 Asn Gly Ala Gln Ile Tyr Glu Leu Val Ala Gln Thr Val Ser Glu Lys
 1105 1110 1115 1120
 Thr Val Trp Gln Asp Leu Ile Cys Arg Met Ala Ala Ser Val Lys Glu
 1125 1130 1135
 Gln Ser Thr Lys Pro Ile Pro Leu Pro Gln Ser Thr Pro Gly Glu Gly
 1140 1145 1150
 Asp Asn Asp Glu Glu Asp Pro Ser Lys Leu Lys Glu Glu Gln His Gly
 1155 1160 1165
 Ile Ser Val Thr Gly Leu Gln Ser Pro Asp Arg Asp Leu Gly Leu Glu
 1170 1175 1180
 Ser Thr Leu Ile Ser Ser Lys Pro Gln Ser His Ser Leu Ser Thr Ser
 1185 1190 1195 1200
 Gly Lys Ser Glu Val Arg Asp Leu Phe Val Ala Glu Arg Gln Phe Ala
 1205 1210 1215
 Lys Glu Gln His Thr Asp Gly Thr Leu Lys Glu Val Gly Glu Asp Tyr
 1220 1225 1230
 Gln Ile Ala Ile Pro Asp Ser His Leu Pro Val Ser Glu Glu Arg Trp
 1235 1240 1245
 Ala Leu Asp Ala Leu Arg Asn Leu Gly Leu Leu Lys Gln Leu Leu Val
 1250 1255 1260
 Gln Gln Leu Gly Leu Thr Glu Lys Ser Val Gln Glu Asp Trp Gln His
 1265 1270 1275 1280
 Phe Pro Arg Tyr Arg Thr Ala Ser Gln Gly Pro Gln Thr Asp Ser Val
 1285 1290 1295
 Ile Gln Asn Ser Glu Asn Ile Lys Ala Tyr His Ser Gly Glu Gly His
 1300 1305 1310
 Met Pro Phe Arg Thr Gly Thr Gly Asp Ile Ala Thr Cys Tyr Ser Pro
 1315 1320 1325
 Arg Thr Ser Thr Glu Ser Phe Ala Pro Arg Asp Ser Val Gly Leu Ala
 1330 1335 1340
 Pro Gln Asp Ser Gln Ala Ser Asn Ile Leu Val Met Asp His Met Ile
 1345 1350 1355 1360
 Met Thr Pro Glu Met Pro Thr Met Glu Pro Glu Gly Gly Leu Asp Asp
 1365 1370 1375
 Ser Gly Glu His Phe Phe Asp Ala Arg Glu Ala His Ser Asp Glu Asn
 1380 1385 1390
 Pro Ser Glu Gly Asp Gly Ala Val Asn Lys Glu Glu Lys Asp Val Asn
 1395 1400 1405
 Leu Arg Ile Ser Gly Asn Tyr Leu Ile Leu Asp Gly Tyr Asp Pro Val
 1410 1415 1420
 Gln Glu Ser Ser Thr Asp Glu Glu Val Ala Ser Ser Leu Thr Leu Gln
 1425 1430 1435 1440
 Pro Met Thr Gly Ile Pro Ala Val Glu Ser Thr His Gln Gln Gln His
 1445 1450 1455
 Ser Pro Gln Asn Thr His Ser Asp Gly Ala Ile Ser Pro Phe Thr Pro
 1460 1465 1470
 Glu Phe Leu Val Gln Gln Arg Trp Gly Ala Met Glu Tyr Ser Cys Phe
 1475 1480 1485
 Glu Ile Gln Ser Pro Ser Ser Cys Ala Asp Ser Gln Ser Gln Ile Met

1490 1495 1500
 Glu Tyr Ile His Lys Ile Glu Ala Asp Leu Glu His Leu Lys Lys Val
 1505 1510 1515 1520
 Glu Glu Ser Tyr Thr Ile Leu Cys Gln Arg Leu Ala Gly Ser Ala Leu
 1525 1530 1535
 Thr Asp Lys His Ser Asp Lys Ser
 1540

<210> 134
 <211> 486
 <212> PRT
 <213> Homo sapiens

<400> 134
 Met Met Gly Gln Asp Lys Ile Gln Gly His Ser Val Ile Ser Glu Glu
 1 5 10 15
 Ser Asp Gly Lys Leu Ile Glu Asp Ser Leu Ile Gln Leu Arg Cys His
 20 25 30
 Phe Thr Trp Lys Leu Leu Ile Glu Ala Pro Glu Ile Pro Asp Leu Glu
 35 40 45
 Asn Arg Ile Trp Glu Glu Ile Gln Phe Leu Asp Thr Lys Tyr Asn Val
 50 55 60
 Gly Ile His Asn Leu Leu Ala Tyr Val Lys His Leu Lys Gly Gln Asn
 65 70 75 80
 Glu Glu Ala Leu Val Ser Leu Lys Lys Ala Glu Asp Leu Ile Gln Lys
 85 90 95
 Glu His Ala Asn Gln Ala Asp Ile Arg Ser Leu Val Thr Trp Gly Asn
 100 105 110
 Phe Ala Trp Val Tyr Tyr His Met Gly Arg Leu Ala Glu Ala Gln Thr
 115 120 125
 Tyr Leu Asp Lys Val Glu Asn Thr Cys Lys Lys Phe Ala Asn Pro Ser
 130 135 140
 Arg Tyr Arg Met Glu Cys Pro Glu Val Asp Cys Glu Glu Gly Trp Ala
 145 150 155 160
 Leu Ala Lys Cys Gly Gly Lys Asn Tyr Glu Arg Ala Lys Thr Cys Phe
 165 170 175
 Glu Lys Ala Leu Glu Gly Asn Pro Glu Asn Pro Glu Phe Asn Thr Gly
 180 185 190
 Tyr Ala Ile Thr Val Tyr Arg Leu Asp Lys Phe Asn Thr Ala Ser Gly
 195 200 205
 Arg Asn Lys Ala Phe Ser Leu His Val Leu Lys Arg Ala Val Arg Leu
 210 215 220
 Asn Pro Asp Asp Val Tyr Ile Arg Val Leu Leu Ala Leu Lys Leu Gln
 225 230 235 240
 Asp Glu Gly Gln Glu Ala Glu Gly Glu Lys Tyr Ile Glu Glu Ala Leu
 245 250 255
 Thr Ser Ile Ser Ser Gln Ala Tyr Val Phe Gln Tyr Ala Ala Lys Phe
 260 265 270
 Tyr Arg Arg Lys Gly Ser Val Asp Lys Ala Leu Glu Leu Leu Lys Met
 275 280 285
 Ala Leu Glu Thr Thr Pro Thr Ser Ala Phe Leu His His Gln Met Gly
 290 295 300
 Leu Cys Tyr Arg Ala Gln Met Ile Gln Ile Lys Glu Ala Thr Asn Trp
 305 310 315 320
 Gln Pro Arg Gly Gln Asp Arg Glu Thr Val Asp Arg Leu Val Gln Leu
 325 330 335
 Ala Ile Cys Lys Phe Glu Lys Thr Ile Met Leu Lys Arg Thr Phe Glu
 340 345 350

Met Ala Tyr Val Asp Leu Ala Glu Thr Tyr Ala Glu Ile Gly His His
 355 360 365
 Arg Lys Ala Glu Glu His Phe Gln Lys Gly Leu Arg Met Lys Ile Phe
 370 375 380
 Glu Asp Gln Leu Lys Gln Glu Ile His Tyr His Tyr Gly Arg Phe Gln
 385 390 395 400
 Glu His His Gly Lys Ser Gln Asp Lys Ala Ile Thr His Tyr Leu Lys
 405 410 415
 Gly Leu Lys Ile Glu Lys Met Ser His Ser Arg Glu Lys Leu Leu Asn
 420 425 430
 Ala Leu Glu Lys Leu Ala Lys Arg Cys Ile His Gln Asn Val Arg Val
 435 440 445
 Val Glu Ser Val Ser Leu Leu Gly Leu Ile His Lys Leu Lys Gly Glu
 450 455 460
 Val Ser Asp Ala Leu Leu Cys Tyr Glu Arg Ala Leu Arg Leu Ala Ala
 465 470 475 480
 Asp Leu Asn Pro Ile Phe
 485

<210> 135
 <211> 403
 <212> PRT
 <213> Homo sapiens

<400> 135
 Met Glu Thr Tyr Ala Glu Val Gly Lys Glu Gly Lys Pro Ser Cys Ala
 1 5 10 15
 Ser Val Asp Leu Gln Gly Asp Ser Ser Leu Gln Val Glu Ile Ser Asp
 20 25 30
 Ala Val Ser Glu Arg Asp Lys Val Lys Phe Thr Val Gln Thr Lys Ser
 35 40 45
 Cys Leu Pro His Phe Ala Gln Thr Glu Phe Ser Val Val Arg Gln His
 50 55 60
 Glu Glu Phe Ile Trp Leu His Asp Ala Tyr Val Glu Asn Glu Glu Tyr
 65 70 75 80
 Ala Gly Leu Ile Ile Pro Pro Ala Pro Pro Arg Pro Asp Phe Glu Ala
 85 90 95
 Ser Arg Glu Lys Leu Gln Lys Leu Gly Glu Gly Asp Ser Ser Val Thr
 100 105 110
 Arg Glu Glu Phe Ala Lys Met Lys Gln Glu Leu Glu Ala Glu Tyr Leu
 115 120 125
 Ala Ile Phe Lys Lys Thr Val Ala Met His Glu Val Phe Leu Gln Arg
 130 135 140
 Leu Ala Ala His Pro Thr Leu Arg Arg Asp His Asn Phe Phe Val Phe
 145 150 155 160
 Leu Glu Tyr Gly Gln Asp Leu Ser Val Arg Gly Lys Asn Arg Lys Glu
 165 170 175
 Leu Leu Gly Gly Phe Leu Arg Asn Ile Val Lys Ser Ala Asp Glu Ala
 180 185 190
 Leu Ile Thr Gly Met Ser Gly Leu Lys Glu Val Asp Asp Phe Phe Glu
 195 200 205
 His Glu Arg Thr Phe Leu Leu Glu Tyr His Thr Arg Ile Arg Asp Ala
 210 215 220
 Cys Leu Arg Ala Asp Arg Val Met Arg Ala His Lys Cys Leu Ala Asp
 225 230 235 240
 Asp Tyr Ile Pro Ile Ser Ala Ala Leu Ser Ser Leu Gly Thr Gln Glu
 245 250 255
 Val Asn Gln Leu Arg Thr Ser Phe Leu Lys Leu Ala Glu Leu Phe Glu

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<210> 136
<211> 273
<212> PRT
<213> Homo sapiens
```

286

Arg Arg Ala His Gly Arg Arg Val Gly Thr Arg Leu Pro Ala Phe Phe
 260 265 270
 Phe

<210> 137
 <211> 806
 <212> PRT
 <213> Homo sapiens

<400> 137
 Met Ala Val Arg Ala Leu Lys Leu Leu Thr Thr Leu Leu Ala Val Val
 1 5 10 15
 Ala Ala Ala Ser Gln Ala Glu Val Glu Ser Glu Ala Gly Trp Gly Met
 20 25 30
 Val Thr Pro Asp Leu Leu Phe Ala Glu Gly Thr Ala Ala Tyr Ala Arg
 35 40 45
 Gly Asp Trp Pro Gly Val Val Leu Ser Met Glu Arg Ala Leu Arg Ser
 50 55 60
 Arg Ala Ala Leu Arg Ala Leu Arg Leu Arg Cys Arg Thr Gln Cys Ala
 65 70 75 80
 Ala Asp Phe Pro Trp Glu Leu Asp Pro Asp Trp Ser Pro Ser Pro Ala
 85 90 95
 Gln Ala Ser Gly Ala Ala Ala Leu Arg Asp Leu Ser Phe Phe Gly Gly
 100 105 110
 Leu Leu Arg Arg Ala Ala Cys Leu Arg Arg Cys Leu Gly Pro Pro Ala
 115 120 125
 Ala His Ser Leu Ser Glu Glu Met Glu Leu Glu Phe Arg Lys Arg Ser
 130 135 140
 Pro Tyr Asn Tyr Leu Gln Val Ala Tyr Phe Lys Val Gln Thr Cys Leu
 145 150 155 160
 Glu Pro Gly Gly Arg Gly Pro Ser Gly Glu Arg Ser Val Ala Gly Asp
 165 170 175
 Leu Arg Ser Leu Gly Asp Arg Gly Ser Val Arg Arg Glu Gly Lys Val
 180 185 190
 Ala Ser Trp Leu Gly Ser Ser Pro Arg Ser Arg Gly Glu Leu Leu Pro
 195 200 205
 Gly Arg Arg Pro Ser Ser Pro Ser Ser His Gly Gln Met Leu Thr Pro
 210 215 220
 Lys Ile Asn Lys Leu Glu Lys Ala Val Ala Ala His Thr Phe Phe
 225 230 235 240
 Val Gly Asn Pro Glu His Met Glu Met Gln Gln Asn Leu Asp Tyr Tyr
 245 250 255
 Gln Thr Met Ser Gly Val Lys Glu Ala Asp Phe Lys Asp Leu Glu Thr
 260 265 270
 Gln Pro His Met Gln Glu Phe Arg Leu Gly Val Arg Leu Tyr Ser Glu
 275 280 285
 Glu Gln Pro Gln Glu Ala Val Pro His Leu Glu Ala Ala Leu Gln Glu
 290 295 300
 Tyr Phe Val Ala Tyr Glu Glu Cys Arg Ala Leu Cys Glu Gly Pro Tyr
 305 310 315 320
 Asp Tyr Asp Gly Tyr Asn Tyr Leu Glu Tyr Asn Ala Asp Leu Phe Gln
 325 330 335
 Ala Ile Thr Asp His Tyr Ile Gln Val Leu Asn Cys Lys Gln Asn Cys
 340 345 350
 Val Thr Glu Leu Ala Ser His Pro Ser Arg Glu Lys Pro Phe Glu Asp
 355 360 365
 Phe Leu Pro Ser His Tyr Asn Tyr Leu Gln Phe Ala Tyr Tyr Asn Ile

370	375	380
Gly Asn Tyr Thr Gln Ala Val Glu Cys Ala Lys Thr Tyr Leu Leu Phe		
385	390	395
Phe Pro Asn Asp Glu Val Met Asn Gln Asn Leu Ala Tyr Tyr Ala Ala		400
	405	410
Met Leu Gly Glu Glu His Thr Arg Ser Ile Gly Pro Arg Glu Ser Ala		415
	420	425
Lys Glu Tyr Arg Gln Arg Ser Leu Glu Lys Glu Leu Leu Phe Phe		430
	435	440
Ala Tyr Asp Val Phe Gly Ile Pro Phe Val Asp Pro Asp Ser Trp Thr		445
	450	455
Pro Glu Glu Val Ile Pro Lys Arg Leu Gln Glu Lys Gln Lys Ser Glu		460
	465	470
Arg Glu Thr Ala Val Arg Ile Ser Gln Glu Ile Gly Asn Leu Met Lys		475
	485	490
Glu Ile Glu Thr Leu Val Glu Glu Lys Thr Lys Glu Ser Leu Asp Val		495
	500	505
Ser Arg Leu Thr Arg Glu Gly Gly Pro Leu Leu Tyr Glu Gly Ile Ser		510
	515	520
Leu Thr Met Asn Ser Lys Leu Leu Asn Gly Ser Gln Arg Val Val Met		525
	530	535
Asp Gly Val Ile Ser Asp His Glu Cys Gln Glu Leu Gln Arg Leu Thr		540
	545	550
Asn Val Ala Ala Thr Ser Gly Asp Gly Tyr Arg Gly Gln Thr Ser Pro		555
	565	570
His Thr Pro Asn Glu Lys Phe Tyr Gly Val Thr Val Phe Lys Ala Leu		575
	580	585
Lys Leu Gly Gln Glu Gly Lys Val Pro Leu Gln Ser Ala His Leu Tyr		590
	595	600
Tyr Asn Val Thr Glu Lys Val Arg Arg Ile Met Glu Ser Tyr Phe Arg		605
	610	615
Leu Asp Thr Pro Leu Tyr Phe Ser Tyr Ser His Leu Val Cys Arg Thr		620
	625	630
Ala Ile Glu Glu Val Gln Ala Glu Arg Lys Asp Asp Ser His Pro Val		635
	645	650
His Val Asp Asn Cys Ile Leu Asn Ala Glu Thr Leu Val Cys Val Lys		655
	660	665
Glu Pro Pro Ala Tyr Thr Phe Arg Asp Tyr Ser Ala Ile Leu Tyr Leu		670
	675	680
Asn Gly Asp Phe Asp Gly Gly Asn Phe Tyr Phe Thr Glu Leu Asp Ala		685
	690	695
Lys Thr Val Thr Ala Glu Val Gln Pro Gln Cys Gly Arg Ala Val Gly		700
	705	710
Phe Ser Ser Gly Thr Glu Asn Pro His Gly Val Lys Ala Val Thr Arg		715
	725	730
Gly Gln Arg Cys Ala Ile Ala Leu Trp Phe Thr Leu Asp Pro Arg His		735
	740	745
Ser Glu Arg Asp Arg Val Gln Ala Asp Asp Leu Val Lys Met Leu Phe		750
	755	760
Ser Pro Glu Glu Met Asp Leu Ser Gln Glu Gln Pro Leu Asp Ala Gln		765
	770	775
Gln Gly Pro Pro Glu Pro Ala Gln Glu Ser Leu Ser Gly Ser Glu Ser		780
	785	790
Lys Pro Lys Asp Glu Leu		795
	805	800

<210> 138

<211> 244

<212> PRT

<213> Homo sapiens

<400> 138

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Met Arg Phe Val Leu Cys Val Lys Ala Lys Pro Ser Gly Leu Val Thr
 1           5           10           15
Ile Ser Arg Lys Ile Thr Gln Asp Tyr Gly Gln Asp Ala Ala Phe Thr
          20           25           30
Ala Ile Leu Asp Thr Leu Asp Ile Phe Leu Glu Ile Val Thr Asn Pro
          35           40           45
Asp Gly Phe Ala Phe Thr His Ser Thr Asn Arg Met Trp Arg Lys Thr
          50           55           60
Arg Ser His Thr Ala Gly Ser Leu Cys Ile Gly Val Asp Pro Asn Arg
          65           70           75           80
Asn Trp Asp Ala Gly Phe Gly Leu Ser Gly Ala Ser Ser Asn Pro Cys
          85           90           95
Ser Glu Thr Tyr His Gly Lys Phe Ala Asn Ser Glu Val Glu Val Lys
          100          105          110
Ser Ile Val Asp Phe Val Lys Asp His Gly Asn Ile Lys Ala Phe Ile
          115          120          125
Ser Ile His Ser Tyr Ser Gln Leu Leu Met Tyr Pro Tyr Gly Tyr Lys
          130          135          140
Thr Glu Pro Val Pro Asp Gln Asp Glu Leu Asp Gln Leu Ser Lys Ala
          145          150          155          160
Ala Val Thr Ala Leu Ala Ser Leu Tyr Gly Thr Lys Phe Asn Tyr Gly
          165          170          175
Ser Ile Ile Lys Ala Ile Tyr Gln Ala Ser Gly Ser Thr Ile Asp Trp
          180          185          190
Thr Tyr Ser Gln Gly Ile Lys Tyr Ser Phe Thr Phe Glu Leu Arg Asp
          195          200          205
Thr Gly Arg Tyr Gly Phe Leu Leu Pro Ala Ser Gln Ile Ile Pro Thr
          210          215          220
Ala Lys Glu Thr Trp Leu Ala Leu Leu Thr Ile Met Glu His Thr Leu
          225          230          235          240
Asn His Pro Tyr

```

<210> 139

<211> 538

<212> PRT

<213> Homo sapiens

<400> 139

```

Met Ala Leu Tyr Asp Glu Asp Leu Leu Lys Asn Pro Phe Tyr Leu Ala
 1           5           10           15
Leu Gln Lys Cys Arg Pro Asp Leu Cys Ser Lys Val Ala Gln Ile His
          20           25           30
Gly Ile Val Leu Val Pro Cys Lys Gly Ser Leu Ser Ser Ser Ile Gln
          35           40           45
Ser Thr Cys Gln Phe Glu Ser Tyr Ile Leu Ile Pro Val Glu Glu His
          50           55           60
Phe Gln Thr Leu Asn Gly Lys Asp Val Phe Ile Gln Gly Asn Arg Ile
          65           70           75           80
Lys Leu Gly Ala Gly Phe Ala Cys Leu Leu Ser Val Pro Ile Leu Phe
          85           90           95
Glu Glu Thr Phe Tyr Asn Glu Lys Glu Glu Ser Phe Ser Ile Leu Cys
          100          105          110
Ile Ala His Pro Leu Glu Lys Arg Glu Ser Ser Glu Glu Pro Leu Ala

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			115						120						125		
Pro	Ser	Asp	Pro	Phe	Ser	Leu	Lys	Thr	Ile	Glu	Asp	Val	Arg	Glu	Phe		
	130						135						140				
Leu	Gly	Arg	His	Ser	Glu	Arg	Phe	Asp	Arg	Asn	Ile	Ala	Ser	Phe	His		
145					150					155					160		
Arg	Thr	Phe	Arg	Glu	Cys	Glu	Arg	Lys	Ser	Leu	Arg	His	His	Ile	Asp		
				165						170					175		
Ser	Ala	Asn	Ala	Leu	Tyr	Thr	Lys	Cys	Leu	Gln	Gln	Leu	Leu	Arg	Asp		
				180						185			190				
Ser	His	Leu	Lys	Met	Leu	Ala	Lys	Gln	Glu	Ala	Gln	Met	Asn	Leu	Met		
		195					200						205				
Lys	Gln	Ala	Val	Glu	Ile	Tyr	Val	His	His	Glu	Ile	Tyr	Asn	Leu	Ile		
	210						215						220				
Phe	Lys	Tyr	Val	Gly	Thr	Met	Glu	Ala	Ser	Glu	Asp	Ala	Ala	Phe	Asn		
225					230					235					240		
Lys	Ile	Thr	Arg	Ser	Leu	Gln	Asp	Leu	Gln	Gln	Lys	Asp	Ile	Gly	Val		
				245						250					255		
Lys	Pro	Glu	Phe	Ser	Phe	Asn	Ile	Pro	Arg	Ala	Lys	Arg	Glu	Leu	Ala		
				260						265			270				
Gln	Leu	Asn	Lys	Cys	Thr	Ser	Pro	Gln	Gln	Lys	Leu	Val	Cys	Leu	Arg		
		275					280						285				
Lys	Val	Val	Gln	Leu	Ile	Thr	Gln	Ser	Pro	Ser	Gln	Arg	Val	Asn	Leu		
	290						295						300				
Glu	Thr	Met	Cys	Ala	Asp	Asp	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Leu	Leu		
305					310					315					320		
Val	Lys	Thr	Glu	Ile	Pro	Asn	Trp	Met	Ala	Asn	Leu	Ser	Tyr	Ile	Lys		
				325						330					335		
Asn	Phe	Arg	Phe	Ser	Ser	Leu	Ala	Lys	Asp	Glu	Leu	Gly	Tyr	Cys	Leu		
				340						345			350				
Thr	Ser	Phe	Glu	Ala	Ala	Ile	Glu	Tyr	Ile	Arg	Gln	Gly	Ser	Leu	Ser		
		355					360						365				
Ala	Lys	Pro	Pro	Glu	Ser	Glu	Gly	Phe	Gly	Asp	Arg	Leu	Phe	Leu	Lys		
		370					375						380				
Gln	Arg	Met	Ser	Leu	Leu	Ser	Gln	Met	Thr	Ser	Ser	Pro	Thr	Asp	Cys		
385					390					395					400		
Leu	Phe	Lys	His	Ile	Ala	Ser	Gly	Asn	Gln	Lys	Glu	Val	Glu	Arg	Leu		
				405						410					415		
Leu	Ser	Gln	Glu	Asp	His	Asp	Lys	Asp	Thr	Val	Gln	Lys	Met	Cys	His		
				420						425			430				
Pro	Leu	Cys	Phe	Cys	Asp	Asp	Cys	Glu	Lys	Leu	Val	Ser	Gly	Arg	Leu		
		435					440						445				

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<210> 140
<211> 232
<212> PRT
<213> Homo sapiens
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<400> 140
 Met Ala Thr Gly Ile Arg Leu Pro Ala Leu Pro Ala Ser Pro Arg Val
 1 5 10 15
 Pro Ser Glu Gly Pro Gly Phe Ser Glu His Pro Glu Gly Pro Pro Ala
 20 25 30
 Leu Pro Pro Ala Ile Pro Phe Ser Phe Thr Leu Leu Val Gln Ala Val
 35 40 45
 Phe Phe Leu Tyr Gln Ala Trp Trp Leu Leu His Gly Ala Pro Gln Gly
 50 55 60
 Lys Gly Trp Pro Gln Ala Ser Gly Leu Glu Asp Arg Val Thr Arg Glu
 65 70 75 80
 Glu Gly Ser Pro Arg Gly Pro Ser Ile Ser Leu Asn Cys Gly Cys Pro
 85 90 95
 Ala Trp Val Pro Cys Glu Arg Pro Ala Cys Val Gly Trp Gly Gly Pro
 100 105 110
 Pro Gln Pro Pro Gly Ala Ile Cys Glu Ala Thr Ala Pro Pro Ser Ile
 115 120 125
 Phe Leu Pro Phe Pro Phe Gln Pro Leu Phe Gln Glu Pro Cys His Thr
 130 135 140
 His Thr Cys Ser Leu Pro Ser Pro Ala Leu Pro Pro Leu Leu Arg Arg
 145 150 155 160
 Gly Arg Pro Arg Pro Cys Ala Ala Leu Ala Leu Pro Ala Leu Ser Ser
 165 170 175
 Leu Phe Ser Pro Val Phe Ser Leu Leu Ser Leu Gln Leu Pro Ala Asp
 180 185 190
 Arg Val Arg Gln Val His Pro Val Leu Arg Ala Pro Gly Pro Pro Ser
 195 200 205
 Thr Ser Lys Gln Ile Pro Pro Leu Leu Gly Asp Leu Pro Phe Gln Ala
 210 215 220
 Cys Leu Asp Gly Cys Ser Val Thr
 225 230

<210> 141
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 141
 Met Thr Ser Ile Ile Lys Leu Thr Thr Leu Ser Gly Val Gln Glu Glu
 1 5 10 15
 Ser Ala Leu Cys Tyr Leu Leu Gln Val Asp Glu Phe Arg Phe Leu Leu
 20 25 30
 Asp Cys Gly Trp Asp Glu His Phe Ser Met Asp Ile Ile Asp Ser Leu
 35 40 45
 Arg Lys His Val His Gln Ile Asp Ala Val Leu Leu Ser His Pro Asp
 50 55 60
 Pro Leu His Leu Gly Ala Leu Pro Tyr Ala Val Gly Lys Leu Gly Leu
 65 70 75 80
 Asn Cys Ala Ile Tyr Ala Thr Ile Pro Val Tyr Lys Met Gly Gln Met
 85 90 95
 Phe Met Tyr Asp Leu Tyr Gln Val Ile
 100 105

<210> 142
 <211> 333

<212> PRT

<213> Homo sapiens

<400> 142

```

Met Asn Leu Ser Leu Val Leu Ala Ala Phe Cys Leu Gly Ile Ala Ser
 1           5           10           15
Ala Val Pro Lys Phe Asp Gln Asn Leu Asp Thr Lys Trp Tyr Gln Trp
          20           25           30
Lys Ala Thr His Arg Arg Leu Tyr Gly Ala Asn Glu Glu Gly Trp Arg
          35           40           45
Arg Ala Val Trp Glu Lys Asn Met Lys Met Ile Glu Leu His Asn Gly
          50           55           60
Glu Tyr Ser Gln Gly Lys His Ser Phe Thr Met Ala Met Asn Ala Phe
          65           70           75           80
Gly Asp Met Thr Asn Glu Glu Phe Arg Gln Val Met Asn Gly Phe Gln
          85           90           95
Tyr Gln Lys His Arg Lys Gly Lys Gln Phe Gln Glu Arg Leu Leu Leu
          100          105          110
Glu Ile Pro Thr Ser Val Asp Trp Arg Glu Lys Gly Tyr Met Thr Pro
          115          120          125
Val Lys Asp Gln Gly Gln Cys Gly Ser Cys Trp Ala Phe Ser Ala Thr
          130          135          140
Gly Ala Leu Glu Gly Gln Met Phe Trp Lys Thr Gly Lys Leu Ile Ser
145          150          155          160
Leu Asn Glu Gln Asn Leu Val Asp Cys Ser Gly Pro Gln Gly Asn Glu
          165          170          175
Gly Cys Asn Gly Asp Phe Met Asp Asn Pro Phe Arg Tyr Val Gln Glu
          180          185          190
Asn Gly Gly Leu Asp Ser Glu Glu Ser Tyr Pro Tyr Glu Ala Thr Glu
          195          200          205
Glu Ser Cys Lys Tyr Asn Pro Lys Tyr Ser Val Ala Asn Asp Thr Gly
          210          215          220
Phe Val Asp Ile Pro Lys Gln Glu Lys Ala Leu Met Lys Ala Val Ala
225          230          235          240
Thr Val Gly Pro Ile Ser Val Ala Ile Asp Ala Gly His Glu Ser Phe
          245          250          255
Leu Phe Tyr Lys Glu Gly Ile Tyr Phe Glu Pro Asp Cys Ser Ser Glu
          260          265          270
Asp Met Asp His Gly Val Leu Val Val Gly Tyr Gly Phe Glu Ser Thr
          275          280          285
Glu Ser Asp Asn Asn Lys Tyr Trp Leu Val Lys Asn Ser Trp Gly Glu
          290          295          300
Glu Trp Gly Met Gly Gly Tyr Val Lys Met Ala Lys Asp Arg Arg Asn
305          310          315          320
His Cys Gly Ile Ala Ser Ala Ala Ser Tyr Pro Thr Val
          325          330

```

<210> 143

<211> 208

<212> PRT

<213> Homo sapiens

<400> 143

```

Met Leu Gly Cys Gln Gly Arg Met Tyr Thr Leu Leu Ser Gly Leu Tyr
 1           5           10           15
Lys Tyr Met Phe Gln Lys Asp Glu Tyr Cys Ile Leu Ile Leu Gly Leu
          20           25           30

```

```

Asp Asn Ala Gly Lys Thr Thr Phe Leu Glu Gln Ser Lys Thr Arg Phe
      35              40              45
Asn Lys Asn Tyr Lys Gly Met Ser Leu Ser Lys Ile Thr Thr Thr Val
      50              55              60
Gly Leu Asn Ile Gly Thr Val Asp Val Gly Lys Ala Arg Leu Met Phe
      65              70              75
Trp Asp Leu Gly Gly Gln Glu Glu Leu Gln Ser Leu Trp Asp Lys Tyr
      85              90              95
Tyr Ala Glu Cys His Gly Val Ile Tyr Val Ile Asp Ser Thr Asp Glu
      100             105             110
Glu Arg Leu Ala Glu Ser Lys Gln Ala Phe Glu Lys Val Val Thr Ser
      115             120             125
Glu Ala Leu Cys Gly Val Pro Val Leu Val Leu Ala Asn Lys Gln Asp
      130             135             140
Val Glu Thr Cys Leu Ser Ile Pro Asp Ile Lys Thr Ala Phe Ser Asp
      145             150             155
Cys Thr Ser Lys Ile Gly Arg Arg Asp Cys Leu Thr Gln Ala Cys Ser
      165             170             175
Ala Leu Thr Gly Lys Gly Val Arg Glu Gly Ile Glu Trp Met Val Lys
      180             185             190
Cys Val Val Arg Asn Val His Arg Pro Pro Arg Gln Arg Asp Ile Thr
      195             200             205

```

```

<210> 144
<211> 229
<212> PRT
<213> Homo sapiens

```

```

<400> 144
Met Leu Ser Val Asp Ile Thr Ser Arg Tyr Arg Ala Pro Ser Thr Tyr
  1              5              10              15
Leu Leu Asn Ser Leu Lys Glu Gly Leu Glu Gly Leu His Gly Glu Ser
      20              25              30
Cys Ser Ser Phe Leu Leu Gly Pro Ser Val Ala Met Asn Met Gln Thr
      35              40              45
Ala Gly Leu Glu Met Asp Ile Cys Asp Gly His Phe Arg Gln Asn Gly
      50              55              60
Gly Cys Gly Tyr Val Leu Lys Pro Asp Phe Leu Arg Asp Ile Gln Ser
      65              70              75
Ser Phe His Pro Glu Lys Pro Ile Ser Pro Phe Lys Ala Gln Thr Leu
      85              90              95
Leu Ile Gln Val Ile Ser Gly Gln Gln Leu Pro Lys Val Asp Lys Thr
      100             105             110
Lys Glu Gly Ser Ile Val Asp Pro Leu Val Lys Val Gln Ile Phe Gly
      115             120             125
Val Arg Leu Asp Thr Ala Arg Gln Glu Thr Asn Tyr Val Glu Asn Asn
      130             135             140
Gly Phe Asn Pro Tyr Trp Gly Gln Thr Leu Cys Phe Arg Val Leu Val
      145             150             155
Pro Glu Leu Ala Met Leu Arg Phe Val Val Met Asp Tyr Asp Trp Lys
      165             170             175
Ser Arg Asn Asp Phe Ile Gly Gln Tyr Thr Leu Pro Trp Thr Cys Met
      180             185             190
Gln Gln Gly Tyr Arg His Ile His Leu Leu Ser Lys Asp Gly Ile Ser
      195             200             205
Leu Arg Pro Ala Ser Ile Phe Val Tyr Ile Cys Ile Gln Glu Gly Leu

```

210
Glu Gly Asp Glu Ser
225

215

220

<210> 145
<211> 223
<212> PRT
<213> Homo sapiens

<400> 145
Met Arg Gly Pro Gly Gln Ala Asp Cys Ala Val Ala Ile Gly Arg Pro
1 5 10 15
Leu Gly Glu Val Val Thr Leu Arg Val Leu Glu Ser Ser Leu Asn Cys
20 25 30
Ser Ala Gly Asp Met Leu Leu Leu Trp Gly Arg Leu Thr Trp Arg Lys
35 40 45
Met Cys Arg Lys Leu Leu Asp Met Thr Phe Ser Ser Lys Thr Asn Thr
50 55 60
Leu Val Val Arg Gln Arg Cys Gly Arg Pro Gly Gly Gly Val Leu Leu
65 70 75 80
Arg Tyr Gly Ser Gln Leu Ala Pro Glu Thr Phe Tyr Arg Glu Cys Asp
85 90 95
Met Gln Leu Phe Gly Pro Trp Gly Glu Ile Val Ser Pro Ser Leu Ser
100 105 110
Pro Ala Thr Ser Asn Ala Gly Gly Cys Arg Leu Phe Ile Asn Val Ala
115 120 125
Pro His Ala Arg Ile Ala Ile His Ala Leu Ala Thr Asn Met Gly Ala
130 135 140
Gly Thr Glu Gly Ala Asn Ala Ser Tyr Ile Leu Ile Arg Asp Thr His
145 150 155 160
Ser Leu Arg Thr Thr Ala Phe His Gly Gln Gln Val Leu Tyr Trp Glu
165 170 175
Ser Glu Ser Ser Gln Ala Glu Met Glu Phe Ser Glu Gly Phe Leu Lys
180 185 190
Ala Gln Ala Ser Leu Arg Gly Gln Tyr Trp Thr Leu Gln Ser Trp Val
195 200 205
Pro Glu Met Gln Asp Pro Gln Ser Trp Lys Gly Lys Glu Gly Thr
210 215 220

<210> 146
<211> 73
<212> PRT
<213> Homo sapiens

<400> 146
Met Thr Asp Pro Asp Gly Asn Pro Lys Cys Leu Thr Lys Ile Asn Tyr
1 5 10 15
Gly Gly Glu Val Pro Lys Ser Tyr Tyr Leu Cys Lys Gln Val Arg Leu
20 25 30
Gln Tyr Glu His Thr Arg Ser Val Gly Arg Gly Ser Ser Leu Gln Val
35 40 45
Glu Asn Glu Ile Leu Phe Pro Gly Cys Val Leu Arg Cys Pro Glu Val
50 55 60
Leu Gln His Leu Gln Pro Gly Ser Phe
65 70

<210> 147
 <211> 202
 <212> PRT
 <213> Homo sapiens

<400> 147
 Met Ala Glu Tyr Leu Ala Ser Ile Phe Gly Thr Glu Lys Asp Lys Val
 1 5 10 15
 Asn Cys Ser Phe Tyr Phe Lys Ile Gly Val Cys Arg His Gly Asp Arg
 20 25 30
 Cys Ser Arg Leu His Asn Lys Pro Thr Phe Ser Gln Glu Val Phe Thr
 35 40 45
 Glu Leu Gln Glu Lys Tyr Gly Glu Ile Glu Glu Met Asn Val Cys Asp
 50 55 60
 Asn Leu Gly Asp His Leu Val Gly Asn Val Tyr Val Lys Phe Arg Arg
 65 70 75 80
 Glu Glu Asp Gly Glu Arg Ala Val Ala Glu Leu Ser Asn Arg Trp Phe
 85 90 95
 Asn Gly Gln Ala Val His Gly Asn Val Pro Glu Val Ala Ser Ala Thr
 100 105 110
 Ser Cys Ile Cys Gly Pro Phe Pro Arg Thr Ser Arg Gly Ser Ser Met
 115 120 125
 Gly Gly Asp Pro Gly Ala Gly His Pro Arg Gly Ser Ile Leu Ala Thr
 130 135 140
 Ile Pro Glu Arg Gly Thr Ile Gly Val Pro Leu Ile Thr Gly Met Ala
 145 150 155 160
 Ala Ser Glu Ala Leu Ala Pro Leu Pro Phe Thr Pro Asn Arg Asp Arg
 165 170 175
 Cys Ser Trp Gln Asp Leu Ser Ser Lys Pro Pro Ser Leu Ser Cys Pro
 180 185 190
 Ile Leu Pro Arg Leu Pro Gly Ser Ile Met
 195 200

<210> 148
 <211> 241
 <212> PRT
 <213> Homo sapiens

<400> 148
 Met Ala Glu Tyr Leu Ala Ser Ile Phe Gly Thr Glu Lys Asp Lys Val
 1 5 10 15
 Asn Cys Ser Phe Tyr Phe Lys Ile Gly Ala Cys Arg His Gly Asp Arg
 20 25 30
 Cys Ser Arg Leu His Asn Lys Pro Thr Phe Ser Gln Thr Ile Val Leu
 35 40 45
 Leu Asn Leu Tyr Arg Asn Pro Gln Asn Thr Ala Gln Thr Ala Asp Gly
 50 55 60
 Ser His Cys His Val Ser Asp Val Glu Val Gln Glu His Tyr Asp Ser
 65 70 75 80
 Phe Phe Glu Glu Val Phe Thr Glu Leu Gln Glu Lys Tyr Gly Glu Ile
 85 90 95
 Glu Glu Met Asn Val Cys Asp Asn Leu Gly Asp His Leu Val Gly Asn
 100 105 110
 Val Tyr Val Lys Phe Arg Arg Glu Glu Asp Gly Glu Arg Ala Val Ala

```

      115      120      125
Glu Leu Ser Asn Arg Trp Phe Asn Gly Gln Ala Val His Gly Asn Val
130      135      140
Pro Glu Val Ala Ser Ala Thr Ser Cys Ile Cys Gly Pro Phe Pro Arg
145      150      155      160
Thr Ser Arg Gly Ser Ser Met Gly Gly Asp Pro Gly Ala Gly His Pro
      165      170      175
Arg Gly Ser Ile Leu Ala Thr Ile Pro Glu Arg Gly Thr Ile Val Val
      180      185      190
Pro Leu Ile Thr Gly Met Ala Ala Ser Glu Ala Leu Ala Pro Leu Pro
      195      200      205
Phe Thr Pro Asn Arg Asp Arg Cys Ser Trp Gln Asp Leu Ser Ser Lys
      210      215      220
Pro Pro Ser Leu Ser Cys Pro Ile Leu Pro Arg Leu Pro Gly Ser Ile
225      230      235      240
Met

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```

<210> 149
<211> 794
<212> PRT
<213> Homo sapiens

```

```

      <400> 149
Met Leu Cys Gly Arg Trp Arg Arg Cys Arg Arg Pro Pro Glu Glu Pro
1      5      10      15
Pro Val Ala Ala Gln Val Ala Ala Gln Val Ala Ala Pro Val Ala Leu
      20      25      30
Pro Ser Pro Pro Thr Pro Ser Asp Gly Gly Thr Lys Arg Pro Gly Leu
      35      40      45
Arg Ala Leu Lys Lys Met Gly Leu Thr Glu Asp Glu Asp Val Arg Ala
      50      55      60
Met Leu Arg Gly Ser Arg Leu Arg Lys Ile Arg Ser Arg Thr Trp His
      65      70      75      80
Lys Glu Arg Leu Tyr Arg Leu Gln Glu Asp Gly Leu Ser Val Trp Phe
      85      90      95
Gln Arg Arg Ile Pro Arg Ala Pro Ser Gln His Ile Phe Phe Val Gln
      100      105      110
His Ile Glu Ala Val Arg Glu Gly His Gln Ser Glu Gly Leu Arg Arg
      115      120      125
Phe Gly Gly Ala Phe Ala Pro Ala Arg Cys Leu Thr Ile Ala Phe Lys
      130      135      140
Gly Arg Arg Lys Asn Leu Asp Leu Ala Ala Pro Thr Ala Glu Glu Ala
145      150      155      160
Gln Arg Trp Val Arg Gly Leu Thr Lys Leu Arg Ala Arg Leu Asp Ala
      165      170      175
Met Ser Gln Arg Glu Arg Leu Asp His Trp Ile His Ser Tyr Leu His
      180      185      190
Arg Ala Asp Ser Asn Gln Asp Ser Lys Met Ser Phe Lys Glu Ile Lys
      195      200      205
Ser Leu Leu Arg Met Val Asn Val Asp Met Asn Asp Met Tyr Ala Tyr
      210      215      220
Leu Leu Phe Lys Glu Cys Asp His Ser Asn Asn Asp Arg Leu Glu Gly
225      230      235      240
Ala Glu Ile Glu Glu Phe Leu Arg Arg Leu Leu Lys Arg Pro Glu Leu
      245      250      255
Glu Glu Ile Phe His Gln Tyr Ser Gly Glu Asp Arg Val Leu Ser Ala
      260      265      270

```

Pro	Glu	Leu	Leu	Glu	Phe	Leu	Glu	Asp	Gln	Gly	Glu	Glu	Gly	Ala	Thr
	275						280					285			
Leu	Ala	Arg	Ala	Gln	Gln	Leu	Ile	Gln	Thr	Tyr	Glu	Leu	Asn	Glu	Thr
	290						295					300			
Ala	Lys	Gln	His	Glu	Leu	Met	Thr	Leu	Asp	Gly	Phe	Met	Met	Tyr	Leu
305					310					315					320
Leu	Ser	Pro	Glu	Gly	Ala	Ala	Leu	Asp	Asn	Thr	His	Thr	Cys	Val	Phe
				325					330					335	
Gln	Asp	Met	Asn	Gln	Pro	Leu	Ala	His	Tyr	Phe	Ile	Ser	Ser	Ser	His
			340					345						350	
Asn	Thr	Tyr	Leu	Thr	Asp	Ser	Gln	Ile	Gly	Gly	Pro	Ser	Ser	Thr	Glu
	355						360							365	
Ala	Tyr	Val	Arg	Tyr	Cys	Ser	Arg	Gly	Ala	Phe	Ala	Gln	Gly	Cys	Arg
	370						375					380			
Cys	Val	Glu	Leu	Asp	Cys	Trp	Glu	Gly	Pro	Gly	Gly	Glu	Pro	Val	Ile
385					390					395					400
Tyr	His	Gly	His	Thr	Leu	Thr	Ser	Lys	Ile	Leu	Phe	Arg	Asp	Val	Val
				405					410					415	
Gln	Ala	Val	Arg	Asp	His	Ala	Phe	Thr	Leu	Ser	Pro	Tyr	Pro	Val	Ile
			420					425						430	
Leu	Ser	Leu	Glu	Asn	His	Cys	Gly	Leu	Glu	Gln	Gln	Ala	Ala	Met	Ala
			435				440						445		
Arg	His	Leu	Cys	Thr	Ile	Leu	Gly	Asp	Met	Leu	Val	Thr	Gln	Ala	Leu
	450						455					460			
Asp	Ser	Pro	Asn	Pro	Glu	Glu	Leu	Pro	Ser	Pro	Glu	Gln	Leu	Lys	Gly
465					470						475				480
Arg	Val	Leu	Val	Lys	Gly	Lys	Lys	Leu	Pro	Ala	Ala	Arg	Ser	Glu	Asp
				485					490					495	
Gly	Arg	Ala	Leu	Ser	Asp	Arg	Glu	Glu	Glu	Glu	Glu	Asp	Asp	Glu	Glu
			500					505					510		
Glu	Glu	Glu	Glu	Val	Glu	Ala	Ala	Ala	Gln	Arg	Arg	Leu	Ala	Lys	Gln
		515					520						525		
Ile	Ser	Pro	Glu	Leu	Ser	Ala	Leu	Ala	Val	Tyr	Cys	His	Ala	Thr	Arg
	530					535					540				
Leu	Arg	Thr	Leu	His	Pro	Ala	Pro	Asn	Ala	Pro	Gln	Pro	Cys	Gln	Val
545					550					555					560
Ser	Ser	Leu	Ser	Glu	Arg	Lys	Ala	Lys	Lys	Leu	Ile	Arg	Glu	Ala	Gly
				565					570					575	
Asn	Ser	Phe	Val	Arg	His	Asn	Ala	Arg	Gln	Leu	Thr	Arg	Val	Tyr	Pro
			580					585						590	
Leu	Gly	Leu	Arg	Met	Asn	Ser	Ala	Asn	Tyr	Ser	Pro	Gln	Glu	Met	Trp
			595				600					605			
Asn	Ser	Gly	Cys	Gln	Leu	Val	Ala	Leu	Asn	Phe	Gln	Thr	Pro	Gly	Tyr
	610					615					620				
Glu	Met	Asp	Leu	Asn	Ala	Gly	Arg	Phe	Leu	Val	Asn	Gly	Gln	Cys	Gly
625					630					635					640
Tyr	Val	Leu	Lys	Pro	Ala	Cys	Leu	Arg	Gln	Pro	Asp	Ser	Thr	Phe	Asp
				645					650					655	
Pro	Glu	Tyr	Pro	Gly	Pro	Pro	Arg	Thr	Thr	Leu	Ser	Ile	Gln	Val	Leu
			660					665						670	
Thr	Ala	Gln	Gln	Leu	Pro	Lys	Leu	Asn	Ala	Glu	Lys	Pro	His	Ser	Ile
		675					680						685		
Val	Asp	Pro	Leu	Val	Arg	Ile	Glu	Ile	His	Gly	Val	Pro	Ala	Asp	Cys
	690					695					700				
Ala	Arg	Gln	Glu	Thr	Asp	Tyr	Val	Leu	Asn	Asn	Gly	Phe	Asn	Pro	Arg
705					710					715					720
Trp	Gly	Gln	Thr	Leu	Gln	Phe	Gln	Leu	Arg	Ala	Pro	Glu	Leu	Ala	Leu
				725					730					735	
Val	Arg	Phe	Val	Val	Glu	Asp	Tyr	Asp	Ala	Thr	Ser	Pro	Asn	Asp	Phe
			740				745						750		
Val	Gly	Gln	Phe	Thr	Leu	Pro	Leu	Ser	Ser	Leu	Lys	Gln	Gly	Tyr	Arg

	755		760		765
His	Ile	His	Leu	Leu	Ser
	770		775		780
Leu	Phe	Ile	Gln	Ile	Arg
785			790		

<210> 150
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 150															
Met	Ala	Ala	Val	Pro	Met	Val	Leu	Ser	Ala	Met	Gly	Phe	Thr	Ala	Ala
1				5					10					15	
Gly	Ile	Ala	Ser	Ser	Ser	Ile	Ala	Ala	Lys	Met	Met	Ser	Ala	Ala	Ala
			20					25					30		
Ile	Ala	Asn	Gly	Gly	Gly	Val	Ser	Ala	Gly	Ser	Leu	Val	Ala	Thr	Leu
		35					40					45			
Gln	Ser	Val	Gly	Ala	Ala	Gly	Leu	Ser	Thr	Ser	Ser	Asn	Ile	Leu	Leu
	50					55				60					
Ala	Ser	Val	Gly	Ser	Val	Leu	Gly	Ala	Cys	Leu	Gly	Asn	Ser	Pro	Ser
65					70				75					80	
Ser	Ser	Leu	Pro	Ala	Glu	Pro	Glu	Ala	Lys	Glu	Asp	Glu	Ala	Arg	Glu
				85				90					95		
Asn	Val	Pro	Gln	Gly	Glu	Pro	Pro	Lys	Pro	Pro	Leu	Lys	Ser	Glu	Lys
			100					105					110		
His	Glu	Glu													
		115													

<210> 151
 <211> 294
 <212> PRT
 <213> Homo sapiens

<400> 151															
Met	Ala	Gln	Ala	Pro	Ala	Asp	Pro	Gly	Arg	Glu	Ala	Lys	Arg	Pro	Gln
1				5					10					15	
Gln	His	Ala	Ala	Thr	Ile	Pro	Glu	Thr	Pro	Gly	Pro	Gln	Phe	Ser	Gln
			20					25					30		
Gln	Arg	Glu	Glu	Asp	Ile	Tyr	Arg	Phe	Leu	Lys	Asp	Asn	Gly	Pro	Gln
	35					40					45				
Arg	Ala	Leu	Val	Ile	Ala	Gln	Ala	Leu	Gly	Met	Arg	Thr	Ala	Lys	Asp
	50					55				60					
Val	Asn	Arg	Asp	Leu	Tyr	Arg	Met	Lys	Ser	Arg	His	Leu	Leu	Asp	Met
65					70				75					80	
Asp	Glu	Gln	Ser	Lys	Ala	Trp	Thr	Ile	Tyr	Arg	Pro	Glu	Asp	Ser	Gly
				85				90					95		
Arg	Arg	Ala	Lys	Ser	Ala	Ser	Ile	Ile	Tyr	Gln	His	Asn	Pro	Ile	Asn
			100					105					110		
Met	Ile	Cys	Gln	Asn	Gly	Pro	Asn	Ser	Trp	Ile	Ser	Ile	Ala	Asn	Ser
	115					120					125				
Glu	Ala	Ile	Gln	Ile	Gly	His	Gly	Asn	Ile	Ile	Thr	Arg	Gln	Thr	Val
	130				135				140						
Ser	Arg	Glu	Asp	Gly	Ser	Ala	Gly	Pro	Arg	His	Leu	Pro	Ser	Met	Ala
145					150				155						160

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<210> 152
<211> 328
<212> PRT
<213> Homo sapiens
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299

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                260                265                270
Gln His Ser Thr Lys Gly Pro Pro Arg Ser Gly Lys Thr Pro Ala Ser
      275                280                285
Ile Arg Lys Pro Pro Ser Ser Val Lys Asp Ala Asp Ser Gly Asp Lys
      290                295                300
Lys Pro Thr Ala Lys Lys Lys Glu Asp Asp Asp His Tyr Phe Val Met
305                310                315                320
Thr Gly Ser Lys Lys Pro Arg Lys
                325

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<210> 153
<211> 1651
<212> PRT
<213> Homo sapiens

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Met Ala Pro Thr Leu Phe Gln Lys Leu Phe Ser Lys Arg Thr Gly Leu
  1                5                10                15
Gly Ala Pro Gly Arg Asp Ala Arg Asp Pro Asp Cys Gly Phe Ser Trp
      20                25                30
Pro Leu Pro Glu Phe Asp Pro Ser Gln Ile Arg Leu Ile Val Tyr Gln
      35                40                45
Asp Cys Glu Arg Arg Gly Arg Asn Val Leu Phe Asp Ser Ser Val Lys
      50                55                60
Arg Arg Asn Glu Asp Ile Ser Val Ser Asp Leu Asn Thr Ile Tyr Ser
      65                70                75                80
Tyr Leu His Gly Met Glu Ile Leu Ser Asn Leu Arg Glu His Gln Leu
      85                90                95
Arg Leu Met Ser Ala Arg Ala Arg Tyr Glu Arg Tyr Ser Gly Asn Gln
      100                105                110
Val Leu Phe Cys Ser Glu Thr Ile Ala Arg Cys Trp Tyr Ile Leu Leu
      115                120                125
Ser Gly Ser Val Leu Val Lys Gly Ser Met Val Leu Pro Pro Cys Ser
      130                135                140
Phe Gly Lys Gln Phe Gly Gly Lys Arg Gly Cys Asp Cys Leu Val Leu
145                150                155                160
Glu Pro Ser Glu Met Ile Val Val Glu Asn Ala Lys Asp Asn Glu Asp
      165                170                175
Ser Ile Leu Gln Arg Glu Ile Pro Ala Arg Gln Ser Arg Arg Arg Phe
      180                185                190
Arg Lys Ile Asn Tyr Lys Gly Glu Arg Gln Thr Ile Thr Asp Asp Val
      195                200                205
Glu Val Asn Ser Tyr Leu Ser Leu Pro Ala Asp Leu Thr Lys Met His
      210                215                220
Leu Thr Glu Asn Pro His Pro Gln Val Thr His Val Ser Ser Ser Gln
225                230                235                240
Ser Gly Cys Ser Ile Ala Ser Asp Ser Gly Ser Ser Ser Leu Ser Asp
      245                250                255
Ile Tyr Gln Ala Thr Glu Ser Glu Val Gly Asp Val Asp Leu Thr Arg
      260                265                270
Leu Pro Glu Gly Pro Val Asp Ser Glu Asp Asp Glu Glu Glu Asp Glu
      275                280                285
Glu Ile Asp Arg Thr Asp Pro Leu Gln Gly Arg Asp Leu Val Arg Glu
      290                295                300
Cys Leu Glu Lys Glu Pro Ala Asp Lys Thr Asp Asp Asp Ile Glu Gln
305                310                315                320
Leu Leu Glu Phe Met His Gln Leu Pro Ala Phe Ala Asn Met Thr Met
      325                330                335

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Ser Val Arg Arg Glu Leu Cys Ser Val Met Ile Phe Glu Val Val Glu
 340 345 350
 Gln Ala Gly Ala Ile Ile Leu Glu Asp Gly Gln Glu Leu Asp Ser Trp
 355 360 365
 Tyr Val Ile Leu Asn Gly Thr Val Glu Ile Ser His Pro Asp Gly Lys
 370 375 380
 Val Glu Asn Leu Phe Met Gly Asn Ser Phe Gly Ile Thr Pro Thr Leu
 385 390 395 400
 Asp Lys Gln Tyr Met His Gly Ile Val Arg Thr Lys Val Asp Asp Cys
 405 410 415
 Gln Phe Val Cys Ile Ala Gln Gln Asp Tyr Trp Arg Ile Leu Asn His
 420 425 430
 Val Glu Lys Asn Thr His Lys Val Glu Glu Gly Glu Ile Val Met
 435 440 445
 Val His Glu His Arg Glu Leu Asp Arg Ser Gly Thr Arg Lys Gly His
 450 455 460
 Ile Val Ile Lys Ala Thr Pro Glu Arg Leu Ile Met His Leu Ile Glu
 465 470 475 480
 Glu His Ser Ile Val Asp Pro Thr Tyr Ile Glu Asp Phe Leu Leu Thr
 485 490 495
 Tyr Arg Thr Phe Leu Glu Ser Pro Leu Asp Val Gly Ile Lys Leu Leu
 500 505 510
 Glu Trp Phe Lys Ile Asp Ser Leu Arg Asp Lys Val Thr Arg Ile Val
 515 520 525
 Leu Leu Trp Val Asn Asn His Phe Asn Asp Phe Glu Gly Asp Pro Ala
 530 535 540
 Met Thr Arg Phe Leu Glu Glu Phe Glu Lys Asn Leu Glu Asp Thr Lys
 545 550 555 560
 Met Asn Gly His Leu Arg Leu Leu Asn Ile Ala Cys Ala Ala Lys Ala
 565 570 575
 Lys Trp Arg Gln Val Val Leu Gln Lys Ala Ser Arg Glu Ser Pro Leu
 580 585 590
 Gln Phe Ser Leu Asn Gly Gly Ser Glu Lys Gly Phe Gly Ile Phe Val
 595 600 605
 Glu Gly Val Glu Pro Gly Ser Lys Ala Ala Asp Ser Gly Leu Lys Arg
 610 615 620
 Gly Asp Gln Ile Met Glu Val Asn Gly Gln Asn Phe Glu Asn Ile Thr
 625 630 635 640
 Phe Met Lys Ala Val Glu Ile Leu Arg Asn Asn Thr His Leu Ala Leu
 645 650 655
 Thr Val Lys Thr Asn Ile Phe Val Phe Lys Glu Leu Leu Phe Arg Thr
 660 665 670
 Glu Gln Glu Lys Ser Gly Val Pro His Ile Pro Lys Ile Ala Glu Lys
 675 680 685
 Lys Ser Asn Arg His Ser Ile Gln His Val Pro Gly Asp Ile Glu Gln
 690 695 700
 Thr Ser Gln Glu Lys Gly Ser Lys Lys Val Lys Ala Asn Thr Val Ser
 705 710 715 720
 Gly Gly Arg Asn Lys Ile Arg Lys Ile Leu Asp Lys Thr Arg Phe Ser
 725 730 735
 Ile Leu Pro Pro Lys Leu Phe Ser Asp Gly Gly Leu Ser Gln Ser Gln
 740 745 750
 Asp Asp Ser Ile Val Gly Thr Arg His Cys Arg His Ser Leu Ala Ile
 755 760 765
 Met Pro Ile Pro Gly Thr Leu Ser Ser Ser Ser Pro Asp Leu Leu Gln
 770 775 780
 Pro Thr Thr Ser Met Leu Asp Phe Ser Asn Pro Ser Asp Ile Pro Asp
 785 790 795 800
 Gln Val Ile Arg Val Phe Lys Val Asp Gln Gln Ser Cys Tyr Ile Ile
 805 810 815
 Ile Ser Lys Asp Thr Thr Ala Lys Glu Val Val Phe His Ala Val His

			820					825				830			
Glu	Phe	Gly	Leu	Thr	Gly	Ala	Ser	Asp	Thr	Tyr	Ser	Leu	Cys	Glu	Val
		835						840				845			
Ser	Val	Thr	Pro	Glu	Gly	Val	Ile	Lys	Gln	Arg	Arg	Leu	Pro	Asp	Gln
		850				855						860			
Phe	Ser	Lys	Leu	Ala	Asp	Arg	Ile	Gln	Leu	Asn	Gly	Arg	Tyr	Tyr	Leu
865					870					875					880
Lys	Asn	Asn	Met	Glu	Thr	Glu	Thr	Leu	Cys	Ser	Asp	Glu	Asp	Ala	Gln
				885					890					895	
Glu	Leu	Val	Lys	Glu	Ser	Gln	Leu	Ser	Met	Leu	Gln	Leu	Ser	Thr	Ile
			900						905					910	
Glu	Val	Ala	Thr	Gln	Leu	Ser	Met	Arg	Asp	Phe	Asp	Leu	Phe	Arg	Asn
		915					920					925			
Ile	Glu	Pro	Thr	Glu	Tyr	Ile	Asp	Asp	Leu	Phe	Lys	Leu	Asn	Ser	Lys
		930				935					940				
Thr	Gly	Asn	Thr	His	Leu	Lys	Arg	Phe	Glu	Asp	Ile	Val	Asn	Gln	Glu
945					950					955					960
Thr	Phe	Trp	Val	Ala	Ser	Glu	Ile	Leu	Thr	Glu	Ala	Asn	Gln	Leu	Lys
				965					970					975	
Arg	Met	Lys	Ile	Ile	Lys	His	Phe	Ile	Lys	Ile	Ala	Leu	His	Cys	Arg
			980				985						990		
Glu	Cys	Lys	Asn	Phe	Asn	Ser	Met	Phe	Ala	Ile	Ile	Ser	Gly	Leu	Asn
		995				1000						1005			
Leu	Ala	Ser	Val	Ala	Arg	Leu	Arg	Gly	Thr	Trp	Glu	Lys	Leu	Pro	Ser
		1010				1015					1020				
Lys	Tyr	Glu	Lys	His	Leu	Gln	Asp	Leu	Gln	Asp	Ile	Phe	Asp	Pro	Ser
1025					1030				1035						1040
Arg	Asn	Met	Ala	Lys	Tyr	Arg	Asn	Ile	Leu	Ser	Ser	Gln	Ser	Met	Gln
				1045					1050					1055	
Pro	Pro	Ile	Ile	Pro	Leu	Phe	Pro	Val	Val	Lys	Lys	Asp	Met	Thr	Phe
			1060					1065					1070		
Leu	His	Glu	Gly	Asn	Asp	Ser	Lys	Val	Asp	Gly	Leu	Val	Asn	Phe	Glu
		1075				1080					1085				
Lys	Leu	Arg	Met	Ile	Ser	Lys	Glu	Ile	Arg	Gln	Val	Val	Arg	Met	Thr
		1090				1095				1100					
Ser	Ala	Asn	Met	Asp	Pro	Ala	Met	Met	Phe	Arg	Gln	Arg	Ser	Leu	Ser
1105				1110						1115				1120	
Gln	Gly	Ser	Thr	Asn	Ser	Asn	Met	Leu	Asp	Val	Gln	Gly	Gly	Ala	His
				1125					1130					1135	
Lys	Lys	Arg	Ala	Arg	Arg	Ser	Ser	Leu	Leu	Asn	Ala	Lys	Lys	Leu	Tyr
			1140					1145					1150		
Glu	Asp	Ala	Gln	Met	Ala	Arg	Lys	Val	Lys	Gln	Tyr	Leu	Ser	Ser	Leu
		1155				1160						1165			
Asp	Val	Glu	Thr	Asp	Glu	Glu	Lys	Phe	Gln	Met	Met	Ser	Leu	Gln	Trp
		1170				1175					1180				
Glu	Pro	Ala	Tyr	Gly	Thr	Leu	Thr	Lys	Asn	Leu	Ser	Glu	Lys	Arg	Ser
1185				1190					1195						1200
Ala	Lys	Ser	Ser	Glu	Met	Ser	Pro	Val	Pro	Met	Arg	Ser	Ala	Gly	Gln
				1205					1210					1215	
Thr	Thr	Lys	Ala	His	Leu	His	Gln	Pro	His	Arg	Val	Ser	Gln	Val	Leu
			1220					1225					1230		
Gln	Val	Pro	Ala	Val	Asn	Leu	His	Pro	Ile	Arg	Lys	Lys	Gly	Gln	Thr
		1235						1240					1245		
Lys	Asp	Pro	Ala	Leu	Asn	Thr	Ser	Leu	Pro	Gln	Lys	Val	Leu	Gly	Thr
		1250				1255					1260				
Thr	Glu	Glu	Ile	Ser	Gly	Lys	Lys	His	Thr	Glu	Asp	Thr	Ile	Ser	Val
1265				1270					1275						1280
Ala	Ser	Ser	Leu	His	Ser	Ser	Pro	Pro	Ala	Ser	Pro	Gln	Gly	Ser	Pro
				1285					1290					1295	
His	Lys	Gly	Tyr	Thr	Leu	Ile	Pro	Ser	Ala	Lys	Ser	Asp	Asn	Leu	Ser
			1300					1305					1310		

Asp Ser Ser His Ser Glu Ile Ser Ser Arg Ser Ser Ile Val Ser Asn
 1315 1320 1325
 Cys Ser Val Asp Ser Met Ser Ala Ala Leu Gln Asp Glu Arg Cys Ser
 1330 1335 1340
 Ser Gln Ala Leu Ala Val Pro Glu Ser Thr Gly Ala Leu Glu Lys Thr
 1345 1350 1355 1360
 Glu His Ala Ser Gly Ile Gly Asp His Ser Gln His Gly Pro Gly Trp
 1365 1370 1375
 Thr Leu Leu Lys Pro Ser Leu Ile Lys Cys Leu Ala Val Ser Ser Ser
 1380 1385 1390
 Val Ser Asn Glu Glu Ile Ser Gln Glu His Ile Ile Ile Glu Ala Ala
 1395 1400 1405
 Asp Ser Gly Arg Gly Ser Trp Thr Ser Cys Ser Ser Ser Ser His Asp
 1410 1415 1420
 Asn Phe Gln Ser Leu Pro Asn Pro Lys Ser Trp Asp Phe Leu Asn Ser
 1425 1430 1435 1440
 Tyr Arg His Thr His Leu Asp Asp Pro Ile Ala Glu Val Glu Pro Thr
 1445 1450 1455
 Asp Ser Glu Pro Tyr Ser Cys Ser Lys Ser Cys Ser Arg Thr Cys Gly
 1460 1465 1470
 Gln Cys Lys Gly Ser Leu Glu Arg Lys Ser Trp Thr Ser Ser Ser Ser
 1475 1480 1485
 Leu Ser Asp Thr Tyr Glu Pro Asn Tyr Gly Thr Val Lys Arg Arg Val
 1490 1495 1500
 Leu Glu Ser Thr Pro Ala Glu Ser Ser Glu Gly Leu Asp Pro Lys Asp
 1505 1510 1515 1520
 Ala Thr Asp Pro Val Tyr Lys Thr Val Thr Ser Ser Thr Glu Lys Gly
 1525 1530 1535
 Leu Ile Val Tyr Cys Val Thr Ser Pro Lys Lys Asp Asp Arg Tyr Arg
 1540 1545 1550
 Glu Pro Pro Pro Thr Pro Pro Gly Tyr Leu Gly Ile Ser Leu Ala Asp
 1555 1560 1565
 Leu Lys Glu Gly Pro His Thr His Leu Lys Pro Pro Asp Tyr Ser Val
 1570 1575 1580
 Ala Val Gln Arg Ser Lys Met Met His Asn Ser Leu Ser Arg Leu Pro
 1585 1590 1595 1600
 Pro Ala Ser Leu Ser Ser Asn Leu Val Ala Cys Val Pro Ser Lys Ile
 1605 1610 1615
 Val Thr Gln Pro Gln Arg His Asn Leu Gln Pro Phe His Pro Lys Leu
 1620 1625 1630
 Gly Asp Val Thr Asp Ala Asp Ser Glu Ala Asp Glu Asn Glu Gln Val
 1635 1640 1645
 Ser Ala Val
 1650

<210> 154
 <211> 1424
 <212> PRT
 <213> Homo sapiens

<400> 154
 Met Ser Asp Ser Trp Val Pro Asn Ser Ala Ser Gly Gln Asp Pro Gly
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 Gly Arg Arg Arg Ala Trp Ala Glu Leu Leu Ala Gly Arg Val Lys Arg
 20 25 30
 Glu Lys Tyr Asn Pro Glu Arg Ala Gln Lys Leu Lys Glu Ser Ala Val
 35 40 45
 Arg Leu Leu Arg Ser His Gln Asp Leu Asn Ala Leu Leu Leu Glu Val

50	55	60
Glu Gly Pro Leu Cys Lys Lys Leu Ser Leu Ser Lys Val Ile Asp Cys		
65	70	75
Asp Ser Ser Glu Ala Tyr Ala Asn His Ser Ser Ser Phe Ile Gly Ser		80
	85	90
Ala Leu Gln Asp Gln Ala Ser Arg Leu Gly Val Pro Val Gly Ile Leu		95
	100	105
Ser Ala Gly Met Val Ala Ser Ser Val Gly Gln Ile Cys Thr Ala Pro		110
	115	120
Ala Glu Thr Ser His Pro Val Leu Leu Thr Val Glu Gln Arg Lys Lys		125
	130	135
Leu Ser Ser Leu Leu Glu Phe Ala Gln Tyr Leu Leu Ala His Ser Met		140
145	150	155
Phe Ser Arg Leu Ser Phe Cys Gln Glu Leu Trp Lys Ile Gln Ser Ser		160
	165	170
Leu Leu Leu Glu Ala Val Trp His Leu His Val Gln Gly Ile Val Ser		175
	180	185
Leu Gln Glu Leu Leu Glu Ser His Pro Asp Met His Ala Val Gly Ser		190
	195	200
Trp Leu Phe Arg Asn Leu Cys Cys Leu Cys Glu Gln Met Glu Ala Ser		205
210	215	220
Cys Gln His Ala Asp Val Ala Arg Ala Met Leu Ser Asp Phe Val Gln		225
	230	235
Met Phe Val Leu Arg Gly Phe Gln Lys Asn Ser Asp Leu Arg Arg Thr		240
	245	250
Val Glu Pro Glu Lys Met Pro Gln Val Thr Val Asp Val Leu Gln Arg		255
	260	265
Met Leu Ile Phe Ala Leu Asp Ala Leu Ala Ala Gly Val Gln Glu Glu		270
	275	280
Ser Ser Thr His Lys Ile Val Arg Cys Trp Phe Gly Val Phe Ser Gly		285
	290	295
His Thr Leu Gly Ser Val Ile Ser Thr Asp Pro Leu Lys Arg Phe Phe		300
305	310	315
Ser His Thr Leu Thr Gln Ile Leu Thr His Ser Pro Val Leu Lys Ala		320
	325	330
Ser Asp Ala Val Gln Met Gln Arg Glu Trp Ser Phe Ala Arg Thr His		335
	340	345
Pro Leu Leu Thr Ser Leu Tyr Arg Arg Leu Phe Val Met Leu Ser Ala		350
	355	360
Glu Glu Leu Val Gly His Leu Gln Glu Val Leu Glu Thr Gln Glu Val		365
	370	375
His Trp Gln Arg Val Leu Ser Phe Val Ser Ala Leu Val Val Cys Phe		380
385	390	395
Pro Glu Ala Gln Gln Leu Leu Glu Asp Trp Val Ala Arg Leu Met Ala		400
	405	410
Gln Ala Phe Glu Ser Cys Gln Leu Asp Ser Met Val Thr Ala Phe Leu		415
	420	425
Val Val Arg Gln Ala Ala Leu Glu Gly Pro Ser Ala Phe Leu Ser Tyr		430
	435	440
Ala Asp Trp Phe Lys Ala Ser Phe Gly Ser Thr Arg Gly Tyr His Gly		445
	450	455
Cys Ser Lys Lys Ala Leu Val Phe Leu Phe Thr Phe Leu Ser Glu Leu		460
465	470	475
Val Pro Phe Glu Ser Pro Arg Tyr Leu Gln Val His Ile Leu His Pro		480
	485	490
Pro Leu Val Pro Ser Lys Tyr Arg Ser Leu Leu Thr Asp Tyr Ile Ser		495
	500	505
Leu Ala Lys Thr Arg Leu Ala Asp Leu Lys Val Ser Ile Glu Asn Met		510
	515	520
Gly Leu Tyr Glu Asp Leu Ser Ser Ala Gly Asp Ile Thr Glu Pro His		525
	530	535
		540

Ser Gln Ala Leu Gln Asp Val Glu Lys Ala Ile Met Val Phe Glu His
 545 550 555 560
 Thr Gly Asn Ile Pro Val Thr Val Met Glu Ala Ser Ile Phe Arg Arg
 565 570 575
 Pro Tyr Tyr Val Ser His Phe Leu Pro Ala Leu Leu Thr Pro Arg Val
 580 585 590
 Leu Pro Lys Val Pro Asp Ser Arg Val Ala Phe Ile Glu Ser Leu Lys
 595 600 605
 Arg Ala Asp Lys Ile Pro Pro Ser Leu Tyr Ser Thr Tyr Cys Gln Ala
 610 615 620
 Cys Ser Ala Ala Glu Glu Lys Pro Glu Asp Ala Ala Leu Gly Val Arg
 625 630 635 640
 Ala Glu Pro Asn Ser Ala Glu Glu Pro Leu Gly Gln Leu Thr Ala Ala
 645 650 655
 Leu Gly Glu Leu Arg Ala Ser Met Thr Asp Pro Ser Gln Arg Asp Val
 660 665 670
 Ile Ser Ala Gln Val Ala Val Ile Ser Glu Arg Leu Arg Ala Val Leu
 675 680 685
 Gly His Asn Glu Asp Asp Ser Ser Val Glu Ile Ser Lys Ile Gln Leu
 690 695 700
 Ser Ile Asn Thr Pro Arg Leu Glu Pro Arg Glu His Ile Ala Val Asp
 705 710 715 720
 Leu Leu Leu Thr Ser Phe Cys Gln Asn Leu Met Ala Ala Ser Ser Val
 725 730 735
 Ala Pro Pro Glu Arg Gln Gly Pro Trp Ala Ala Leu Phe Val Arg Thr
 740 745 750
 Met Cys Gly Arg Val Leu Pro Ala Val Leu Thr Arg Leu Cys Gln Leu
 755 760 765
 Leu Arg His Gln Gly Pro Ser Leu Ser Ala Pro His Val Leu Gly Leu
 770 775 780
 Ala Ala Leu Ala Val His Leu Gly Glu Ser Arg Ser Ala Leu Pro Glu
 785 790 795 800
 Val Asp Val Gly Pro Pro Ala Pro Gly Ala Gly Leu Pro Val Pro Ala
 805 810 815
 Leu Phe Asp Ser Leu Leu Thr Cys Arg Thr Arg Asp Ser Leu Phe Phe
 820 825 830
 Cys Leu Lys Phe Cys Thr Ala Ala Ile Ser Tyr Ser Leu Cys Lys Phe
 835 840 845
 Ser Ser Gln Ser Arg Asp Thr Leu Cys Ser Cys Leu Ser Pro Gly Leu
 850 855 860
 Ile Lys Lys Phe Gln Phe Leu Met Phe Arg Leu Phe Ser Glu Ala Arg
 865 870 875 880
 Gln Pro Leu Ser Glu Asp Val Ala Ser Leu Ser Trp Arg Pro Leu
 885 890 895
 His Leu Pro Ser Ala Asp Trp Gln Arg Ala Ala Leu Ser Leu Trp Thr
 900 905 910
 His Arg Thr Phe Arg Glu Val Leu Lys Glu Glu Asp Val His Leu Thr
 915 920 925
 Tyr Gln Asp Trp Leu His Leu Glu Leu Glu Ile Gln Pro Glu Ala Asp
 930 935 940
 Ala Leu Ser Asp Thr Glu Arg Gln Asp Phe His Gln Trp Ala Ile His
 945 950 955 960
 Glu His Phe Leu Pro Glu Ser Ser Ala Ser Gly Gly Cys Asp Gly Asp
 965 970 975
 Leu Gln Ala Ala Cys Thr Ile Leu Val Asn Ala Leu Met Asp Phe His
 980 985 990
 Gln Ser Ser Arg Ser Tyr Asp His Ser Glu Asn Ser Asp Leu Val Phe
 995 1000 1005
 Gly Gly Arg Thr Gly Asn Glu Asp Ile Ile Ser Arg Leu Gln Glu Met
 1010 1015 1020
 Val Ala Asp Leu Glu Leu Gln Gln Asp Leu Ile Val Pro Leu Gly His

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1025          1030          1035          1040
Thr Pro Ser Gln Glu His Phe Leu Phe Glu Ile Phe Arg Arg Arg Leu
          1045          1050          1055
Gln Ala Leu Thr Ser Gly Trp Ser Val Ala Ala Ser Leu Gln Arg Gln
          1060          1065          1070
Arg Glu Leu Leu Met Tyr Lys Arg Ile Leu Leu Arg Leu Pro Ser Ser
          1075          1080          1085
Val Leu Cys Gly Ser Ser Phe Gln Ala Glu Gln Pro Ile Thr Ala Arg
          1090          1095          1100
Cys Glu Gln Phe Phe His Leu Val Asn Ser Glu Met Arg Asn Phe Cys
1105          1110          1115          1120
Ser His Gly Gly Ala Leu Thr Gln Asp Ile Thr Ala His Phe Phe Arg
          1125          1130          1135
Gly Leu Leu Asn Ala Cys Leu Arg Ser Arg Asp Pro Ser Leu Met Val
          1140          1145          1150
Asp Phe Ile Leu Ala Lys Cys Gln Thr Lys Cys Pro Leu Ile Leu Thr
          1155          1160          1165
Ser Ala Leu Val Trp Trp Pro Ser Leu Glu Pro Val Leu Leu Cys Arg
          1170          1175          1180
Trp Arg Arg His Cys Gln Ser Pro Leu Pro Arg Glu Leu Gln Lys Leu
1185          1190          1195          1200
Gln Glu Gly Arg Gln Phe Ala Ser Asp Phe Leu Ser Pro Glu Ala Ala
          1205          1210          1215
Ser Pro Ala Pro Asn Pro Asp Trp Leu Ser Ala Ala Ala Leu His Phe
          1220          1225          1230
Ala Ile Gln Gln Val Arg Glu Glu Asn Ile Arg Lys Gln Leu Lys Lys
          1235          1240          1245
Leu Asp Cys Glu Arg Glu Glu Leu Leu Val Phe Leu Phe Phe Phe Ser
          1250          1255          1260
Leu Met Gly Leu Leu Ser Ser His Leu Thr Ser Asn Ser Thr Thr Asp
1265          1270          1275          1280
Leu Pro Lys Ala Phe His Val Cys Ala Ala Ile Leu Glu Cys Leu Glu
          1285          1290          1295
Lys Arg Lys Ile Ser Trp Leu Ala Leu Phe Gln Leu Thr Glu Ser Asp
          1300          1305          1310
Leu Arg Leu Gly Arg Leu Leu Leu Arg Val Ala Pro Asp Gln His Thr
          1315          1320          1325
Arg Leu Leu Pro Phe Ala Phe Tyr Ser Leu Leu Ser Tyr Phe His Glu
          1330          1335          1340
Asp Ala Ala Ile Arg Glu Glu Ala Phe Leu His Val Ala Val Asp Met
1345          1350          1355          1360
Tyr Leu Lys Leu Val Gln Leu Phe Val Ala Gly Asp Thr Ser Thr Val
          1365          1370          1375
Ser Pro Pro Ala Gly Arg Ser Leu Glu Leu Lys Gly Gln Ala Gly Gln
          1380          1385          1390
Pro Arg Gly Thr Asp Asn Lys Ser Ser Ser Phe Ser Ala Ala Val Asn
          1395          1400          1405
Thr Ser Val Pro Glu Lys Glu Leu Leu Thr Arg Gly Arg Ala Ala Gly
          1410          1415          1420

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<210> 155
<211> 1381
<212> PRT
<213> Homo sapiens

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<400> 155

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Met	Ser	Asp	Ser	Trp	Val	Pro	Asn	Ser	Ala	Ser	Gly	Gln	Asp	Pro	Gly
1				5					10					15	
Gly	Arg	Arg	Arg	Ala	Trp	Ala	Glu	Leu	Leu	Ala	Gly	Arg	Val	Lys	Arg
			20					25					30		
Glu	Lys	Tyr	Asn	Pro	Glu	Arg	Ala	Gln	Lys	Leu	Lys	Glu	Ser	Ala	Val
		35					40					45			
Arg	Leu	Leu	Arg	Ser	His	Gln	Asp	Leu	Asn	Ala	Leu	Leu	Leu	Glu	Val
	50				55						60				
Glu	Gly	Pro	Leu	Cys	Lys	Lys	Leu	Ser	Leu	Ser	Lys	Val	Ile	Asp	Cys
	65				70					75				80	
Asp	Ser	Ser	Glu	Ala	Tyr	Ala	Asn	His	Ser	Ser	Ser	Phe	Ile	Gly	Ser
				85					90					95	
Ala	Leu	Gln	Asp	Gln	Ala	Ser	Arg	Leu	Gly	Val	Pro	Val	Gly	Ile	Leu
		100						105					110		
Ser	Ala	Gly	Met	Val	Ala	Ser	Ser	Val	Gly	Gln	Ile	Cys	Thr	Ala	Pro
	115						120					125			
Ala	Glu	Thr	Ser	His	Pro	Val	Leu	Leu	Thr	Val	Glu	Gln	Arg	Lys	Lys
	130					135					140				
Leu	Ser	Ser	Leu	Leu	Glu	Phe	Ala	Gln	Tyr	Leu	Leu	Ala	His	Ser	Met
	145				150				155						160
Phe	Ser	Arg	Leu	Ser	Phe	Cys	Gln	Glu	Leu	Trp	Lys	Ile	Gln	Ser	Ser
			165				170						175		
Leu	Leu	Leu	Glu	Ala	Val	Trp	His	Leu	His	Val	Gln	Gly	Ile	Val	Ser
		180					185						190		
Leu	Gln	Glu	Leu	Leu	Glu	Ser	His	Pro	Asp	Met	His	Ala	Val	Gly	Ser
	195						200					205			
Trp	Leu	Phe	Arg	Asn	Leu	Cys	Cys	Leu	Cys	Glu	Gln	Met	Glu	Ala	Ser
	210					215					220				
Cys	Gln	His	Ala	Asp	Val	Ala	Arg	Ala	Met	Leu	Ser	Asp	Phe	Val	Gln
	225				230					235				240	
Met	Phe	Val	Leu	Arg	Gly	Phe	Gln	Lys	Asn	Ser	Asp	Leu	Arg	Arg	Thr
			245						250					255	
Val	Glu	Pro	Glu	Lys	Met	Pro	Gln	Val	Thr	Val	Asp	Val	Leu	Gln	Arg
		260						265					270		
Met	Leu	Ile	Phe	Ala	Leu	Asp	Ala	Leu	Ala	Ala	Gly	Val	Gln	Glu	Glu
	275						280					285			
Ser	Ser	Thr	His	Lys	Ile	Val	Arg	Cys	Trp	Phe	Gly	Val	Phe	Ser	Gly
	290					295					300				
His	Thr	Leu	Gly	Ser	Val	Ile	Ser	Thr	Asp	Pro	Leu	Lys	Arg	Phe	Phe
	305				310					315					320
Ser	His	Thr	Leu	Thr	Gln	Ile	Leu	Thr	His	Ser	Pro	Val	Leu	Lys	Ala
			325						330					335	
Ser	Asp	Ala	Val	Gln	Met	Gln	Arg	Glu	Trp	Ser	Phe	Ala	Arg	Thr	His
		340						345					350		
Pro	Leu	Leu	Thr	Ser	Leu	Tyr	Arg	Arg	Leu	Phe	Val	Met	Leu	Ser	Ala
	355						360					365			
Glu	Glu	Leu	Val	Gly	His	Leu	Gln	Glu	Val	Leu	Glu	Thr	Gln	Glu	Val
	370					375					380				
His	Trp	Gln	Arg	Val	Leu	Ser	Phe	Val	Ser	Ala	Leu	Val	Val	Cys	Phe
	385				390					395					400
Pro	Glu	Ala	Gln	Gln	Leu	Leu	Glu	Asp	Trp	Val	Ala	Arg	Leu	Met	Ala
			405						410					415	
Gln	Ala	Phe	Glu	Ser	Cys	Gln	Leu	Asp	Ser	Met	Val	Thr	Ala	Phe	Leu
		420						425					430		
Val	Val	Arg	Gln	Ala	Ala	Leu	Glu	Gly	Pro	Ser	Ala	Phe	Leu	Ser	Tyr
	435						440					445			
Ala	Asp	Trp	Phe	Lys	Ala	Ser	Phe	Gly	Ser	Thr	Arg	Gly	Tyr	His	Gly
	450					455					460				
Cys	Ser	Lys	Lys	Ala	Leu	Val	Phe	Leu	Phe	Thr	Phe	Leu	Ser	Glu	Leu
	465				470					475					480
Val	Pro	Phe	Glu	Ser	Pro	Arg	Tyr	Leu	Gln	Val	His	Ile	Leu	His	Pro

				485					490				495				
Pro	Leu	Val	Pro	Ser	Lys	Tyr	Arg	Ser	Leu	Leu	Thr	Asp	Tyr	Ile	Ser		
			500					505					510				
Leu	Ala	Lys	Thr	Arg	Leu	Ala	Asp	Leu	Lys	Val	Ser	Ile	Glu	Asn	Met		
		515					520					525					
Gly	Leu	Tyr	Glu	Asp	Leu	Ser	Ser	Ala	Gly	Asp	Ile	Thr	Glu	Pro	His		
	530				535						540						
Ser	Gln	Ala	Leu	Gln	Asp	Val	Glu	Lys	Ala	Ile	Met	Val	Phe	Glu	His		
545				550						555					560		
Thr	Gly	Asn	Ile	Pro	Val	Thr	Val	Met	Glu	Ala	Ser	Ile	Phe	Arg	Arg		
				565					570						575		
Pro	Tyr	Tyr	Val	Ser	His	Phe	Leu	Pro	Ala	Leu	Leu	Thr	Pro	Arg	Val		
			580					585					590				
Leu	Pro	Lys	Val	Pro	Asp	Ser	Arg	Val	Ala	Phe	Ile	Glu	Ser	Leu	Lys		
		595					600					605					
Arg	Ala	Asp	Lys	Ile	Pro	Pro	Ser	Leu	Tyr	Ser	Thr	Tyr	Cys	Gln	Ala		
	610					615					620						
Cys	Ser	Ala	Ala	Glu	Glu	Lys	Pro	Glu	Asp	Ala	Ala	Leu	Gly	Val	Arg		
625				630						635					640		
Ala	Glu	Pro	Asn	Ser	Ala	Glu	Glu	Pro	Leu	Gly	Gln	Leu	Thr	Ala	Ala		
			645						650					655			
Leu	Gly	Glu	Leu	Arg	Ala	Ser	Met	Thr	Asp	Pro	Ser	Gln	Arg	Asp	Val		
			660					665						670			
Ile	Ser	Ala	Gln	Val	Ala	Val	Ile	Ser	Glu	Arg	Leu	Arg	Ala	Val	Leu		
		675					680					685					
Gly	His	Asn	Glu	Asp	Asp	Ser	Ser	Val	Glu	Ile	Ser	Lys	Ile	Gln	Leu		
	690					695					700						
Ser	Ile	Asn	Thr	Pro	Arg	Leu	Glu	Pro	Arg	Glu	His	Ile	Ala	Val	Asp		
705				710						715					720		
Leu	Leu	Leu	Thr	Ser	Phe	Cys	Gln	Asn	Leu	Met	Ala	Ala	Ser	Ser	Val		
				725					730						735		
Ala	Pro	Pro	Glu	Arg	Gln	Gly	Pro	Trp	Ala	Ala	Leu	Phe	Val	Arg	Thr		
			740					745					750				
Met	Cys	Gly	Arg	Val	Leu	Pro	Ala	Val	Leu	Thr	Arg	Leu	Cys	Gln	Leu		
		755					760					765					
Leu	Arg	His	Gln	Gly	Pro	Ser	Leu	Ser	Ala	Pro	His	Val	Leu	Gly	Leu		
	770					775					780						
Ala	Ala	Leu	Ala	Val	His	Leu	Gly	Glu	Ser	Arg	Ser	Ala	Leu	Pro	Glu		
785				790						795					800		
Val	Asp	Val	Gly	Pro	Pro	Ala	Pro	Gly	Ala	Gly	Leu	Pro	Val	Pro	Ala		
			805						810					815			
Leu	Phe	Asp	Ser	Leu	Leu	Thr	Cys	Arg	Thr	Arg	Asp	Ser	Leu	Phe	Phe		
			820					825					830				
Cys	Leu	Lys	Phe	Cys	Thr	Ala	Ala	Ile	Ser	Tyr	Ser	Leu	Cys	Lys	Phe		
		835					840					845					
Ser	Ser	Gln	Ser	Arg	Asp	Thr	Leu	Cys	Ser	Cys	Leu	Ser	Pro	Gly	Leu		
	850				855						860						
Ile	Lys	Lys	Phe	Gln	Phe	Leu	Met	Phe	Arg	Leu	Phe	Ser	Glu	Ala	Arg		
865				870						875					880		
Gln	Pro	Leu	Ser	Glu	Glu	Asp	Val	Ala	Ser	Leu	Ser	Trp	Arg	Pro	Leu		
			885						890					895			
His	Leu	Pro	Ser	Ala	Asp	Trp	Gln	Arg	Ala	Ala	Leu	Ser	Leu	Trp	Thr		
			900					905					910				
His	Arg	Thr	Phe	Arg	Glu	Val	Leu	Lys	Glu	Glu	Asp	Val	His	Leu	Thr		
		915					920					925					
Tyr	Gln	Asp	Trp	Leu	His	Leu	Glu	Leu	Glu	Ile	Gln	Pro	Glu	Ala	Asp		
	930					935					940						
Ala	Leu	Ser	Asp	Thr	Glu	Arg	Ser	Arg	Ser	Tyr	Asp	His	Ser	Glu	Asn		
945				950						955					960		
Ser	Asp	Leu	Val	Phe	Gly	Gly	Arg	Thr	Gly	Asn	Glu	Asp	Ile	Ile	Ser		
				965					970					975			

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Arg Leu Gln Glu Met Val Ala Asp Leu Glu Leu Gln Gln Asp Leu Ile
          980          985          990
Val Pro Leu Gly His Thr Pro Ser Gln Glu His Phe Leu Phe Glu Ile
          995          1000          1005
Phe Arg Arg Arg Leu Gln Ala Leu Thr Ser Gly Trp Ser Val Ala Ala
1010          1015          1020
Ser Leu Gln Arg Gln Arg Glu Leu Leu Met Tyr Lys Arg Ile Leu Leu
1025          1030          1035          1040
Arg Leu Pro Ser Ser Val Leu Cys Gly Ser Ser Phe Gln Ala Glu Gln
          1045          1050          1055
Pro Ile Thr Ala Arg Cys Glu Gln Phe Phe His Leu Val Asn Ser Glu
          1060          1065          1070
Met Arg Asn Phe Cys Ser His Gly Gly Ala Leu Thr Gln Asp Ile Thr
          1075          1080          1085
Ala His Phe Phe Arg Gly Leu Leu Asn Ala Cys Leu Arg Ser Arg Asp
1090          1095          1100
Pro Ser Leu Met Val Asp Phe Ile Leu Ala Lys Cys Gln Thr Lys Cys
1105          1110          1115          1120
Pro Leu Ile Leu Thr Ser Ala Leu Val Trp Trp Pro Ser Leu Glu Pro
          1125          1130          1135
Val Leu Leu Cys Arg Trp Arg Arg His Cys Gln Ser Pro Leu Pro Arg
          1140          1145          1150
Glu Leu Gln Lys Leu Gln Glu Gly Arg Gln Phe Ala Ser Asp Phe Leu
          1155          1160          1165
Ser Pro Glu Ala Ala Ser Pro Ala Pro Asn Pro Asp Trp Leu Ser Ala
1170          1175          1180
Ala Ala Leu His Phe Ala Ile Gln Gln Val Arg Glu Glu Asn Ile Arg
1185          1190          1195          1200
Lys Gln Leu Lys Lys Leu Asp Cys Glu Arg Glu Glu Leu Leu Val Phe
          1205          1210          1215
Leu Phe Phe Phe Ser Leu Met Gly Leu Leu Ser Ser His Leu Thr Ser
          1220          1225          1230
Asn Ser Thr Thr Asp Leu Pro Lys Ala Phe His Val Cys Ala Ala Ile
          1235          1240          1245
Leu Glu Cys Leu Glu Lys Arg Lys Ile Ser Trp Leu Ala Leu Phe Gln
1250          1255          1260
Leu Thr Glu Ser Asp Leu Arg Leu Gly Arg Leu Leu Arg Val Ala
1265          1270          1275          1280
Pro Asp Gln His Thr Arg Leu Leu Pro Phe Ala Phe Tyr Ser Leu Leu
          1285          1290          1295
Ser Tyr Phe His Glu Asp Ala Ala Ile Arg Glu Glu Ala Phe Leu His
1300          1305          1310
Val Ala Val Asp Met Tyr Leu Lys Leu Val Gln Leu Phe Val Ala Gly
          1315          1320          1325
Asp Thr Ser Thr Val Ser Pro Pro Ala Gly Arg Ser Leu Glu Leu Lys
1330          1335          1340
Gly Gln Ala Gly Gln Pro Arg Gly Thr Asp Asn Lys Ser Ser Ser Phe
1345          1350          1355          1360
Ser Ala Ala Val Asn Thr Ser Val Pro Glu Lys Glu Leu Leu Thr Arg
          1365          1370          1375
Gly Arg Ala Ala Gly
          1380

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<210> 156
<211> 162
<212> PRT
<213> Homo sapiens

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```

<400> 156
Met Leu Arg Ala Val Gly Ser Leu Leu Arg Leu Gly Arg Gly Leu Thr
 1      5      10      15
Val Arg Cys Gly Pro Gly Ala Pro Leu Glu Ala Thr Arg Arg Pro Ala
      20      25      30
Pro Ala Leu Pro Pro Arg Gly Leu Pro Cys Tyr Ser Ser Gly Gly Ala
      35      40      45
Pro Ser Asn Ser Gly Pro Gln Gly His Gly Glu Ile His Arg Val Pro
      50      55      60
Thr Gln Arg Arg Pro Ser Gln Phe Asp Lys Lys Ile Leu Leu Trp Thr
      65      70      75      80
Gly Arg Phe Lys Ser Met Glu Glu Ile Pro Pro Arg Ile Pro Pro Glu
      85      90      95
Met Ile Asp Thr Ala Arg Asn Lys Ala Arg Val Lys Ala Cys Tyr Ile
      100      105      110
Met Ile Gly Leu Thr Ile Ile Ala Cys Phe Ala Val Ile Val Ser Ala
      115      120      125
Lys Arg Ala Val Glu Arg His Glu Ser Leu Thr Ser Trp Asn Leu Ala
      130      135      140
Lys Lys Ala Lys Trp Arg Glu Glu Ala Ala Leu Ala Ala Gln Ala Lys
      145      150      155      160
Ala Lys

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```

<210> 157
<211> 311
<212> PRT
<213> Homo sapiens

```

```

<400> 157
Met His Ala Ala Arg His Gly Trp Asp Val Glu Lys Asp Ala Pro Leu
 1      5      10      15
Phe Arg Asn Trp Ala Ile His Thr Gly Lys His Gln Pro Gly Val Asp
      20      25      30
Lys Pro Asp Pro Lys Thr Trp Lys Ala Asn Phe Arg Cys Ala Met Asn
      35      40      45
Ser Leu Pro Asp Ile Glu Glu Val Lys Asp Lys Ser Ile Lys Lys Gly
      50      55      60
Asn Asn Ala Phe Arg Val Tyr Arg Met Leu Pro Leu Ser Glu Arg Pro
      65      70      75      80
Ser Lys Lys Gly Lys Lys Pro Lys Thr Glu Lys Glu Asp Lys Val Lys
      85      90      95
His Ile Lys Gln Glu Pro Val Glu Ser Ser Leu Gly Leu Ser Asn Gly
      100      105      110
Val Ser Asp Leu Ser Pro Glu Tyr Ala Val Leu Thr Ser Thr Ile Lys
      115      120      125
Asn Glu Val Asp Ser Thr Val Asn Ile Ile Val Val Gly Gln Ser His
      130      135      140
Leu Asp Ser Asn Ile Glu Asn Gln Glu Ile Val Thr Asn Pro Pro Asp
      145      150      155      160
Ile Cys Gln Val Val Glu Val Thr Thr Glu Ser Asp Glu Gln Pro Val
      165      170      175
Ser Met Ser Glu Leu Tyr Pro Leu Gln Ile Ser Pro Val Ser Ser Tyr
      180      185      190
Ala Glu Ser Glu Thr Thr Asp Ser Val Pro Ser Asp Glu Glu Ser Ala
      195      200      205
Glu Gly Arg Pro His Trp Arg Lys Arg Asn Ile Glu Gly Lys Gln Tyr
      210      215      220

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```

Leu Ser Asn Met Gly Thr Arg Gly Ser Tyr Leu Leu Pro Gly Met Ala
225                230                235                240
Ser Phe Val Thr Ser Asn Lys Pro Asp Leu Gln Val Thr Ile Lys Glu
                245                250                255
Glu Ser Asn Pro Val Pro Tyr Asn Ser Ser Trp Pro Pro Phe Gln Asp
                260                265                270
Leu Pro Leu Ser Ser Ser Met Thr Pro Ala Ser Ser Ser Ser Arg Pro
                275                280                285
Asp Arg Glu Thr Arg Ala Ser Val Ile Lys Lys Thr Ser Asp Ile Thr
                290                295                300
Gln Ala Arg Val Lys Ser Cys
305                310

```

```

<210> 158
<211> 210
<212> PRT
<213> Homo sapiens

```

```

<400> 158
Met Asn Ser Leu Pro Asp Ile Glu Glu Val Lys Asp Lys Ser Ile Lys
1      5      10      15
Lys Gly Asn Asn Ala Phe Arg Val Tyr Arg Met Leu Pro Leu Ser Glu
                20      25      30
Arg Pro Ser Lys Lys Val Val Gly Gln Ser His Leu Asp Ser Asn Ile
                35      40      45
Glu Asn Gln Glu Ile Val Thr Asn Pro Pro Asp Ile Cys Gln Val Val
50      55      60
Glu Val Thr Thr Glu Ser Asp Glu Gln Pro Val Ser Met Ser Glu Leu
65      70      75      80
Tyr Pro Leu Gln Ile Ser Pro Val Ser Ser Tyr Ala Glu Ser Glu Thr
                85      90      95
Thr Asp Ser Val Pro Ser Asp Glu Glu Ser Ala Glu Gly Arg Pro His
100      105      110
Trp Arg Lys Arg Asn Ile Glu Gly Lys Gln Tyr Leu Ser Asn Met Gly
115      120      125
Thr Arg Gly Ser Tyr Leu Leu Pro Gly Met Ala Ser Phe Val Thr Ser
130      135      140
Asn Lys Pro Asp Leu Gln Val Thr Ile Lys Glu Glu Ser Asn Pro Val
145      150      155      160
Pro Tyr Asn Ser Ser Trp Pro Pro Phe Gln Asp Leu Pro Leu Ser Ser
165      170      175
Ser Met Thr Pro Ala Ser Ser Ser Ser Arg Pro Asp Arg Glu Thr Arg
180      185      190
Ala Ser Val Ile Lys Lys Thr Ser Asp Ile Thr Gln Ala Arg Val Lys
195      200      205
Ser Cys
210

```

```

<210> 159
<211> 529
<212> PRT
<213> Homo sapiens

```

```

<400> 159
Met Tyr Lys Arg Asn Gly Leu Met Ala Ser Val Leu Val Thr Ser Ala

```

1	5	10	15
Thr Pro Gln Gly Ser Ser Ser Ser Asp Ser Leu Glu Gly Gln Ser Cys			
20	25	30	
Asp Tyr Ala Ser Lys Ser Tyr Asp Ala Val Val Phe Asp Val Leu Lys			
35	40	45	
Val Thr Pro Glu Glu Phe Ala Ser Gln Ile Thr Leu Met Asp Ile Pro			
50	55	60	
Val Phe Lys Ala Ile Gln Pro Glu Glu Leu Ala Ser Cys Gly Trp Ser			
65	70	75	80
Lys Lys Glu Lys His Ser Leu Ala Pro Asn Val Val Ala Phe Thr Arg			
85	90	95	
Arg Phe Asn Gln Val Ser Phe Trp Val Val Arg Glu Ile Leu Thr Ala			
100	105	110	
Gln Thr Leu Lys Ile Arg Ala Glu Ile Leu Ser His Phe Val Lys Ile			
115	120	125	
Ala Lys Lys Leu Leu Glu Leu Asn Asn Leu His Ser Leu Met Ser Val			
130	135	140	
Val Ser Ala Leu Gln Ser Ala Pro Ile Phe Arg Leu Thr Lys Thr Trp			
145	150	155	160
Ala Leu Leu Asn Arg Lys Asp Lys Thr Thr Phe Glu Lys Leu Asp Tyr			
165	170	175	
Leu Met Ser Lys Glu Asp Asn Tyr Lys Arg Thr Arg Glu Tyr Ile Arg			
180	185	190	
Ser Leu Lys Met Val Pro Ser Ile Pro Tyr Leu Gly Ile Tyr Leu Leu			
195	200	205	
Asp Leu Ile Tyr Ile Asp Ser Ala Tyr Pro Ala Ser Gly Ser Ile Met			
210	215	220	
Glu Asn Glu Gln Arg Ser Asn Gln Met Asn Asn Ile Leu Arg Ile Ile			
225	230	235	240
Ala Asp Leu Gln Val Ser Cys Ser Tyr Asp His Leu Thr Thr Leu Pro			
245	250	255	
His Val Gln Lys Tyr Leu Lys Ser Val Arg Tyr Ile Glu Glu Leu Gln			
260	265	270	
Lys Phe Val Glu Asp Asp Asn Tyr Lys Leu Ser Leu Arg Ile Glu Pro			
275	280	285	
Gly Ser Ser Ser Pro Arg Leu Val Ser Ser Lys Glu Asp Leu Ala Gly			
290	295	300	
Pro Ser Ala Gly Ser Gly Ser Ala Arg Phe Ser Arg Arg Pro Thr Cys			
305	310	315	320
Pro Asp Thr Ser Val Ala Gly Ser Leu Pro Thr Pro Pro Val Pro Arg			
325	330	335	
His Arg Lys Ser His Ser Leu Gly Asn Asn Arg Gly Arg Leu Tyr Ala			
340	345	350	
Thr Leu Gly Pro Asn Trp Arg Val Pro Val Arg Asn Ser Pro Arg Thr			
355	360	365	
Arg Ser Cys Val Tyr Ser Pro Thr Gly Pro Cys Ile Cys Ser Leu Gly			
370	375	380	
Asn Ser Ala Ala Val Pro Thr Met Glu Gly Pro Leu Arg Arg Lys Thr			
385	390	395	400
Leu Leu Lys Glu Gly Arg Lys Pro Ala Leu Ser Ser Trp Thr Arg Tyr			
405	410	415	
Trp Val Ile Leu Ser Gly Ser Thr Leu Leu Tyr Tyr Gly Ala Lys Ser			
420	425	430	
Leu Arg Gly Thr Asp Arg Lys His Val Ser Ile Val Gly Trp Met Val			
435	440	445	
Gln Leu Pro Asp Asp Pro Glu His Pro Asp Ile Phe Gln Leu Asn Asn			
450	455	460	
Pro Asp Lys Gly Asn Val Tyr Lys Phe Gln Thr Gly Ser Arg Phe His			
465	470	475	480
Ala Ile Leu Trp His Lys His Leu Asp Asp Ala Cys Lys Ser Asn Arg			
485	490	495	

Pro Gln Glu Ala Gly Ala Ala Pro Gly Pro Thr Gly Thr Asp Ser His
 500 505 510
 Glu Val Asp His Leu Glu Gly Gly Ala Gly Lys Glu Ala Gly Pro Cys
 515 520 525
 Ala

<210> 160
 <211> 404
 <212> PRT
 <213> Homo sapiens

<400> 160
 Met Ala Glu Glu Gln Gln Gln Pro Pro Pro Gln Gln Pro Asp Ala His
 1 5 10 15
 Gln Gln Leu Pro Pro Ser Ala Pro Asn Ser Gly Val Ala Leu Pro Ala
 20 25 30
 Leu Val Pro Gly Leu Pro Gly Thr Glu Ala Ser Ala Leu Gln His Lys
 35 40 45
 Ile Lys Asn Ser Ile Cys Lys Thr Val Gln Ser Lys Val Asp Cys Ile
 50 55 60
 Leu Gln Glu Val Glu Lys Phe Thr Asp Leu Glu Lys Leu Tyr Leu Tyr
 65 70 75 80
 Leu Gln Leu Pro Ser Gly Leu Ser Asn Gly Glu Lys Ser Asp Gln Asn
 85 90 95
 Ala Met Ser Ser Ser Arg Ala Gln Gln Met His Ala Phe Ser Trp Ile
 100 105 110
 Arg Asn Thr Leu Glu Glu His Pro Glu Thr Ser Leu Pro Lys Gln Glu
 115 120 125
 Val Tyr Asp Glu Tyr Lys Ser Tyr Cys Asp Asn Leu Gly Tyr His Pro
 130 135 140
 Leu Ser Ala Ala Asp Phe Gly Lys Ile Met Lys Asn Val Phe Pro Asn
 145 150 155 160
 Met Lys Ala Arg Arg Leu Gly Thr Arg Gly Lys Ser Lys Tyr Cys Tyr
 165 170 175
 Ser Gly Leu Arg Lys Lys Ala Phe Val His Met Pro Thr Leu Pro Asn
 180 185 190
 Leu Asp Phe His Lys Thr Gly Asn Gly Leu Glu Gly Ala Glu Pro Ser
 195 200 205
 Gly Gln Leu Gln Asn Ile Asp Glu Glu Val Ile Ser Ser Ala Cys Arg
 210 215 220
 Leu Val Cys Glu Trp Ala Gln Lys Val Leu Ser Gln Pro Phe Asp Thr
 225 230 235 240
 Val Leu Glu Leu Ala Arg Phe Leu Val Lys Ser His Tyr Ile Gly Thr
 245 250 255
 Lys Ser Met Ala Ala Leu Thr Val Met Ala Ala Ala Pro Ala Gly Met
 260 265 270
 Lys Gly Ile Thr Gln Pro Ser Ala Phe Ile Pro Thr Ala Glu Ser Asn
 275 280 285
 Ser Phe Gln Pro Gln Val Lys Thr Leu Pro Ser Pro Ile Asp Ala Lys
 290 295 300
 Gln Gln Leu Gln Arg Lys Ile Gln Lys Lys Gln Gln Glu Gln Lys Leu
 305 310 315 320
 Gln Ser Pro Leu Pro Gly Glu Ser Ala Ala Lys Lys Ser Glu Ser Ala
 325 330 335
 Thr Ser Asn Gly Val Thr Asn Leu Pro Asn Gly Asn Pro Ser Ile Leu
 340 345 350
 Ser Pro Gln Pro Ile Gly Ile Val Met Ala Ala Val Pro Ser Pro Ile

```

          355          360          365
Pro Val Gln Arg Thr Arg His Leu Val Thr Ser Pro Ser Pro Met Ser
  370          375          380
Ser Ser Asp Gly Lys Val Leu Pro Leu Asn Val Gln Val Ser Leu Ser
  385          390          395          400
Thr Cys Ser Leu

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<210> 161
<211> 157
<212> PRT
<213> Homo sapiens

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```

<400> 161
Met Ser Glu Gly Val Asp Leu Ile Asp Ile Tyr Ala Asp Glu Glu Phe
  1          5          10          15
Asn Gln Asp Pro Glu Phe Asn Asn Thr Asp Gln Ile Asp Leu Tyr Asp
          20          25          30
Asp Val Leu Thr Ala Thr Ser Gln Pro Ser Asp Asp Arg Ser Ser Ser
          35          40          45
Thr Glu Pro Pro Pro Pro Val Arg Gln Glu Pro Ser Pro Lys Pro Asn
          50          55          60
Asn Lys Thr Pro Ala Ile Leu Tyr Thr Tyr Ser Gly Leu Arg Asn Arg
          65          70          75          80
Arg Ala Ala Val Tyr Val Gly Ser Phe Ser Trp Trp Thr Thr Asp Gln
          85          90          95
Gln Leu Ile Gln Val Ile Arg Ser Ile Gly Val Tyr Asp Val Val Glu
          100          105          110
Leu Lys Phe Ala Glu Asn Arg Ala Asn Gly Gln Ser Lys Gly Tyr Ala
          115          120          125
Glu Val Val Val Ala Ser Glu Asn Ser Val His Lys Leu Leu Glu Leu
          130          135          140
Leu Pro Gly Lys Val Leu Asn Trp Gln Lys Lys Trp Thr
          145          150          155

```

```

<210> 162
<211> 354
<212> PRT
<213> Homo sapiens

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```

<400> 162
Met Gln Glu Ala Ile Ile Leu Leu Ala Leu Leu Gly Ala Met Ser Gly
  1          5          10          15
Gly Glu Ala Leu His Leu Ile Leu Leu Pro Ala Thr Gly Asn Val Ala
          20          25          30
Glu Asn Ser Pro Pro Gly Thr Ser Val His Lys Phe Ser Val Lys Leu
          35          40          45
Ser Ala Ser Leu Ser Pro Val Ile Pro Gly Phe Pro Gln Ile Val Asn
          50          55          60
Ser Asn Pro Leu Thr Glu Ala Phe Arg Val Asn Trp Leu Ser Gly Thr
          65          70          75          80
Tyr Phe Glu Val Val Thr Thr Gly Met Glu Gln Leu Asp Phe Glu Thr
          85          90          95
Gly Pro Asn Ile Phe Asp Leu Gln Ile Tyr Val Lys Asp Glu Val Gly
          100          105          110

```

```

Val Thr Asp Leu Gln Val Leu Thr Val Gln Val Thr Asp Val Asn Glu
      115                      120                      125
Pro Pro Gln Phe Gln Gly Asn Leu Ala Glu Gly Leu His Leu Tyr Ile
      130                      135                      140
Val Glu Arg Ala Asn Pro Gly Phe Ile Tyr Gln Val Glu Ala Phe Asp
145                      150                      155                      160
Pro Glu Asp Thr Ser Arg Asn Ile Pro Leu Ser Tyr Phe Leu Ile Ser
      165                      170                      175
Pro Pro Lys Ser Phe Arg Met Ser Ala Asn Gly Thr Leu Phe Ser Thr
      180                      185                      190
Thr Glu Leu Asp Phe Glu Ala Gly His Arg Ser Phe His Leu Ile Val
      195                      200                      205
Glu Val Arg Asp Ser Gly Gly Leu Lys Ala Ser Thr Glu Leu Gln Val
      210                      215                      220
Asn Ile Val Asn Leu Asn Asp Glu Val Pro Arg Phe Thr Ser Pro Thr
225                      230                      235                      240
Arg Val Tyr Thr Val Leu Glu Glu Leu Ser Pro Gly Thr Ile Val Ala
      245                      250                      255
Asn Ile Thr Ala Glu Asp Pro Asp Asp Glu Gly Phe Pro Ser His Leu
      260                      265                      270
Leu Tyr Ser Ile Thr Thr Val Ser Lys Tyr Phe Met Ile Asn Gln Leu
      275                      280                      285
Thr Gly Thr Ile Gln Val Ala Gln Arg Ile Asp Arg Asp Ala Gly Glu
      290                      295                      300
Leu Arg Gln Asn Pro Thr Ile Ser Leu Glu Val Leu Val Lys Asp Arg
305                      310                      315                      320
Pro Tyr Gly Gly Gln Glu Asn Arg Ile Gln Ile Thr Phe Ile Val Glu
      325                      330                      335
Asp Val Asn Asp Asn Pro Ala Thr Cys Gln Lys Phe Thr Phe Arg Trp
      340                      345                      350
Arg Asn

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```

<210> 163
<211> 1579
<212> PRT
<213> Homo sapiens

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```

<400> 163
Met Lys Leu Cys Pro Arg Tyr Asn Ser Gln Glu Glu Thr Leu Glu Phe
 1      5      10      15
Val Ala Asp Tyr Ser Gly Gln Asp Asn Phe Leu Gln Arg Val Gly Gln
      20      25      30
Asn Gly Leu Lys Asn Ser Glu Lys Glu Ser Thr Val Asn Ser Ile Phe
      35      40      45
Gln Val Ile Arg Ser Cys Asn Arg Ser Leu Glu Thr Asp Glu Glu Asp
      50      55      60
Ser Pro Ser Glu Gly Asn Ser Ser Arg Lys Ser Ser Leu Lys Asp Lys
      65      70      75      80
Ser Arg Trp Gln Phe Ile Ile Gly Asp Leu Leu Asp Ser Asp Asn Asp
      85      90      95
Ile Phe Glu Gln Ser Lys Glu Tyr Asp Ser His Gly Ser Glu Asp Ser
      100      105      110
Gln Lys Ala Phe Asp His Gly Thr Glu Leu Ile Pro Trp Tyr Val Leu
      115      120      125
Ser Ile Gln Ala Asp Val His Gln Phe Leu Leu Gln Gly Ala Thr Val
      130      135      140
Ile His Tyr Asp Gln Asp Thr His Leu Ser Ala Arg Cys Phe Leu Gln

```

145		150		155		160									
Leu	Gln	Pro	Asp	Asn	Ser	Thr	Leu	Thr	Trp	Val	Lys	Pro	Thr	Thr	Ala
			165						170						175
Ser	Pro	Ala	Ser	Ser	Lys	Ala	Lys	Leu	Gly	Val	Leu	Asn	Asn	Thr	Ala
			180						185						190
Glu	Pro	Gly	Lys	Phe	Pro	Leu	Leu	Gly	Asn	Ala	Gly	Leu	Ser	Ser	Leu
		195					200					205			
Thr	Glu	Gly	Val	Leu	Asp	Leu	Phe	Ala	Val	Lys	Ala	Val	Tyr	Met	Gly
	210				215						220				
His	Pro	Gly	Ile	Asp	Ile	His	Thr	Val	Cys	Val	Gln	Asn	Lys	Leu	Gly
225				230					235						240
Ser	Met	Phe	Leu	Ser	Glu	Thr	Gly	Val	Thr	Leu	Leu	Tyr	Gly	Leu	Gln
			245						250					255	
Thr	Thr	Asp	Asn	Arg	Leu	Leu	His	Phe	Val	Ala	Pro	Lys	His	Thr	Ala
			260					265						270	
Lys	Met	Leu	Phe	Ser	Gly	Leu	Leu	Glu	Leu	Thr	Arg	Ala	Val	Arg	Lys
	275					280						285			
Met	Arg	Lys	Phe	Pro	Asp	Gln	Arg	Gln	Gln	Trp	Leu	Arg	Lys	Gln	Tyr
	290				295						300				
Val	Ser	Leu	Tyr	Gln	Glu	Asp	Gly	Arg	Tyr	Glu	Gly	Pro	Thr	Leu	Ala
305				310						315					320
His	Ala	Val	Glu	Leu	Phe	Gly	Gly	Arg	Arg	Trp	Ser	Ala	Arg	Asn	Pro
			325						330					335	
Ser	Pro	Gly	Thr	Ser	Ala	Lys	Asn	Ala	Glu	Lys	Pro	Asn	Met	Gln	Arg
			340					345					350		
Asn	Asn	Thr	Leu	Gly	Ile	Ser	Thr	Thr	Lys	Lys	Lys	Lys	Lys	Ile	Leu
	355					360						365			
Met	Arg	Gly	Glu	Ser	Gly	Glu	Val	Thr	Asp	Asp	Glu	Met	Ala	Thr	Arg
	370				375					380					
Lys	Ala	Lys	Met	His	Lys	Glu	Cys	Arg	Ser	Arg	Ser	Gly	Ser	Asp	Pro
385				390					395						400
Gln	Asp	Ile	Asn	Glu	Gln	Glu	Glu	Ser	Glu	Val	Asn	Ala	Ile	Ala	Asn
			405					410						415	
Pro	Pro	Asn	Pro	Leu	Pro	Ser	Arg	Arg	Ala	His	Ser	Leu	Thr	Thr	Ala
			420					425					430		
Gly	Ser	Pro	Asn	Leu	Ala	Ala	Gly	Thr	Ser	Ser	Pro	Ile	Arg	Pro	Val
		435					440					445			
Ser	Ser	Pro	Val	Leu	Ser	Ser	Ser	Asn	Lys	Ser	Pro	Ser	Ser	Ala	Trp
	450					455					460				
Ser	Ser	Ser	Ser	Trp	His	Gly	Arg	Ile	Lys	Gly	Gly	Met	Lys	Gly	Phe
465				470					475						480
Gln	Ser	Phe	Met	Val	Ser	Asp	Ser	Asn	Met	Ser	Phe	Val	Glu	Phe	Val
			485						490					495	
Glu	Leu	Phe	Lys	Ser	Phe	Ser	Val	Arg	Gln	Ala	Lys	Asp	Leu	Lys	Asp
		500						505					510		
Leu	Phe	Asp	Val	Tyr	Ala	Val	Pro	Cys	Asn	Arg	Ser	Gly	Ser	Glu	Ser
		515					520					525			
Ala	Pro	Leu	Tyr	Thr	Asn	Leu	Thr	Ile	Asp	Glu	Asn	Thr	Ser	Asp	Leu
	530					535					540				
Gln	Pro	Asp	Leu	Asp	Leu	Leu	Thr	Arg	Asn	Val	Ser	Asp	Leu	Gly	Leu
545				550					555						560
Phe	Ile	Lys	Ser	Lys	Gln	Gln	Leu	Ser	Asp	Asn	Gln	Arg	Gln	Ile	Ser
			565						570					575	
Asp	Ala	Ile	Ala	Ala	Ala	Ser	Ile	Val	Thr	Asn	Gly	Thr	Gly	Ile	Glu
			580					585					590		
Ser	Thr	Ser	Leu	Gly	Ile	Phe	Gly	Val	Gly	Ile	Leu	Gln	Leu	Asn	Asp
		595					600					605			
Phe	Leu	Val	Asn	Cys	Gln	Gly	Glu	His	Cys	Thr	Tyr	Asp	Glu	Ile	Leu
	610					615					620				
Ser	Ile	Ile	Gln	Lys	Phe	Glu	Pro	Ser	Ile	Ser	Met	Cys	His	Gln	Gly
625					630					635					640

Leu Met Ser Phe Glu Gly Phe Ala Arg Phe Leu Met Asp Lys Glu Asn
 645 650 655
 Phe Ala Ser Lys Asn Asp Glu Ser Gln Glu Asn Ile Lys Glu Leu Gln
 660 665 670
 Leu Pro Leu Ser Tyr Tyr Tyr Ile Glu Ser Ser His Asn Thr Tyr Leu
 675 680 685
 Thr Gly His Gln Leu Lys Gly Glu Ser Ser Val Glu Leu Tyr Ser Gln
 690 695 700
 Val Leu Leu Gln Gly Cys Arg Ser Val Glu Leu Asp Cys Trp Asp Gly
 705 710 715 720
 Asp Asp Gly Met Pro Ile Ile Tyr His Gly His Thr Leu Thr Thr Lys
 725 730 735
 Ile Pro Phe Lys Glu Val Val Glu Ala Ile Asp Arg Ser Ala Phe Ile
 740 745 750
 Asn Ser Asp Leu Pro Ile Ile Ile Ser Ile Glu Asn His Cys Ser Leu
 755 760 765
 Pro Gln Gln Arg Lys Met Ala Glu Ile Phe Lys Thr Val Phe Gly Glu
 770 775 780
 Lys Leu Val Thr Lys Phe Leu Phe Glu Thr Asp Phe Ser Asp Asp Pro
 785 790 795 800
 Met Leu Pro Ser Pro Asp Gln Leu Arg Lys Lys Val Leu Leu Lys Asn
 805 810 815
 Lys Lys Leu Lys Ala His Gln Thr Pro Val Asp Ile Leu Lys Gln Lys
 820 825 830
 Ala His Gln Leu Ala Ser Met Gln Val Gln Ala Tyr Asn Gly Gly Asn
 835 840 845
 Ala Asn Pro Arg Pro Ala Asn Asn Glu Glu Glu Glu Asp Glu Glu Asp
 850 855 860
 Glu Tyr Asp Tyr Asp Tyr Glu Ser Leu Ser Asp Asp Asn Ile Leu Glu
 865 870 875 880
 Asp Arg Pro Glu Asn Lys Ser Cys Asn Asp Lys Leu Gln Phe Glu Tyr
 885 890 895
 Asn Glu Glu Ile Pro Lys Arg Ile Lys Lys Ala Asp Asn Ser Ala Cys
 900 905 910
 Asn Lys Gly Lys Val Tyr Asp Met Glu Leu Gly Glu Glu Phe Tyr Leu
 915 920 925
 Asp Gln Asn Lys Lys Glu Ser Arg Gln Ile Ala Pro Glu Leu Ser Asp
 930 935 940
 Leu Val Ile Tyr Cys Gln Ala Val Lys Phe Pro Gly Leu Ser Thr Leu
 945 950 955 960
 Asn Ala Ser Gly Ser Ser Arg Gly Lys Glu Arg Lys Ser Arg Lys Ser
 965 970 975
 Ile Phe Gly Asn Asn Pro Gly Arg Met Ser Pro Gly Glu Thr Ala Ser
 980 985 990
 Phe Asn Lys Thr Ser Gly Lys Ser Ser Cys Glu Gly Ile Arg Gln Thr
 995 1000 1005
 Trp Glu Glu Ser Ser Ser Pro Leu Asn Pro Thr Thr Ser Leu Ser Ala
 1010 1015 1020
 Ile Ile Arg Thr Pro Lys Cys Tyr His Ile Ser Ser Leu Asn Glu Asn
 1025 1030 1035 1040
 Ala Ala Lys Arg Leu Cys Arg Arg Tyr Ser Gln Lys Leu Thr Gln His
 1045 1050 1055
 Thr Ala Cys Gln Leu Leu Arg Thr Tyr Pro Ala Ala Thr Arg Ile Asp
 1060 1065 1070
 Ser Ser Asn Pro Asn Pro Leu Met Phe Trp Leu His Gly Ile Gln Leu
 1075 1080 1085
 Val Ala Leu Asn Tyr Gln Thr Asp Asp Leu Pro Leu His Leu Asn Ala
 1090 1095 1100
 Ala Met Phe Glu Ala Asn Gly Gly Cys Gly Tyr Val Leu Lys Pro Pro
 1105 1110 1115 1120
 Val Leu Trp Asp Lys Asn Cys Pro Met Tyr Gln Lys Phe Ser Pro Leu

```

1125      1130      1135
Glu Arg Asp Leu Asp Ser Met Asp Pro Ala Val Tyr Ser Leu Thr Ile
1140      1145      1150
Val Ser Gly Gln Asn Val Cys Pro Ser Asn Ser Met Gly Ser Pro Cys
1155      1160      1165
Ile Glu Val Asp Val Leu Gly Met Pro Leu Asp Ser Cys His Phe Arg
1170      1175      1180
Thr Lys Pro Ile His Arg Asn Thr Leu Asn Pro Met Trp Asn Glu Gln
1185      1190      1195      1200
Phe Leu Phe Arg Val His Phe Glu Asp Leu Val Phe Leu Arg Phe Ala
1205      1210      1215
Val Val Glu Asn Ser Ser Ala Val Thr Ala Gln Arg Ile Ile Pro
1220      1225      1230
Leu Lys Ala Leu Lys Arg Gly Tyr Arg His Leu Gln Leu Arg Asn Leu
1235      1240      1245
His Asn Glu Val Leu Glu Ile Ser Ser Leu Phe Ile Asn Ser Arg Arg
1250      1255      1260
Met Glu Glu Asn Ser Ser Gly Asn Thr Met Ser Ala Ser Ser Met Phe
1265      1270      1275      1280
Asn Thr Glu Glu Arg Lys Cys Leu Gln Thr His Arg Val Thr Val His
1285      1290      1295
Gly Val Pro Gly Pro Glu Pro Phe Thr Val Phe Thr Ile Asn Gly Gly
1300      1305      1310
Thr Lys Ala Lys Gln Leu Leu Gln Ile Leu Thr Asn Glu Gln Asp
1315      1320      1325
Ile Lys Pro Val Thr Thr Asp Tyr Phe Leu Met Glu Glu Lys Tyr Phe
1330      1335      1340
Ile Ser Lys Glu Lys Asn Glu Cys Arg Lys Gln Pro Phe Gln Arg Ala
1345      1350      1355      1360
Ile Gly Pro Glu Glu Ile Met Gln Ile Leu Ser Ser Trp Phe Pro
1365      1370      1375
Glu Glu Gly Tyr Met Gly Arg Ile Val Leu Lys Thr Gln Gln Glu Asn
1380      1385      1390
Leu Glu Glu Lys Asn Ile Val Gln Asp Asp Lys Glu Val Ile Leu Ser
1395      1400      1405
Ser Glu Glu Glu Ser Phe Phe Val Gln Val His Asp Val Ser Pro Glu
1410      1415      1420
Gln Pro Arg Thr Val Ile Lys Ala Pro Arg Val Ser Thr Ala Gln Asp
1425      1430      1435      1440
Val Ile Gln Gln Thr Leu Cys Lys Ala Lys Tyr Ser Tyr Ser Ile Leu
1445      1450      1455
Ser Asn Pro Asn Pro Ser Asp Tyr Val Leu Leu Glu Glu Val Val Lys
1460      1465      1470
Asp Thr Thr Asn Lys Lys Thr Thr Pro Lys Ser Ser Gln Arg Val
1475      1480      1485
Leu Leu Asp Gln Glu Cys Val Phe Gln Ala Gln Ser Lys Trp Lys Gly
1490      1495      1500
Ala Gly Lys Phe Ile Leu Lys Leu Lys Glu Gln Val Gln Ala Ser Arg
1505      1510      1515      1520
Glu Asp Lys Lys Lys Gly Ile Ser Phe Ala Ser Glu Leu Lys Lys Leu
1525      1530      1535
Thr Lys Ser Thr Lys Gln Pro Arg Gly Leu Thr Ser Pro Ser Gln Leu
1540      1545      1550
Leu Thr Ser Glu Ser Ile Gln Thr Lys Glu Glu Lys Pro Val Gly Gly
1555      1560      1565
Leu Ser Ser Ser Asp Thr Met Asp Tyr Arg Gln
1570      1575

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<210> 164

<211> 407

<212> PRT

<213> Homo sapiens

<400> 164

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Met Asp Gly Leu Pro Gly Arg Ala Leu Gly Ala Ala Cys Leu Leu Leu
 1      5      10      15
Leu Ala Ala Gly Trp Leu Gly Pro Glu Ala Trp Gly Ser Pro Thr Pro
 20      25      30
Pro Pro Thr Pro Ala Ala Pro Pro Pro Pro Pro Pro Gly Ala Pro
 35      40      45
Gly Gly Ser Gln Asp Thr Cys Thr Ser Cys Gly Gly Phe Arg Arg Pro
 50      55      60
Glu Glu Leu Gly Arg Val Asp Gly Asp Phe Leu Glu Ala Val Lys Arg
 65      70      75      80
His Ile Leu Ser Arg Leu Gln Met Arg Gly Arg Pro Asn Ile Thr His
 85      90      95
Ala Val Pro Lys Ala Ala Met Val Thr Ala Leu Arg Lys Leu His Ala
100      105      110
Gly Lys Val Arg Glu Asp Gly Arg Val Glu Ile Pro His Leu Asp Gly
115      120      125
His Ala Ser Pro Gly Ala Asp Gly Gln Glu Arg Val Ser Glu Ile Ile
130      135      140
Ser Phe Ala Glu Thr Asp Gly Leu Ala Ser Ser Arg Val Arg Leu Tyr
145      150      155      160
Phe Phe Ile Ser Asn Glu Gly Asn Gln Asn Leu Phe Val Val Gln Ala
165      170      175
Ser Leu Trp Leu Tyr Leu Lys Leu Leu Pro Tyr Val Leu Glu Lys Gly
180      185      190
Ser Arg Arg Lys Val Arg Val Lys Val Tyr Phe Gln Glu Gln Gly His
195      200      205
Gly Asp Arg Trp Asn Met Val Glu Lys Arg Val Asp Leu Lys Arg Ser
210      215      220
Gly Trp His Thr Phe Pro Leu Thr Glu Ala Ile Gln Ala Leu Phe Glu
225      230      235      240
Arg Gly Glu Arg Arg Leu Asn Leu Asp Val Gln Cys Asp Ser Cys Gln
245      250      255
Glu Leu Ala Val Val Pro Val Phe Val Asp Pro Gly Glu Glu Ser His
260      265      270
Arg Pro Phe Val Val Val Gln Ala Arg Leu Gly Asp Ser Arg His Arg
275      280      285
Ile Arg Lys Arg Gly Leu Glu Cys Asp Gly Arg Thr Asn Leu Cys Cys
290      295      300
Arg Gln Gln Phe Phe Ile Asp Phe Arg Leu Ile Gly Trp Asn Asp Trp
305      310      315      320
Ile Ile Ala Pro Thr Gly Tyr Tyr Gly Asn Tyr Cys Glu Gly Ser Cys
325      330      335
Pro Ala Tyr Leu Ala Gly Val Pro Gly Ser Ala Ser Ser Phe His Thr
340      345      350
Ala Val Val Asn Gln Tyr Arg Met Arg Gly Leu Asn Pro Gly Thr Val
355      360      365
Asn Ser Cys Cys Ile Pro Thr Lys Leu Ser Thr Met Ser Met Leu Tyr
370      375      380
Phe Asp Asp Glu Tyr Asn Ile Val Lys Arg Asp Val Pro Asn Met Ile
385      390      395      400
Val Glu Glu Cys Gly Cys Ala
405

```

<210> 165
 <211> 407
 <212> PRT
 <213> Homo sapiens

<400> 165
 Met Ala Leu Gly Val Gly Arg Ala Arg Pro Gly Leu Ser Cys Gly Val
 1 5 10 15
 Ile Ser Pro Pro Cys Ala Pro Thr Arg Asn Ser His Pro Gly Pro Gly
 20 25 30
 Cys Thr Ala Ser Pro Pro Ala Pro Pro Gly Trp Pro Phe Ser Gln Arg
 35 40 45
 Gly Pro Gly Arg Trp Ser Thr Thr Glu Leu Arg Lys Glu Lys Ser Arg
 50 55 60
 Asp Ala Ala Arg Ser Arg Arg Ser Gln Glu Thr Glu Val Leu Tyr Gln
 65 70 75 80
 Leu Ala His Thr Leu Pro Phe Ala Arg Gly Val Ser Ala His Leu Asp
 85 90 95
 Lys Ala Ser Ile Met Arg Leu Thr Ile Ser Tyr Leu Arg Met His Arg
 100 105 110
 Leu Cys Ala Ala Gly Glu Trp Asn Gln Val Gly Ala Gly Gly Glu Pro
 115 120 125
 Leu Asp Ala Cys Tyr Leu Lys Ala Leu Glu Gly Phe Val Met Val Leu
 130 135 140
 Thr Ala Glu Gly Asp Met Ala Tyr Leu Ser Glu Asn Val Ser Lys His
 145 150 155 160
 Leu Gly Leu Ser Gln Leu Glu Leu Ile Gly His Ser Ile Phe Asp Phe
 165 170 175
 Ile His Pro Cys Asp Gln Glu Glu Leu Gln Asp Ala Leu Thr Pro Gln
 180 185 190
 Gln Thr Leu Ser Arg Arg Lys Val Glu Ala Pro Thr Glu Arg Cys Phe
 195 200 205
 Ser Leu Arg Met Lys Ser Thr Leu Thr Ser Arg Gly Arg Thr Leu Asn
 210 215 220
 Leu Lys Ala Ala Thr Trp Lys Val Leu Asn Cys Ser Gly His Met Arg
 225 230 235 240
 Ala Tyr Lys Pro Pro Ala Gln Thr Ser Pro Ala Gly Ser Pro Asp Ser
 245 250 255
 Glu Pro Pro Leu Gln Cys Leu Val Leu Ile Cys Glu Ala Ile Pro His
 260 265 270
 Pro Gly Ser Leu Glu Pro Pro Leu Gly Arg Gly Ala Phe Leu Ser Arg
 275 280 285
 His Ser Leu Asp Met Lys Phe Thr Tyr Cys Asp Asp Arg Ile Ala Glu
 290 295 300
 Val Ala Gly Tyr Ser Pro Asp Asp Leu Ile Gly Cys Ser Ala Tyr Glu
 305 310 315 320
 Tyr Ile His Ala Leu Asp Ser Asp Ala Val Ser Lys Ser Ile His Thr
 325 330 335
 Cys Met Tyr Pro Ile Ser Pro Gly Ala Lys Pro Ala Ala Thr Trp Pro
 340 345 350
 Pro Ala Asp Thr Arg Thr Pro Gln Leu Pro Ile Pro Gln Asp Ala Leu
 355 360 365
 Pro Pro His Leu Asn Thr Ser Ser Leu Leu Pro Lys Pro Gln Gly Thr
 370 375 380
 Val Ser Phe Leu Ala Pro Ser Tyr Pro Val Pro Arg Ser Phe Ser Pro
 385 390 395 400
 His Leu Pro Pro Trp Trp Pro
 405

<210> 166
 <211> 418
 <212> PRT
 <213> Homo sapiens

<400> 166
 Met Ser Glu Gly Val Asp Leu Ile Asp Ile Tyr Ala Asp Glu Glu Phe
 1 5 10 15
 Asn Gln Asp Pro Glu Phe Asn Asn Thr Asp Gln Ile Asp Leu Tyr Asp
 20 25 30
 Asp Val Leu Thr Ala Thr Ser Gln Pro Ser Asp Asp Arg Ser Ser Ser
 35 40 45
 Thr Glu Pro Pro Pro Pro Val Arg Gln Glu Pro Ser Pro Lys Pro Asn
 50 55 60
 Asn Lys Thr Pro Ala Ile Leu Tyr Thr Tyr Ser Gly Leu Arg Asn Arg
 65 70 75 80
 Arg Ala Ala Val Tyr Val Gly Ser Phe Ser Trp Trp Thr Thr Asp Gln
 85 90 95
 Gln Leu Ile Gln Val Ile Arg Ser Ile Gly Val Tyr Asp Val Val Glu
 100 105 110
 Leu Lys Phe Ala Glu Asn Arg Ala Asn Gly Gln Ser Lys Gly Tyr Ala
 115 120 125
 Glu Val Val Val Ala Ser Glu Asn Ser Val His Lys Leu Leu Glu Leu
 130 135 140
 Leu Pro Gly Lys Val Leu Asn Gly Glu Lys Val Asp Val Arg Pro Ala
 145 150 155 160
 Thr Arg Gln Asn Leu Ser Gln Phe Glu Ala Gln Ala Arg Lys Arg Glu
 165 170 175
 Cys Val Arg Val Pro Arg Gly Gly Ile Pro Pro Arg Ala His Ser Arg
 180 185 190
 Asp Ser Ser Asp Ser Ala Asp Gly Arg Ala Thr Pro Ser Glu Asn Leu
 195 200 205
 Val Pro Ser Ser Ala Arg Val Asp Lys Pro Pro Ser Val Leu Pro Tyr
 210 215 220
 Phe Asn Arg Pro Pro Ser Ala Leu Pro Leu Met Gly Leu Pro Pro Pro
 225 230 235 240
 Pro Ile Pro Pro Pro Pro Pro Leu Ser Ser Ser Phe Gly Val Pro Pro
 245 250 255
 Pro Pro Pro Gly Ile His Tyr Gln His Leu Met Pro Pro Pro Pro Arg
 260 265 270
 Leu Pro Pro His Leu Ala Val Pro Pro Pro Gly Ala Ile Pro Pro Ala
 275 280 285
 Leu His Leu Asn Pro Ala Phe Leu Pro Pro Pro Asn Ala Thr Val Gly
 290 295 300
 Pro Pro Pro Asp Thr Tyr Met Lys Ala Ser Ala Pro Tyr Asn His His
 305 310 315 320
 Gly Ser Arg Asp Ser Gly Pro Pro Pro Ser Thr Val Ser Glu Ala Glu
 325 330 335
 Phe Glu Asp Ile Met Lys Arg Asn Arg Ala Ile Ser Ser Ser Ala Ile
 340 345 350
 Ser Lys Ala Val Ser Gly Ala Ser Ala Gly Asp Tyr Ser Asp Ala Ile
 355 360 365
 Glu Thr Leu Leu Thr Ala Ile Ala Val Ile Lys Gln Ser Arg Val Ala
 370 375 380
 Asn Asp Glu Arg Cys Arg Val Leu Ile Ser Ser Leu Lys Asp Cys Leu
 385 390 395 400
 His Gly Ile Glu Ala Lys Ser Tyr Ser Val Gly Ala Ser Gly Ser Ser
 405 410 415
 Ser Arg

<210> 167
 <211> 694
 <212> PRT
 <213> Homo sapiens

<400> 167
 Met Gly Ala Pro Ala Cys Ala Leu Ala Leu Cys Val Ala Val Ala Ile
 1 5 10 15
 Val Ala Gly Ala Ser Ser Glu Ser Leu Gly Thr Glu Gln Arg Val Val
 20 25 30
 Gly Arg Ala Ala Glu Val Pro Gly Pro Glu Pro Gly Gln Gln Glu Gln
 35 40 45
 Leu Val Phe Gly Ser Gly Asp Ala Val Glu Leu Ser Cys Pro Pro Pro
 50 55 60
 Gly Gly Gly Pro Met Gly Pro Thr Val Trp Val Lys Asp Gly Thr Gly
 65 70 75 80
 Leu Val Pro Ser Glu Arg Val Leu Val Gly Pro Gln Arg Leu Gln Val
 85 90 95
 Leu Asn Ala Ser His Glu Asp Ser Gly Ala Tyr Ser Cys Arg Gln Arg
 100 105 110
 Leu Thr Gln Arg Val Leu Cys His Phe Ser Val Arg Val Thr Asp Ala
 115 120 125
 Pro Ser Ser Gly Asp Asp Glu Asp Gly Glu Asp Glu Ala Glu Asp Thr
 130 135 140
 Gly Val Asp Thr Gly Ala Pro Tyr Trp Thr Arg Pro Glu Arg Met Asp
 145 150 155 160
 Lys Lys Leu Leu Ala Val Pro Ala Ala Asn Thr Val Arg Phe Arg Cys
 165 170 175
 Pro Ala Ala Gly Asn Pro Thr Pro Ser Ile Ser Trp Leu Lys Asn Gly
 180 185 190
 Arg Glu Phe Arg Gly Glu His Arg Ile Gly Gly Ile Lys Leu Arg His
 195 200 205
 Gln Gln Trp Ser Leu Val Met Glu Ser Val Val Pro Ser Asp Arg Gly
 210 215 220
 Asn Tyr Thr Cys Val Val Glu Asn Lys Phe Gly Ser Ile Arg Gln Thr
 225 230 235 240
 Tyr Thr Leu Asp Val Leu Glu Arg Ser Pro His Arg Pro Ile Leu Gln
 245 250 255
 Ala Gly Leu Pro Ala Asn Gln Thr Ala Val Leu Gly Ser Asp Val Glu
 260 265 270
 Phe His Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Leu
 275 280 285
 Lys His Val Glu Val Asn Gly Ser Lys Val Gly Pro Asp Gly Thr Pro
 290 295 300
 Tyr Val Thr Val Leu Lys Val Ser Leu Glu Ser Asn Ala Ser Met Ser
 305 310 315 320
 Ser Asn Thr Pro Leu Val Arg Ile Ala Arg Leu Ser Ser Gly Glu Gly
 325 330 335
 Pro Thr Leu Ala Asn Val Ser Glu Leu Glu Leu Pro Ala Asp Pro Lys
 340 345 350
 Trp Glu Leu Ser Arg Ala Arg Leu Thr Leu Gly Lys Pro Leu Gly Glu
 355 360 365
 Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Ile Gly Ile Asp Lys
 370 375 380
 Asp Arg Ala Ala Lys Pro Val Thr Val Ala Val Lys Met Leu Lys Asp
 385 390 395 400

Asp Ala Thr Asp Lys Asp Leu Ser Asp Leu Val Ser Glu Met Glu Met
 405 410 415
 Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gly Ala
 420 425 430
 Cys Thr Gln Gly Gly Pro Leu Tyr Val Leu Val Glu Tyr Ala Ala Lys
 435 440 445
 Gly Asn Leu Arg Glu Phe Leu Arg Ala Arg Arg Pro Pro Gly Leu Asp
 450 455 460
 Tyr Ser Phe Asp Thr Cys Lys Pro Pro Glu Glu Gln Leu Thr Phe Lys
 465 470 475 480
 Asp Leu Val Ser Cys Ala Tyr Gln Val Ala Arg Gly Met Glu Tyr Leu
 485 490 495
 Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu
 500 505 510
 Val Thr Glu Asp Asn Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg
 515 520 525
 Asp Val His Asn Leu Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu
 530 535 540
 Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr
 545 550 555 560
 His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe
 565 570 575
 Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe
 580 585 590
 Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn Cys Thr
 595 600 605
 His Asp Leu Tyr Met Ile Met Arg Glu Cys Trp His Ala Ala Pro Ser
 610 615 620
 Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg Val Leu
 625 630 635 640
 Thr Val Thr Ser Thr Asp Glu Tyr Leu Asp Leu Ser Ala Pro Phe Glu
 645 650 655
 Gln Tyr Ser Pro Gly Gly Gln Asp Thr Pro Ser Ser Ser Ser Ser Gly
 660 665 670
 Asp Asp Ser Val Phe Ala His Asp Leu Leu Pro Pro Ala Pro Pro Ser
 675 680 685
 Ser Gly Gly Ser Arg Thr
 690

<210> 168
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 168
 Met Met Glu Thr Met Gln Leu Lys Val Asn Arg His Pro Phe Cys Phe
 1 5 10 15
 Ser Val Lys Gly Gln Val Lys Met Leu Gln Leu Met Arg Leu Gly Leu
 20 25 30
 Arg Val Arg Gly Val Val Glu Ser Ala Cys Gly Arg Glu Met Trp Leu
 35 40 45
 Cys Gly Tyr Lys Gly
 50

<210> 169
 <211> 42

<212> PRT
 <213> Homo sapiens

<400> 169
 Met Ser Ser Phe Ser Thr Thr Thr Val Ser Phe Leu Leu Leu Leu Ala
 1 5 10 15
 Phe Gln Leu Leu Gly Gln Thr Arg Ala Asn Pro Met Tyr Asn Ala Val
 20 25 30
 Ser Asn Ala Asp Leu Leu Leu Lys Val Val
 35 40

<210> 170
 <211> 289
 <212> PRT
 <213> Homo sapiens

<400> 170
 Met Phe Val Leu Leu Tyr Val Thr Ser Phe Ala Ile Cys Ala Ser Gly
 1 5 10 15
 Gln Pro Arg Gly Asn Gln Leu Lys Gly Glu Asn Tyr Ser Pro Arg Tyr
 20 25 30
 Ile Cys Ser Ile Pro Gly Leu Pro Gly Pro Pro Gly Pro Pro Gly Ala
 35 40 45
 Asn Gly Ser Pro Gly Pro His Gly Arg Ile Gly Leu Pro Gly Arg Asp
 50 55 60
 Gly Arg Asp Gly Arg Lys Gly Glu Lys Gly Glu Lys Gly Thr Ala Gly
 65 70 75 80
 Leu Arg Gly Lys Thr Gly Pro Leu Gly Leu Ala Gly Glu Lys Gly Asp
 85 90 95
 Gln Gly Glu Thr Gly Lys Lys Gly Pro Ile Gly Pro Glu Gly Glu Lys
 100 105 110
 Gly Glu Val Gly Pro Ile Gly Pro Pro Gly Pro Lys Gly Asp Arg Gly
 115 120 125
 Glu Gln Gly Asp Pro Gly Leu Pro Gly Val Cys Arg Cys Gly Ser Ile
 130 135 140
 Val Leu Lys Ser Ala Phe Ser Val Gly Ile Thr Thr Ser Tyr Pro Glu
 145 150 155 160
 Glu Arg Leu Pro Ile Ile Phe Asn Lys Val Leu Phe Asn Glu Gly Glu
 165 170 175
 His Tyr Asn Pro Ala Thr Gly Lys Phe Ile Cys Ala Phe Pro Gly Ile
 180 185 190
 Tyr Tyr Phe Ser Tyr Asp Ile Thr Leu Ala Asn Lys His Leu Ala Ile
 195 200 205
 Gly Leu Val His Asn Gly Gln Tyr Arg Ile Lys Thr Phe Asp Ala Asn
 210 215 220
 Thr Gly Asn His Asp Val Ala Ser Gly Ser Thr Val Ile Tyr Leu Gln
 225 230 235 240
 Pro Glu Asp Glu Val Trp Leu Glu Ile Phe Phe Thr Asp Gln Asn Gly
 245 250 255
 Leu Phe Ser Asp Pro Gly Trp Ala Asp Ser Leu Phe Ser Gly Phe Leu
 260 265 270
 Leu Tyr Val Asp Thr Asp Tyr Leu Asp Ser Ile Ser Glu Asp Asp Glu
 275 280 285
 Leu

<210> 171
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 171
 Met Asp Ala Leu Ser Glu Ala Asn Gly Thr Phe Ala Leu Asn Leu Leu
 1 5 10 15
 Lys Lys Leu Gly Glu Asn Asn Ser Asn Asn Leu Phe Phe Ser Pro Leu
 20 25 30
 Ser Ile Ser Ser Ala Leu Ala Met Val Phe Met Gly Ala Lys Gly Asn
 35 40 45
 Thr Ala Ala Gln Met Ser Gln Ala Leu Cys Phe Ser Lys Ile Gly Gly
 50 55 60
 Glu Asp Gly Asp Ile His Arg Gly Phe Gln Ser Leu Leu Val Ala Ile
 65 70 75 80
 Asn Arg Thr Asp Thr Glu Tyr Val Leu Arg Thr Ala Asn Gly Leu Phe
 85 90 95
 Gly Glu Lys Ser Tyr Asp Phe Leu Thr Gly Phe Thr Asp Ser Cys Gly
 100 105 110
 Lys Phe Tyr Gln Ala Thr Ile Lys Gln Leu Asp Phe Val Asn Asp Thr
 115 120 125
 Glu Lys Ser Thr Thr Arg Val Asn Ser Trp Val Ala Asp Lys Thr Lys
 130 135 140
 Gly Glu Asn Ile Leu Leu Phe Tyr Phe Asp Asn Ile Leu Asn Ser Phe
 145 150 155 160
 Ile Val Ser Ser Leu Gln Asn Cys Gln Ile
 165 170

<210> 172
 <211> 212
 <212> PRT
 <213> Homo sapiens

<400> 172
 Met Leu Ser Ser Val Val Phe Trp Gly Leu Ile Ala Leu Ile Gly Thr
 1 5 10 15
 Ser Arg Gly Ser Tyr Pro Phe Ser His Ser Met Lys Pro His Leu His
 20 25 30
 Pro Arg Leu Tyr His Gly Cys Tyr Gly Asp Ile Met Thr Met Lys Thr
 35 40 45
 Ser Gly Ala Thr Cys Asp Ala Asn Ser Val Met Asn Cys Gly Ile Arg
 50 55 60
 Gly Ser Glu Met Phe Ala Glu Met Asp Leu Arg Ala Ile Lys Pro Tyr
 65 70 75 80
 Gln Thr Leu Ile Lys Glu Val Gly Gln Arg His Cys Val Asp Pro Ala
 85 90 95
 Val Ile Ala Ala Ile Ile Ser Arg Glu Ser His Gly Gly Ser Val Leu
 100 105 110
 Gln Asp Gly Trp Asp His Arg Gly Leu Lys Phe Gly Leu Met Gln Leu
 115 120 125
 Asp Lys Gln Thr Tyr His Pro Val Gly Ala Trp Asp Ser Lys Glu His
 130 135 140
 Leu Ser Gln Ala Thr Gly Ile Leu Thr Glu Arg Ile Lys Ala Ile Gln
 145 150 155 160
 Lys Lys Phe Pro Thr Trp Ser Val Ala Gln His Leu Lys Gly Gly Leu

				165					170					175			
Ser	Ala	Phe	Lys	Ser	Gly	Ile	Glu	Ala	Ile	Ala	Thr	Pro	Ser	Asp	Ile		
			180					185						190			
Asp	Asn	Asp	Phe	Val	Asn	Asp	Ile	Ile	Ala	Arg	Ala	Lys	Phe	Tyr	Lys		
			195				200					205					
Arg	Gln	Ser	Phe														
	210																

<210> 173
 <211> 581
 <212> PRT
 <213> Homo sapiens

<400> 173

Met	Val	Phe	Arg	Asn	Val	Gly	Arg	Pro	Pro	Glu	Glu	Glu	Asp	Val	Glu		
1				5					10					15			
Ala	Ala	Pro	Glu	Pro	Gly	Pro	Ser	Glu	Leu	Leu	Cys	Pro	Arg	His	Arg		
			20					25					30				
Cys	Ala	Leu	Asp	Pro	Lys	Ala	Leu	Pro	Pro	Gly	Leu	Ala	Leu	Glu	Arg		
			35				40					45					
Thr	Trp	Gly	Pro	Ala	Ala	Gly	Leu	Glu	Ala	Gln	Leu	Ala	Ala	Leu	Gly		
	50					55					60						
Leu	Gly	Gln	Pro	Ala	Gly	Pro	Gly	Val	Lys	Thr	Val	Gly	Gly	Gly	Cys		
	65				70					75					80		
Cys	Pro	Cys	Pro	Cys	Pro	Pro	Gln	Pro	Pro	Pro	Pro	Gln	Pro	Gln	Pro		
				85				90					95				
Pro	Ala	Ala	Ala	Pro	Gln	Ala	Gly	Glu	Asp	Pro	Thr	Glu	Thr	Ser	Asp		
			100					105					110				
Ala	Leu	Leu	Val	Leu	Glu	Gly	Leu	Glu	Ser	Glu	Ala	Glu	Ser	Leu	Glu		
			115				120					125					
Thr	Asn	Ser	Cys	Ser	Glu	Glu	Glu	Leu	Ser	Ser	Pro	Gly	Arg	Gly	Gly		
	130				135						140						
Gly	Gly	Gly	Gly	Arg	Leu	Leu	Gln	Pro	Pro	Gly	Pro	Glu	Leu	Pro			
	145				150				155					160			
Pro	Val	Pro	Phe	Pro	Leu	Gln	Asp	Leu	Val	Pro	Leu	Gly	Arg	Leu	Ser		
				165				170						175			
Arg	Gly	Glu	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Pro	Pro	Pro	Pro		
			180					185					190				
Pro	Pro	Pro	Gly	Pro	Leu	Arg	Pro	Leu	Ala	Gly	Pro	Ser	Arg	Lys	Gly		
			195				200					205					
Ser	Phe	Lys	Ile	Arg	Leu	Ser	Arg	Leu	Phe	Arg	Thr	Lys	Ser	Cys	Asn		
	210				215						220						
Gly	Gly	Ser	Gly	Gly	Gly	Asp	Gly	Thr	Gly	Lys	Arg	Pro	Ser	Gly	Glu		
	225				230					235					240		
Leu	Ala	Ala	Ser	Ala	Ala	Ser	Leu	Thr	Asp	Met	Gly	Gly	Ser	Ala	Gly		
				245					250					255			
Arg	Glu	Leu	Asp	Ala	Gly	Arg	Lys	Pro	Lys	Leu	Thr	Arg	Thr	Gln	Ser		
			260					265						270			
Ala	Phe	Ser	Pro	Val	Ser	Phe	Ser	Pro	Leu	Phe	Thr	Gly	Glu	Thr	Val		
			275				280					285					
Ser	Leu	Val	Asp	Val	Asp	Ile	Ser	Gln	Arg	Gly	Leu	Thr	Ser	Pro	His		
	290				295						300						
Pro	Pro	Thr	Pro	Pro	Pro	Pro	Arg	Arg	Ser	Leu	Ser	Leu	Leu	Asp			
	305				310				315					320			
Asp	Ile	Ser	Gly	Thr	Leu	Pro	Thr	Ser	Val	Leu	Val	Ala	Pro	Met	Gly		
				325				330					335				
Ser	Ser	Leu	Gln	Ser	Phe	Pro	Leu	Pro	Pro	Pro	Pro	Pro	Pro	His	Ala		
			340				345					350					

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Pro Asp Ala Phe Pro Arg Ile Ala Pro Ile Arg Ala Ala Glu Ser Leu
      355                      360                      365
His Ser Gln Pro Pro Gln His Leu Gln Cys Pro Leu Tyr Arg Pro Asp
      370                      375                      380
Ser Ser Ser Phe Ala Ala Ser Leu Arg Glu Leu Glu Lys Cys Gly Trp
385                      390                      395                      400
Tyr Trp Gly Pro Met Asn Trp Glu Asp Ala Glu Met Lys Leu Lys Gly
      405                      410                      415
Lys Pro Asp Gly Ser Phe Leu Val Arg Asp Ser Ser Asp Pro Arg Tyr
      420                      425                      430
Ile Leu Ser Leu Ser Phe Arg Ser Gln Gly Ile Thr His His Thr Arg
      435                      440                      445
Met Glu His Tyr Arg Gly Thr Phe Ser Leu Trp Cys His Pro Lys Phe
      450                      455                      460
Glu Asp Arg Cys Gln Ser Val Val Glu Phe Ile Lys Arg Ala Ile Met
465                      470                      475                      480
His Ser Lys Asn Gly Lys Phe Leu Tyr Phe Leu Arg Ser Arg Val Pro
      485                      490                      495
Gly Leu Pro Pro Thr Pro Val Gln Leu Leu Tyr Pro Val Ser Arg Phe
      500                      505                      510
Ser Asn Val Lys Ser Leu Gln His Leu Cys Arg Phe Arg Ile Arg Gln
      515                      520                      525
Leu Val Arg Ile Asp His Ile Pro Asp Leu Pro Leu Pro Lys Pro Leu
      530                      535                      540
Ile Ser Tyr Ile Arg Lys Phe Tyr Tyr Tyr Asp Pro Gln Glu Glu Val
545                      550                      555                      560
Tyr Leu Ser Leu Lys Glu Ala Gln Leu Ile Ser Lys Gln Lys Gln Glu
      565                      570                      575
Val Glu Pro Ser Thr
      580

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<210> 174
<211> 87
<212> PRT
<213> Homo sapiens

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      <400> 174
Met His Ser Tyr Pro Gly Ile Phe Phe Phe Pro Leu Ala Val Phe Gln
  1                      5                      10                      15
Ile Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr
      20                      25                      30
Leu His Asp Asn Pro Ala Val Asn Tyr Ile Tyr Asn Trp Ala Tyr Gly
      35                      40                      45
Phe Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly Cys Ser Phe Phe Phe
      50                      55                      60
Cys Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly Ala Ala Lys Pro
      65                      70                      75                      80
Arg Tyr Phe Tyr Pro Pro Ala
      85

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<210> 175
<211> 193
<212> PRT
<213> Homo sapiens

```

<400> 175

```

Met Leu Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro
 1           5           10           15
Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly
           20           25           30
Arg Gly Trp Leu Gln Ser Ser Asn His Ile Gln Thr Ser Ser Leu Trp
           35           40           45
Trp Arg Cys Phe Asp Glu Gly Gly Gly Ser Gly Ser Tyr Asp Asp Gly
           50           55           60
Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Ala Thr
           65           70           75           80
Leu Phe Cys Gly Phe Ile Ile Leu Cys Ile Cys Phe Ile Leu Ser Phe
           85           90           95
Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly
           100          105          110
Gly Leu Leu Ala Leu Ala Ala Ile Phe Gln Ile Ile Ser Leu Val Ile
           115          120          125
Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu His Asp Asn Pro Ala
           130          135          140
Val Asn Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr
           145          150          155          160
Ile Ile Leu Ile Gly Cys Ser Phe Phe Phe Cys Cys Leu Pro Asn Tyr
           165          170          175
Glu Asp Asp Leu Leu Gly Ala Ala Lys Pro Arg Tyr Phe Tyr Pro Pro
           180          185          190
Ala

```

<210> 176

<211> 87

<212> PRT

<213> Homo sapiens

<400> 176

```

Met Gly Leu Met Phe Leu Pro Cys Leu Ile Asn Leu Phe Gln Arg Phe
 1           5           10           15
Phe Lys Leu Thr Gly Ser Trp Pro Phe His Arg Gln Leu Pro Lys Asn
           20           25           30
Ile Tyr Arg Arg His Cys Ser Tyr Gln His Asp Thr Arg Glu Leu Ser
           35           40           45
Val Pro Ser Ser Ala Gly Ser Ser Gln Lys Glu His Ala Ala Pro Arg
           50           55           60
Pro Phe Tyr Asn Tyr Glu Val Trp Ile Asp Arg Ala Glu Ala Ser Pro
           65           70           75           80
Leu Trp Ile Ser Ala Ser Phe
           85

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<210> 177

<211> 83

<212> PRT

<213> Homo sapiens

<400> 177

```

Met Ser Leu Leu Arg Leu His Arg Leu Ser Ile Ile Trp Lys Asn Leu
 1           5           10           15

```

```

Ile Phe His Gln Glu Tyr Glu His Val Phe Gln Val Glu Asn Ala Lys
      20      25      30
Asp Asn Glu Asp Ser Ile Leu Gln Arg Glu Ile Pro Ala Arg Gln Ser
      35      40      45
Arg Arg Arg Phe Arg Lys Ile Asn Tyr Lys Gly Glu Arg Gln Thr Ile
      50      55      60
Thr Asp Asp Val Glu Val Asn Ser Tyr Leu Ser Val Ser Ile Phe Arg
      65      70      75      80
Asn Thr Ser

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<210> 178
<211> 662
<212> PRT
<213> Homo sapiens

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      <400> 178
Met Lys Glu Val Thr Phe His Cys His Glu Gly Tyr Ile Leu His Gly
  1      5      10      15
Ala Pro Lys Leu Thr Cys Gln Ser Asp Gly Asn Trp Asp Ala Glu Ile
      20      25      30
Pro Leu Cys Lys Pro Val Asn Cys Gly Pro Pro Glu Asp Leu Ala His
      35      40      45
Gly Phe Pro Asn Gly Phe Ser Phe Ile His Gly Gly His Ile Gln Tyr
      50      55      60
Gln Cys Phe Pro Gly Tyr Lys Leu His Gly Asn Ser Ser Arg Arg Cys
      65      70      75      80
Leu Ser Asn Gly Ser Trp Ser Gly Ser Ser Pro Ser Cys Leu Pro Cys
      85      90      95
Arg Cys Ser Thr Pro Val Ile Glu Tyr Gly Thr Val Asn Gly Thr Asp
      100      105      110
Phe Asp Cys Gly Lys Ala Ala Arg Ile Gln Cys Phe Lys Gly Phe Lys
      115      120      125
Leu Leu Gly Leu Ser Glu Ile Thr Cys Glu Ala Asp Gly Gln Trp Ser
      130      135      140
Ser Gly Phe His His Phe Glu His Thr Ser Cys Gly Ser Leu Pro Met
      145      150      155      160
Ile Pro Asn Ala Phe Ile Ser Glu Thr Ser Ser Trp Lys Glu Asn Val
      165      170      175
Ile Thr Tyr Ser Cys Arg Ser Gly Tyr Val Ile Gln Gly Ser Ser Asp
      180      185      190
Leu Ile Cys Thr Glu Lys Gly Val Trp Ser Gln Pro Tyr Pro Val Cys
      195      200      205
Glu Pro Leu Ser Cys Gly Ser Pro Pro Ser Val Ala Asn Ala Val Ala
      210      215      220
Thr Gly Glu Ala His Thr Tyr Glu Ser Glu Val Lys Leu Arg Cys Leu
      225      230      235      240
Glu Gly Tyr Thr Met Asp Thr Asp Thr Arg Ser Ile Thr Cys Gln Lys
      245      250      255
Asp Gly Arg Trp Phe Pro Glu Arg Ile Ser Cys Ser Pro Lys Lys Cys
      260      265      270
Pro Leu Pro Glu Asn Ile Thr His Ile Leu Val His Gly Asp Asp Phe
      275      280      285
Ser Val Asn Arg Gln Val Ser Val Ser Cys Ala Glu Gly Tyr Thr Phe
      290      295      300
Glu Gly Val Asn Ile Ser Val Cys Gln Leu Asp Gly Thr Trp Glu Pro
      305      310      315      320
Pro Phe Ser Asp Glu Ser Cys Ser Pro Val Ser Cys Gly Lys Pro Glu

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          325          330          335
Ser Pro Glu His Gly Phe Val Val Gly Ser Lys Tyr Thr Phe Glu Ser
          340          345          350
Thr Ile Ile Tyr Gln Cys Glu Pro Gly Tyr Glu Leu Glu Gly Asn Arg
          355          360          365
Glu Arg Val Cys Gln Glu Asn Arg Gln Trp Ser Gly Gly Val Ala Ile
          370          375          380
Cys Lys Glu Thr Arg Cys Glu Thr Pro Leu Glu Phe Leu Asn Gly Lys
          385          390          395          400
Ala Asp Ile Glu Asn Arg Thr Thr Gly Pro Asn Val Val Tyr Ser Cys
          405          410          415
Asn Arg Gly Tyr Ser Leu Glu Gly Pro Ser Glu Ala His Cys Thr Glu
          420          425          430
Asn Gly Thr Trp Ser His Pro Val Pro Leu Cys Lys Pro Asn Pro Cys
          435          440          445
Pro Val Pro Phe Val Ile Pro Glu Asn Ala Leu Leu Ser Glu Lys Glu
          450          455          460
Phe Tyr Val Asp Gln Asn Val Ser Ile Lys Cys Arg Glu Gly Phe Leu
          465          470          475          480
Leu Gln Gly His Gly Ile Ile Thr Cys Asn Pro Asp Glu Thr Trp Thr
          485          490          495
Gln Thr Ser Ala Lys Cys Glu Lys Ile Ser Cys Gly Pro Pro Ala His
          500          505          510
Val Glu Asn Ala Ile Ala Arg Gly Val His Tyr Gln Tyr Gly Asp Met
          515          520          525
Ile Thr Tyr Ser Cys Tyr Ser Gly Tyr Met Leu Glu Gly Phe Leu Arg
          530          535          540
Ser Val Cys Leu Glu Asn Gly Thr Trp Thr Ser Pro Pro Ile Cys Arg
          545          550          555          560
Ala Val Cys Arg Phe Pro Cys Gln Asn Gly Gly Ile Cys Gln Arg Pro
          565          570          575
Asn Ala Cys Ser Cys Pro Glu Gly Trp Met Gly Arg Leu Cys Glu Glu
          580          585          590
Leu Ile Cys Ile Leu Pro Cys Leu Asn Gly Gly Arg Cys Val Ala Pro
          595          600          605
Tyr Gln Cys Asp Cys Pro Pro Gly Trp Thr Gly Ser Arg Cys His Thr
          610          615          620
Ala Val Cys Gln Ser Pro Cys Leu Asn Gly Gly Lys Cys Val Arg Pro
          625          630          635          640
Asn Arg Cys His Cys Leu Ser Ser Trp Thr Gly His Asn Cys Ser Arg
          645          650          655
Lys Arg Arg Thr Gly Phe
          660

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<210> 179

<211> 1867

<212> PRT

<213> Homo sapiens

<400> 179

```

Met Ala Arg Leu Ala Asp Tyr Phe Val Leu Val Ala Phe Gly Pro His
  1          5          10          15
Pro Arg Gly Ser Gly Glu Gly Gln Gly Ile Leu Gln Arg Phe Pro
          20          25          30
Glu Lys Asp Trp Glu Asp Asn Pro Phe Pro Gln Gly Ile Glu Leu Phe
          35          40          45
Cys Gln Pro Ser Gly Trp Gln Leu Cys Pro Glu Arg Asn Pro Pro Thr
          50          55          60

```

Phe	Phe	Val	Ala	Val	Leu	Thr	Asp	Ile	Asn	Ser	Glu	Arg	His	Tyr	Cys	65	70	75	80
Ala	Cys	Leu	Thr	Phe	Trp	Glu	Pro	Ala	Glu	Pro	Ser	Gln	Glu	Thr	Thr	85	90	95	
Arg	Val	Glu	Asp	Ala	Thr	Glu	Arg	Glu	Glu	Glu	Gly	Asp	Glu	Gly	Gly	100	105	110	
Gln	Thr	His	Leu	Ser	Pro	Thr	Ala	Pro	Ala	Pro	Ser	Ala	Gln	Leu	Phe	115	120	125	
Ala	Pro	Lys	Thr	Leu	Val	Leu	Val	Ser	Arg	Leu	Asp	His	Thr	Glu	Val	130	135	140	
Phe	Arg	Asn	Ser	Leu	Gly	Leu	Ile	Tyr	Ala	Ile	His	Val	Glu	Gly	Leu	145	150	155	160
Asn	Val	Cys	Leu	Glu	Asn	Val	Ile	Gly	Asn	Leu	Leu	Thr	Cys	Thr	Val	165	170	175	
Pro	Leu	Ala	Gly	Gly	Ser	Gln	Arg	Thr	Ile	Ser	Leu	Gly	Ala	Gly	Asp	180	185	190	
Arg	Gln	Val	Ile	Gln	Thr	Pro	Leu	Ala	Asp	Ser	Leu	Pro	Val	Ser	Arg	195	200	205	
Cys	Ser	Val	Ala	Leu	Leu	Phe	Arg	Gln	Leu	Gly	Ile	Thr	Asn	Val	Leu	210	215	220	
Ser	Leu	Phe	Cys	Ala	Ala	Leu	Thr	Glu	His	Lys	Val	Leu	Phe	Leu	Ser	225	230	235	240
Arg	Ser	Tyr	Gln	Arg	Leu	Ala	Asp	Ala	Cys	Arg	Gly	Leu	Leu	Ala	Leu	245	250	255	
Leu	Phe	Pro	Leu	Arg	Tyr	Ser	Phe	Thr	Tyr	Val	Pro	Ile	Leu	Pro	Ala	260	265	270	
Gln	Leu	Leu	Glu	Val	Leu	Ser	Thr	Pro	Thr	Pro	Phe	Ile	Ile	Gly	Val	275	280	285	
Asn	Ala	Ala	Phe	Gln	Ala	Glu	Thr	Gln	Glu	Leu	Leu	Asp	Val	Ile	Val	290	295	300	
Ala	Asp	Leu	Asp	Gly	Gly	Thr	Val	Thr	Ile	Pro	Glu	Cys	Val	His	Ile	305	310	315	320
Pro	Pro	Leu	Pro	Glu	Pro	Leu	Gln	Ser	Gln	Thr	His	Ser	Val	Leu	Ser	325	330	335	
Met	Val	Leu	Asp	Pro	Glu	Leu	Glu	Leu	Ala	Asp	Leu	Ala	Phe	Pro	Pro	340	345	350	
Pro	Thr	Thr	Ser	Thr	Ser	Ser	Leu	Lys	Met	Gln	Asp	Lys	Glu	Leu	Arg	355	360	365	
Ala	Val	Phe	Leu	Arg	Leu	Phe	Ala	Gln	Leu	Leu	Gln	Gly	Tyr	Arg	Trp	370	375	380	
Cys	Leu	His	Val	Val	Arg	Ile	His	Pro	Glu	Pro	Val	Ile	Arg	Phe	His	385	390	395	400
Lys	Ala	Ala	Phe	Leu	Gly	Gln	Arg	Gly	Leu	Val	Glu	Asp	Asp	Phe	Leu	405	410	415	
Met	Lys	Val	Leu	Glu	Gly	Met	Ala	Phe	Ala	Gly	Phe	Val	Ser	Glu	Arg	420	425	430	
Gly	Val	Pro	Tyr	Arg	Pro	Thr	Asp	Leu	Phe	Asp	Glu	Leu	Val	Ala	His	435	440	445	
Glu	Val	Ala	Arg	Met	Arg	Ala	Asp	Glu	Asn	His	Pro	Gln	Arg	Val	Leu	450	455	460	
Arg	His	Val	Gln	Glu	Leu	Ala	Glu	Gln	Leu	Tyr	Lys	Asn	Glu	Asn	Pro	465	470	475	480
Tyr	Pro	Ala	Val	Ala	Met	His	Lys	Val	Gln	Arg	Pro	Gly	Glu	Ser	Ser	485	490	495	
His	Leu	Arg	Arg	Val	Pro	Arg	Pro	Phe	Pro	Arg	Leu	Asp	Glu	Gly	Thr	500	505	510	
Val	Gln	Trp	Ile	Val	Asp	Gln	Ala	Ala	Lys	Met	Gln	Gly	Ala	Pro		515	520	525	
Pro	Ala	Val	Lys	Ala	Glu	Arg	Arg	Thr	Thr	Val	Pro	Ser	Gly	Pro	Pro	530	535	540	
Met	Thr	Ala	Ile	Leu	Glu	Arg	Cys	Ser	Gly	Leu	His	Val	Asn	Ser	Ala				

545	Arg	Arg	Leu	Glu	Val	Val	Arg	Asn	Cys	Ile	Ser	Tyr	Val	Phe	Glu	Gly	560
					565					570							575
Lys	Met	Leu	Glu	Ala	Lys	Lys	Leu	Leu	Pro	Ala	Val	Leu	Arg	Ala	Leu		
			580					585									590
Lys	Gly	Arg	Val	Ala	Arg	Arg	Cys	Leu	Ala	Gln	Glu	Leu	His	Leu	His		
		595					600					605					
Val	Gln	Gln	Asn	Arg	Ala	Val	Leu	Asp	His	Gln	Gln	Phe	Asp	Phe	Val		
	610					615					620						
Val	Arg	Met	Met	Asn	Cys	Cys	Leu	Gln	Asp	Cys	Thr	Ser	Leu	Asp	Glu		
	625				630					635					640		
His	Gly	Ile	Ala	Ala	Ala	Leu	Leu	Pro	Leu	Val	Thr	Ala	Phe	Cys	Arg		
			645						650						655		
Lys	Leu	Ser	Pro	Gly	Val	Thr	Gln	Phe	Ala	Tyr	Ser	Cys	Val	Gln	Glu		
			660					665						670			
His	Val	Val	Trp	Ser	Thr	Pro	Gln	Phe	Trp	Glu	Ala	Met	Phe	Tyr	Gly		
	675						680					685					
Asp	Val	Gln	Thr	His	Ile	Arg	Ala	Leu	Tyr	Leu	Glu	Pro	Thr	Glu	Asp		
	690				695						700						
Leu	Ala	Pro	Ala	Gln	Glu	Val	Gly	Glu	Ala	Pro	Ser	Gln	Glu	Asp	Glu		
	705			710					715						720		
Arg	Ser	Ala	Leu	Asp	Val	Ala	Ser	Glu	Gln	Arg	Arg	Leu	Trp	Pro	Thr		
			725					730						735			
Leu	Ser	Arg	Glu	Lys	Gln	Gln	Glu	Leu	Val	Gln	Lys	Glu	Glu	Ser	Thr		
			740					745						750			
Val	Phe	Ser	Gln	Ala	Ile	His	Tyr	Ala	Asn	Arg	Met	Ser	Tyr	Leu	Leu		
	755						760					765					
Leu	Pro	Leu	Asp	Ser	Ser	Lys	Ser	Arg	Leu	Leu	Arg	Glu	Arg	Ala	Gly		
	770					775					780						
Leu	Gly	Asp	Leu	Glu	Ser	Ala	Ser	Asn	Ser	Leu	Val	Thr	Asn	Ser	Met		
	785				790						795				800		
Ala	Gly	Ser	Val	Ala	Glu	Ser	Tyr	Asp	Thr	Glu	Ser	Gly	Phe	Glu	Asp		
			805						810					815			
Ala	Glu	Thr	Cys	Asp	Val	Ala	Gly	Ala	Val	Val	Arg	Phe	Ile	Asn	Arg		
			820					825					830				
Phe	Val	Asp	Lys	Val	Cys	Thr	Glu	Ser	Gly	Val	Thr	Ser	Asp	His	Leu		
	835						840					845					
Lys	Gly	Leu	His	Val	Met	Val	Pro	Asp	Ile	Val	Gln	Met	His	Ile	Glu		
	850					855					860						
Thr	Leu	Glu	Ala	Val	Gln	Arg	Glu	Ser	Arg	Arg	Leu	Pro	Pro	Ile	Gln		
	865				870					875					880		
Lys	Pro	Lys	Leu	Leu	Arg	Pro	Arg	Leu	Leu	Pro	Gly	Glu	Glu	Cys	Val		
			885						890					895			
Leu	Asp	Gly	Leu	Arg	Val	Tyr	Leu	Leu	Pro	Asp	Gly	Arg	Glu	Glu	Gly		
			900				905						910				
Ala	Gly	Gly	Ser	Ala	Gly	Gly	Pro	Ala	Leu	Leu	Pro	Ala	Glu	Gly	Ala		
			915				920					925					
Val	Phe	Leu	Thr	Thr	Tyr	Arg	Val	Ile	Phe	Thr	Gly	Met	Pro	Thr	Asp		
	930				935						940						
Pro	Leu	Val	Gly	Glu	Gln	Val	Val	Val	Arg	Ser	Phe	Pro	Val	Ala	Ala		
	945				950					955					960		
Leu	Thr	Lys	Glu	Lys	Arg	Ile	Ser	Val	Gln	Thr	Pro	Val	Asp	Gln	Leu		
			965						970					975			
Leu	Gln	Asp	Gly	Leu	Gln	Leu	Arg	Ser	Cys	Thr	Phe	Gln	Leu	Leu	Lys		
			980					985					990				
Met	Ala	Phe	Asp	Glu	Glu	Val	Gly	Ser	Asp	Ser	Ala	Glu	Leu	Phe	Arg		
			995				1000					1005					
Lys	Gln	Leu	His	Lys	Leu	Arg	Tyr	Pro	Pro	Asp	Ile	Arg	Ala	Thr	Phe		
	1010				1015					1020							
Ala	Phe	Thr	Leu	Gly	Ser	Ala	His	Thr	Pro	Gly	Arg	Pro	Pro	Arg	Val		
	1025				1030					1035				1040			

Thr Lys Asp Lys Gly Pro Ser Leu Arg Thr Leu Ser Arg Asn Leu Val
 1045 1050 1055
 Lys Asn Ala Lys Lys Thr Ile Gly Arg Gln His Val Thr Arg Lys Lys
 1060 1065 1070
 Tyr Asn Pro Pro Ser Trp Glu His Arg Gly Gln Pro Pro Pro Glu Asp
 1075 1080 1085
 Gln Glu Asp Glu Ile Ser Val Ser Glu Glu Leu Glu Pro Ser Thr Leu
 1090 1095 1100
 Thr Pro Ser Ser Ala Leu Lys Pro Ser Asp Arg Met Thr Met Ser Ser
 1105 1110 1115 1120
 Leu Val Glu Arg Ala Cys Cys Arg Asp Tyr Gln Arg Leu Gly Leu Gly
 1125 1130 1135
 Thr Leu Ser Ser Ser Leu Ser Arg Ala Lys Ser Glu Pro Phe Arg Ile
 1140 1145 1150
 Ser Pro Val Asn Arg Met Tyr Ala Ile Cys Arg Ser Tyr Pro Gly Leu
 1155 1160 1165
 Leu Ile Val Arg Gln Ser Val Gln Asp Asn Ala Leu Gln Arg Val Ser
 1170 1175 1180
 Arg Cys Tyr Arg Gln Asn Arg Phe Pro Val Val Cys Trp Arg Ser Gly
 1185 1190 1195 1200
 Arg Ser Lys Ala Val Leu Leu Arg Ser Gly Gly Leu His Gly Lys Gly
 1205 1210 1215
 Val Val Gly Leu Phe Lys Ala Gln Asn Ala Pro Ser Pro Gly Gln Ser
 1220 1225 1230
 Gln Ala Asp Ser Ser Ser Leu Glu Gln Glu Lys Tyr Leu Gln Ala Val
 1235 1240 1245
 Val Ser Ser Met Pro Arg Tyr Ala Asp Ala Ser Gly Arg Asn Thr Leu
 1250 1255 1260
 Ser Gly Phe Ser Ser Ala His Met Gly Ser His Gly Lys Trp Gly Ser
 1265 1270 1275 1280
 Val Arg Thr Ser Gly Arg Ser Ser Gly Leu Gly Thr Asp Val Gly Ser
 1285 1290 1295
 Arg Leu Ala Gly Arg Asp Ala Leu Ala Pro Pro Gln Ala Asn Gly Gly
 1300 1305 1310
 Pro Pro Asp Pro Gly Phe Leu Arg Pro Gln Arg Ala Ala Leu Tyr Ile
 1315 1320 1325
 Leu Gly Asp Lys Ala Gln Leu Lys Gly Val Arg Ser Asp Pro Leu Gln
 1330 1335 1340
 Gln Trp Glu Leu Val Pro Ile Glu Val Phe Glu Ala Arg Gln Val Lys
 1345 1350 1355 1360
 Ala Ser Phe Lys Lys Leu Leu Lys Ala Cys Val Pro Gly Cys Pro Ala
 1365 1370 1375
 Ala Glu Pro Ser Pro Ala Ser Phe Leu Arg Ser Leu Glu Asp Ser Glu
 1380 1385 1390
 Trp Leu Ile Gln Ile His Lys Leu Leu Gln Val Ser Val Leu Val Val
 1395 1400 1405
 Glu Leu Leu Asp Ser Gly Ser Ser Val Leu Val Gly Leu Glu Asp Gly
 1410 1415 1420
 Trp Asp Ile Thr Thr Gln Val Val Ser Leu Val Gln Leu Leu Ser Asp
 1425 1430 1435 1440
 Pro Phe Tyr Arg Thr Leu Glu Gly Phe Arg Leu Leu Val Glu Lys Glu
 1445 1450 1455
 Trp Leu Ser Phe Gly His Arg Phe Ser His Arg Gly Ala His Thr Leu
 1460 1465 1470
 Ala Gly Gln Ser Ser Gly Phe Thr Pro Val Phe Leu Gln Phe Leu Asp
 1475 1480 1485
 Cys Val His Gln Val His Leu Gln Phe Pro Met Glu Phe Glu Phe Ser
 1490 1495 1500
 Gln Phe Tyr Leu Lys Phe Leu Gly Tyr His His Val Ser Arg Arg Phe
 1505 1510 1515 1520
 Arg Thr Phe Leu Leu Asp Ser Asp Tyr Glu Arg Ile Glu Leu Gly Leu

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1525      1530      1535
Leu Tyr Glu Glu Lys Gly Glu Arg Arg Gly Gln Val Pro Cys Arg Ser
1540      1545      1550
Val Trp Glu Tyr Val Asp Arg Leu Ser Lys Arg Thr Pro Val Phe His
1555      1560      1565
Asn Tyr Met Tyr Ala Pro Glu Asp Ala Glu Val Leu Arg Pro Tyr Ser
1570      1575      1580
Asn Val Ser Asn Leu Lys Val Trp Asp Phe Tyr Thr Glu Glu Thr Leu
1585      1590      1595      1600
Ala Glu Gly Pro Pro Tyr Asp Trp Glu Leu Ala Gln Gly Pro Pro Glu
1605      1610      1615
Pro Pro Glu Glu Glu Arg Ser Asp Gly Gly Ala Pro Gln Ser Arg Arg
1620      1625      1630
Arg Val Val Trp Pro Cys Tyr Asp Ser Cys Pro Arg Ala Gln Pro Asp
1635      1640      1645
Ala Ile Ser Arg Leu Leu Glu Leu Gln Arg Leu Glu Thr Glu Leu
1650      1655      1660
Gly Gln Pro Ala Glu Arg Trp Lys Asp Thr Trp Asp Arg Val Lys Ala
1665      1670      1675      1680
Ala Gln Arg Leu Glu Gly Arg Pro Asp Gly Arg Gly Thr Pro Ser Ser
1685      1690      1695
Leu Leu Val Ser Thr Ala Pro His His Arg Arg Ser Leu Gly Val Tyr
1700      1705      1710
Leu Gln Glu Gly Pro Val Gly Ser Thr Leu Ser Leu Ser Leu Asp Ser
1715      1720      1725
Asp Gln Ser Ser Gly Ser Thr Thr Ser Gly Ser Arg Gln Ala Ala Arg
1730      1735      1740
Arg Ser Thr Ser Thr Leu Tyr Ser Gln Phe Gln Thr Ala Glu Ser Glu
1745      1750      1755      1760
Asn Arg Ser Tyr Glu Gly Thr Leu Tyr Lys Lys Gly Ala Phe Met Lys
1765      1770      1775
Pro Trp Lys Ala Arg Trp Phe Val Leu Asp Lys Thr Lys His Gln Leu
1780      1785      1790
Arg Tyr Tyr Asp His Arg Val Asp Thr Glu Cys Lys Gly Val Ile Asp
1795      1800      1805
Leu Ala Glu Val Glu Ala Val Ala Pro Gly Thr Pro Thr Met Gly Ala
1810      1815      1820
Pro Lys Thr Val Asp Glu Lys Ala Phe Phe Asp Val Lys Thr Thr Arg
1825      1830      1835      1840
Arg Val Tyr Asn Phe Cys Ala Gln Asp Val Pro Ser Ala Gln Gln Trp
1845      1850      1855
Val Asp Arg Ile Gln Ser Cys Leu Ser Asp Ala
1860      1865

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<210> 180
<211> 495
<212> PRT
<213> Homo sapiens

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<400> 180
Met Glu Tyr Phe Asp Leu Lys Arg His Glu Leu Cys Gly Asp Tyr Ile
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Lys Asp Ile Leu Cys Gln Glu Cys Ser Pro Tyr Ala Ala His Leu Tyr
20      25      30
Asp Ala Glu Asn Thr Gln Thr Pro Leu Arg Asn Leu Pro Gly Leu Cys
35      40      45
Ser Asp Tyr Cys Ser Ala Phe His Ser Asn Cys His Ser Ala Ile Ser
50      55      60

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Leu Leu Thr Asn Asp Arg Gly Leu Gln Glu Ser His Gly Arg Asp Gly
 65 70 75 80
 Thr Arg Phe Cys His Leu Leu Asp Leu Pro Asp Lys Asp Tyr Cys Phe
 85 90 95
 Pro Asn Val Leu Arg Asn Asp Tyr Leu Asn Arg His Leu Gly Met Val
 100 105 110
 Ala Gln Asp Pro Gln Gly Cys Leu Gln Leu Cys Leu Ser Glu Val Ala
 115 120 125
 Asn Gly Leu Arg Asn Pro Val Ser Met Val His Ala Gly Asp Gly Thr
 130 135 140
 His Arg Phe Phe Val Ala Glu Gln Val Gly Val Val Trp Val Tyr Leu
 145 150 155 160
 Pro Asp Gly Ser Arg Leu Glu Gln Pro Phe Leu Asp Leu Lys Asn Ile
 165 170 175
 Val Leu Thr Thr Pro Trp Ile Gly Asp Glu Arg Gly Phe Leu Gly Leu
 180 185 190
 Ala Phe His Pro Lys Phe Arg His Asn Arg Lys Phe Tyr Ile Tyr Tyr
 195 200 205
 Ser Cys Leu Asp Lys Lys Lys Val Glu Lys Ile Arg Ile Ser Glu Met
 210 215 220
 Lys Val Ser Arg Ala Asp Pro Asn Lys Ala Asp Leu Lys Ser Glu Arg
 225 230 235 240
 Val Ile Leu Glu Ile Glu Glu Pro Ala Ser Asn His Asn Gly Gly Gln
 245 250 255
 Leu Leu Phe Gly Leu Asp Gly Tyr Met Tyr Ile Phe Thr Gly Asp Gly
 260 265 270
 Gly Gln Ala Gly Asp Pro Phe Gly Leu Phe Gly Asn Ala Gln Asn Lys
 275 280 285
 Ser Ser Leu Leu Gly Lys Val Leu Arg Ile Asp Val Asn Arg Ala Gly
 290 295 300
 Ser His Gly Lys Arg Tyr Arg Val Pro Ser Asp Asn Pro Phe Val Ser
 305 310 315 320
 Glu Pro Gly Ala His Pro Ala Ile Tyr Ala Tyr Gly Ile Arg Asn Met
 325 330 335
 Trp Arg Cys Ala Val Asp Arg Gly Asp Pro Ile Thr Arg Gln Gly Arg
 340 345 350
 Gly Arg Ile Phe Cys Gly Asp Val Gly Gln Asn Arg Phe Glu Glu Val
 355 360 365
 Asp Leu Ile Leu Lys Gly Gly Asn Tyr Gly Trp Arg Ala Lys Glu Gly
 370 375 380
 Phe Ala Cys Tyr Asp Lys Lys Leu Cys His Asn Ala Ser Leu Glu Glu
 385 390 395 400
 Gln Ala Thr Glu Asp Gly Ser Pro Glu Ser Leu Gly Arg Pro Ala Ser
 405 410 415
 Gly Val Pro Ile Ser Gly Val Val Leu Asp Thr Gly Val Ser Gly Arg
 420 425 430
 Gly Glu Ala Pro Pro Pro Pro Ala Ala Phe Thr Lys Gly Asp Asp Glu
 435 440 445
 Leu Ala Met Gly Ala Asp Gln Pro Trp Glu Gly Thr Gly Arg Gly Ala
 450 455 460
 Ala Gln Ala Lys Ile Leu Leu Pro Phe Leu Val Phe Ser Ile Phe
 465 470 475 480
 Leu Gln Ser His Lys Ser Thr Arg Gln Lys Ile Asn Pro Tyr Val
 485 490 495

<210> 181

<211> 217

<212> PRT

<213> Homo sapiens

<400> 181
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 Gly Ile Asn Arg Asn Glu Gly Pro Leu Val Tyr Ile Gln Glu Ile Ile
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 Pro Gly Gly Asp Cys Tyr Lys Asp Gly Arg Leu Lys Pro Gly Asp Gln
 35 40 45
 Leu Val Ser Val Asn Lys Glu Ser Met Ile Gly Val Ser Phe Glu Glu
 50 55 60
 Ala Lys Ser Ile Ile Thr Arg Ala Lys Leu Arg Leu Glu Ser Ala Trp
 65 70 75 80
 Glu Ile Ala Phe Ile Arg Gln Lys Ser Asp Asn Ile Gln Pro Glu Asn
 85 90 95
 Leu Ser Cys Thr Ser Leu Ile Glu Ala Ser Gly Glu Tyr Gly Pro Gln
 100 105 110
 Ala Ser Thr Leu Ser Leu Phe Ser Ser Pro Pro Glu Ile Leu Ile Pro
 115 120 125
 Lys Thr Ser Ser Thr Pro Lys Thr Asn Asn Asp Ile Leu Ser Ser Cys
 130 135 140
 Glu Ile Lys Thr Gly Tyr Asn Lys Thr Val Gln Ile Pro Ile Thr Ser
 145 150 155 160
 Glu Asn Ser Thr Val Gly Leu Ser Asn Thr Gly Ser Lys Leu Ser Trp
 165 170 175
 Tyr Ser Ala His Lys Gly Thr Thr Pro Ser Pro Glu Thr Ala Ser Thr
 180 185 190
 Ser Arg Leu Lys Arg Asp Ser Val Phe Trp Arg Phe Cys Pro Gly Cys
 195 200 205
 Gln Lys Leu Val Leu Leu Ala Val Gly
 210 215

<210> 182
 <211> 179
 <212> PRT
 <213> Homo sapiens

<400> 182
 Met Gly Leu Ile Phe Ala Lys Leu Trp Ser Leu Phe Cys Asn Gln Glu
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 His Lys Val Ile Ile Val Gly Leu Asp Asn Ala Gly Lys Thr Thr Ile
 20 25 30
 Leu Tyr Gln Phe Leu Met Asn Glu Val Val His Thr Ser Pro Thr Ile
 35 40 45
 Gly Ser Asn Val Glu Glu Ile Val Val Lys Asn Thr His Phe Leu Met
 50 55 60
 Trp Asp Ile Gly Gly Gln Glu Ser Leu Arg Ser Ser Trp Asn Thr Tyr
 65 70 75 80
 Tyr Ser Asn Thr Glu Phe Ile Ile Leu Val Val Asp Ser Ile Asp Arg
 85 90 95
 Glu Arg Leu Ala Ile Thr Lys Glu Glu Leu Tyr Arg Met Leu Ala His
 100 105 110
 Glu Asp Leu Arg Lys Ala Ala Val Leu Ile Phe Ala Asn Lys Gln Asp
 115 120 125
 Met Lys Gly Cys Met Thr Ala Ala Glu Ile Ser Lys Tyr Leu Thr Leu
 130 135 140
 Ser Ser Ile Lys Asp His Pro Trp His Ile Gln Ser Cys Cys Ala Leu
 145 150 155 160

Thr Gly Glu Gly Leu Cys Gln Gly Leu Glu Trp Met Thr Ser Arg Ile
 165 170 175
 Gly Val Arg

<210> 183
 <211> 1364
 <212> PRT
 <213> Homo sapiens

<400> 183
 Met Gly Pro Asp Glu Ala Thr Pro Pro Asp Leu Val Leu Pro Ala Trp
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 Arg Leu Arg His Gly Ala Phe Arg Thr Leu Val Thr Arg Glu Pro Gly
 20 25 30
 Ala Pro Arg Met Gly Ala Pro Ser Ala Cys Arg Thr Leu Val Leu Ala
 35 40 45
 Leu Ala Ala Met Leu Val Val Pro Gln Ala Glu Thr Gln Gly Pro Val
 50 55 60
 Glu Pro Ser Trp Glu Asn Ala Gly His Thr Met Asp Gly Gly Ala Pro
 65 70 75 80
 Thr Ser Ser Pro Thr Arg Arg Val Ser Phe Val Pro Pro Val Thr Val
 85 90 95
 Phe Pro Ser Leu Ser Pro Leu Asn Pro Ala His Asn Gly Arg Val Cys
 100 105 110
 Ser Thr Trp Gly Asp Phe His Tyr Lys Thr Phe Asp Gly Asp Val Phe
 115 120 125
 Arg Phe Pro Gly Leu Cys Asn Tyr Val Phe Ser Glu His Cys Arg Ala
 130 135 140
 Ala Tyr Glu Asp Phe Asn Val Gln Leu Arg Arg Gly Leu Val Gly Ser
 145 150 155 160
 Arg Pro Val Val Thr Arg Val Val Ile Lys Ala Gln Gly Leu Val Leu
 165 170 175
 Glu Ala Ser Asn Gly Ser Val Leu Ile Asn Gly Gln Arg Glu Glu Leu
 180 185 190
 Pro Tyr Ser Arg Thr Gly Leu Leu Val Glu Gln Ser Gly Asp Tyr Ile
 195 200 205
 Lys Val Ser Ile Arg Leu Val Leu Thr Phe Leu Trp Asn Gly Glu Asp
 210 215 220
 Ser Ala Leu Leu Glu Leu Asp Pro Lys Tyr Ala Asn Gln Thr Cys Gly
 225 230 235 240
 Leu Cys Gly Asp Phe Asn Gly Leu Pro Ala Phe Asn Glu Phe Tyr Ala
 245 250 255
 His Ser Glu Cys His Leu Asp Ala Arg Leu Thr Pro Leu Gln Phe Gly
 260 265 270
 Asn Leu Gln Lys Leu Asp Gly Pro Thr Glu Gln Cys Pro Asp Pro Leu
 275 280 285
 Pro Leu Pro Ala Gly Asn Cys Thr Asp Glu Glu Gly Ile Cys His Arg
 290 295 300
 Thr Leu Leu Gly Pro Ala Phe Ala Glu Cys His Ala Leu Val Asp Ser
 305 310 315 320
 Thr Ala Tyr Leu Ala Ala Cys Ala Gln Asp Leu Cys Arg Cys Pro Thr
 325 330 335
 Cys Pro Cys Ala Thr Phe Val Glu Tyr Ser Arg Gln Cys Ala His Ala
 340 345 350
 Gly Gly Gln Pro Arg Asn Trp Arg Cys Pro Glu Leu Cys Pro Arg Thr
 355 360 365
 Cys Pro Leu Asn Met Gln His Gln Glu Cys Gly Ser Pro Cys Thr Asp

370	375	380
Thr Cys Ser Asn Pro Gln Arg Ala Gln Leu Cys Glu Asp His Cys Val		
385	390	395
Asp Gly Cys Phe Cys Pro Pro Gly Thr Val Leu Asp Asp Ile Thr His		
	405	410
Ser Gly Cys Leu Pro Leu Gly Gln Cys Pro Cys Thr His Gly Gly Arg		
	420	425
Thr Tyr Ser Pro Gly Thr Ser Phe Asn Thr Thr Cys Ser Ser Cys Thr		
	435	440
Cys Ser Gly Gly Leu Trp Gln Cys Gln Asp Leu Pro Cys Pro Gly Thr		
	450	455
Cys Ser Val Gln Gly Gly Ala His Ile Ser Thr Tyr Asp Glu Lys Leu		
465	470	475
Tyr Asp Leu His Gly Asp Cys Ser Tyr Val Leu Ser Lys Lys Cys Ala		
	485	490
Asp Ser Ser Phe Thr Val Leu Ala Glu Leu Arg Lys Cys Gly Leu Thr		
	500	505
Asp Asn Glu Asn Cys Leu Lys Ala Val Thr Leu Ser Leu Asp Gly Gly		
	515	520
Asp Thr Ala Ile Arg Val Gln Ala Asp Gly Gly Val Phe Leu Asn Ser		
	530	535
Ile Tyr Thr Gln Leu Pro Leu Ser Ala Ala Asn Ile Thr Leu Phe Thr		
545	550	555
Pro Ser Ser Phe Phe Ile Val Val Gln Thr Gly Leu Gly Leu Gln Leu		
	565	570
Leu Val Gln Leu Val Pro Leu Met Gln Val Phe Val Arg Leu Asp Pro		
	580	585
Ala His Gln Gly Gln Met Cys Gly Leu Cys Gly Asn Phe Asn Gln Asn		
	595	600
Gln Ala Asp Asp Phe Thr Ala Leu Ser Gly Val Val Glu Ala Thr Gly		
	610	615
Ala Ala Phe Ala Asn Thr Trp Lys Ala Gln Ala Ala Cys Ala Asn Ala		
625	630	635
Arg Asn Ser Phe Glu Asp Pro Cys Ser Leu Ser Val Glu Asn Glu Asn		
	645	650
Tyr Ala Arg His Trp Cys Ser Arg Leu Thr Asp Pro Asn Ser Ala Phe		
	660	665
Ser Arg Cys His Ser Ile Ile Asn Pro Lys Pro Phe His Ser Asn Cys		
	675	680
Met Phe Asp Thr Cys Asn Cys Glu Arg Ser Glu Asp Cys Leu Cys Ala		
	690	695
Ala Leu Ser Ser Tyr Val His Ala Cys Ala Ala Lys Gly Val Gln Leu		
705	710	715
Ser Asp Trp Arg Asp Gly Val Cys Thr Lys Tyr Met Gln Asn Cys Pro		
	725	730
Lys Ser Gln Arg Tyr Ala Tyr Val Val Asp Ala Cys Gln Pro Thr Cys		
	740	745
Arg Gly Leu Ser Glu Ala Asp Val Thr Cys Ser Val Ser Phe Val Pro		
	755	760
Val Asp Gly Cys Thr Cys Pro Ala Gly Thr Phe Leu Asn Asp Ala Gly		
	770	775
Ala Cys Val Pro Ala Gln Lys Cys Pro Cys Tyr Ala His Gly Thr Val		
785	790	795
Leu Ala Pro Gly Glu Val Val His Asp Glu Gly Ala Val Cys Ser Cys		
	805	810
Thr Gly Gly Lys Leu Ser Cys Leu Gly Ala Ser Leu Gln Lys Ser Thr		
	820	825
Gly Cys Ala Ala Pro Met Val Tyr Leu Asp Cys Ser Asn Ser Ser Ala		
	835	840
Gly Thr Pro Gly Ala Glu Cys Leu Arg Ser Cys His Thr Leu Asp Val		
	850	855
		860

Gly Cys Phe Ser Thr His Cys Val Ser Gly Cys Val Cys Pro Pro Gly
 865 870 875 880
 Leu Val Ser Asp Gly Ser Gly Gly Cys Ile Ala Glu Glu Asp Cys Pro
 885 890 895
 Cys Val His Asn Glu Ala Thr Tyr Lys Pro Gly Glu Thr Ile Arg Val
 900 905 910
 Asp Cys Asn Thr Cys Thr Cys Arg Asn Arg Arg Trp Glu Cys Ser His
 915 920 925
 Arg Leu Cys Leu Gly Thr Cys Val Ala Tyr Gly Asp Gly His Phe Ile
 930 935 940
 Thr Phe Asp Gly Asp Arg Tyr Ser Phe Glu Gly Ser Cys Glu Tyr Ile
 945 950 955 960
 Leu Ala Gln Asp Tyr Cys Gly Asp Asn Thr Thr His Gly Thr Phe Arg
 965 970 975
 Ile Val Thr Glu Asn Ile Pro Cys Gly Thr Thr Gly Thr Thr Cys Ser
 980 985 990
 Lys Ala Ile Lys Leu Phe Val Glu Ser Tyr Glu Leu Ile Leu Gln Glu
 995 1000 1005
 Gly Thr Phe Lys Ala Val Ala Arg Gly Pro Gly Gly Asp Pro Pro Tyr
 1010 1015 1020
 Lys Ile Arg Tyr Met Gly Ile Phe Leu Val Ile Glu Thr His Gly Met
 1025 1030 1035 1040
 Ala Val Ser Trp Asp Arg Lys Thr Ser Val Phe Ile Arg Leu His Gln
 1045 1050 1055
 Asp Tyr Lys Gly Arg Val Cys Gly Leu Cys Gly Asn Phe Asp Asp Asn
 1060 1065 1070
 Ala Ile Asn Asp Phe Ala Thr Arg Ser Arg Ser Val Val Gly Asp Ala
 1075 1080 1085
 Leu Glu Phe Gly Asn Ser Trp Lys Leu Ser Pro Ser Cys Pro Asp Ala
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 Leu Ala Pro Lys Asp Pro Cys Thr Ala Asn Pro Phe Arg Lys Ser Trp
 1105 1110 1115 1120
 Ala Gln Lys Gln Cys Ser Ile Leu His Gly Pro Thr Phe Ala Ala Cys
 1125 1130 1135
 Arg Ser Gln Val Asp Ser Thr Lys Tyr Tyr Glu Ala Cys Val Asn Asp
 1140 1145 1150
 Ala Cys Ala Cys Asp Ser Gly Gly Asp Cys Glu Cys Phe Cys Thr Ala
 1155 1160 1165
 Val Ala Ala Tyr Ala Gln Ala Cys His Asp Ala Gly Leu Cys Val Ser
 1170 1175 1180
 Trp Arg Thr Pro Asp Thr Cys Pro Leu Phe Cys Asp Phe Tyr Asn Pro
 1185 1190 1195 1200
 His Gly Gly Cys Glu Trp His Tyr Gln Pro Cys Gly Ala Pro Cys Leu
 1205 1210 1215
 Lys Thr Cys Arg Asn Pro Ser Gly His Cys Leu Val Asp Leu Pro Gly
 1220 1225 1230
 Leu Glu Gly Cys Tyr Pro Lys Cys Pro Pro Ser Gln Pro Phe Phe Asn
 1235 1240 1245
 Glu Asp Gln Met Lys Cys Val Ala Gln Cys Gly Cys Tyr Asp Lys Asp
 1250 1255 1260
 Gly Asn Tyr Tyr Asp Val Gly Ala Arg Val Pro Thr Ala Glu Asn Cys
 1265 1270 1275 1280
 Gln Ser Cys Asn Cys Thr Pro Ser Gly Ile Gln Cys Ala His Ser Leu
 1285 1290 1295
 Glu Ala Cys Thr Cys Thr Tyr Glu Asp Arg Thr Tyr Ser Tyr Gln Asp
 1300 1305 1310
 Val Ile Tyr Asn Thr Thr Asp Gly Leu Gly Ala Cys Leu Ile Ala Ile
 1315 1320 1325
 Cys Gly Ser Asn Gly Thr Ile Ile Arg Lys Ala Val Ala Cys Pro Gly
 1330 1335 1340
 Thr Pro Ala Thr Thr Pro Phe Thr Phe Thr Ala Trp Val Pro His

1345
Ser Thr Thr Ser

1350

1355

1360

<210> 184
<211> 1296
<212> PRT
<213> Homo sapiens

<400> 184
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Pro Thr Phe Thr Ser Thr His Asn Thr Leu Thr Ser Ser Leu Leu Thr
35 40 45
Thr Phe Pro Gly Thr Tyr Ser Phe Ser Ser Ser Met Ser Ala Ser Ser
50 55 60
Asp Gly Thr Thr His Thr Glu Thr Ile Thr Ser Leu Pro Ala Ser Thr
65 70 75 80
Ser Thr Leu His Thr Thr Ala Glu Ser Thr Thr Ala His Thr Thr Thr
85 90 95
Thr Ser Phe Thr Thr Ser Thr Thr Met Glu Ser Pro Ser Ser Ser Val
100 105 110
Ala Thr Thr Ser Thr Gly Gln Thr Thr Phe Ser Ser Ser Thr Ala Thr
115 120 125
Phe Thr Glu Thr Thr Thr Leu Thr Pro Thr Thr Asp Phe Ser Glu Glu
130 135 140
Thr Leu Thr Thr Ala Met Thr Ser Thr Pro Pro Ile Thr Ser Ser Ile
145 150 155 160
Thr Pro Thr Asn Thr Val Thr Ser Met Thr Thr Met Thr Ser Trp Pro
165 170 175
Thr Ala Thr Asn Thr Leu Ser Ser Leu Thr Thr Asn Ile Leu Ser Ser
180 185 190
Thr Pro Val Pro Ser Thr Glu Arg Thr Thr Ser His Thr Thr Asn Ile
195 200 205
Asn Pro Val Ser Thr Leu Val Thr Thr Leu Pro Thr Thr Ile Thr Arg
210 215 220
Ser Thr Pro Thr Ser Glu Thr Thr Tyr Pro Ile Ser Ser Thr Ser Thr
225 230 235 240
Val Thr Glu Ser Thr Thr Glu Ile Thr Tyr Ser Thr Thr Met Thr Glu
245 250 255
Thr Ser Ser Ser Ala Thr Ser Leu Pro Leu Thr Ser Pro Leu Val Ser
260 265 270
Thr Thr Glu Thr Ala Lys Thr Pro Thr Thr Ile Leu Val Thr Thr Thr
275 280 285
Thr Lys Thr Thr Ser His Ser Thr Thr Ser Phe Thr Ser Ser Thr Val
290 295 300
Tyr Ser Thr Ala Ser Thr His Thr Thr Ala Ile Thr Ser Val Pro Thr
305 310 315 320
Thr Leu Gly Thr Met Val Thr Ser Thr Ser Arg Ile Pro Ser Thr Val
325 330 335
Ser Thr Ser Ile Pro Thr Ser Gln Pro Lys Thr Val Asn Ser Ser Ser
340 345 350
Gly Gly Ile Thr Gly Ser Leu Pro Met Met Thr Asp Leu Thr Ser Gly
355 360 365
Tyr Thr Val Ser Ser Met Ser Ala Ile Pro Thr Thr Val Ile Pro Thr
370 375 380

Ser	Leu	Thr	Val	Gln	Asn	Thr	Glu	Thr	Ser	Ile	Phe	Val	Ser	Met	Thr
385					390					395					400
Ser	Ala	Thr	Thr	Pro	Ser	Gly	Arg	Pro	Thr	Phe	Thr	Ser	Thr	Val	Asn
				405					410					415	
Thr	Pro	Thr	Arg	Ser	Leu	Leu	Thr	Ser	Phe	Pro	Thr	Thr	His	Leu	Phe
			420					425					430		
Ser	Ser	Ser	Met	Ser	Glu	Ser	Ser	Ala	Gly	Thr	Thr	His	Thr	Glu	Ser
		435					440					445			
Ile	Ser	Ser	Pro	Pro	Ala	Thr	Thr	Ser	Thr	Leu	His	Thr	Thr	Ala	Glu
	450					455					460				
Ser	Thr	Pro	Ser	Cys	Thr	Thr	Thr	Ser	Phe	Ile	Thr	Ser	Thr	Thr	
465					470				475						480
Met	Glu	Pro	Leu	Ser	Thr	Ile	Val	Ala	Thr	Thr	Gly	Thr	Val	Lys	Thr
				485					490					495	
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		515					520					525			
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Leu	Thr	Ser	Ser	Ile	Leu	Ser	Ser	Thr	Leu	Val	Pro	Ser	Thr	Asp	Met
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		690				695					700				
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705					710				715						720
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Thr	Thr	Thr	Thr	Asp	Phe	Pro	Ser	Ile	Pro	Thr	Asp	Ile	Ser	Thr	Leu
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785					790				795						800
Thr	Ser	Ile	Val	Val	Ile	Pro	Glu	Thr	Pro	Thr	Gln	Thr	Pro	Pro	Val
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Leu	Thr	Ser	Ala	Thr	Gly	Thr	Gln	Thr	Ser	Pro	Ala	Pro	Thr	Thr	Val
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865		870		875		880									
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<211> 84

<212> PRT

<213> Homo sapiens

<400> 185

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          20           25           30
Val Ala Ala Leu Ser Trp Val Gln Lys Asn Ile Glu Phe Phe Gly Gly
          35           40           45
Asp Pro Ser Ser Val Thr Ile Phe Asp Ser Val Ser His Gly Arg Arg
          50           55           60
Leu Ile Pro Gln Ser Arg His Gly Glu Trp Gly Gly His His Pro Leu
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Pro Glu Gly Pro

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<210> 186

<211> 207

<212> PRT

<213> Homo sapiens

<400> 186

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Cys Val Phe Val Cys Ala Val Phe Met Cys Ala Val His Ala Cys Val
          20           25           30
Leu Cys Ala Cys Val Cys Cys Val Leu Cys Ser Cys Val Cys Cys Val
          35           40           45
Cys Met Cys Cys Val His Val Cys Ala Val Phe Val Cys Val Leu Cys
          50           55           60
Val Leu Cys Ser Cys Val Leu Cys Ser Arg Val Cys Ala Val Cys Ala
          65           70           75           80
Cys Val Cys Cys Val Phe Val Cys Val Leu Cys Ala Ser Val Leu Cys
          85           90           95
Val His Val Cys Ala Cys Ala Val Arg Leu Cys Ala Val Cys Ser Cys
          100          105          110
Val Cys Cys Val Cys Val Cys Ala Val Arg Leu Cys Val Arg Val Arg
          115          120          125
Leu Arg Val Cys Cys Val Cys Met Cys Val Arg Val Cys Ala Val Arg
          130          135          140
Leu Cys Ala Val Cys Ala Cys Val Cys Val Cys Val Leu Cys Val Cys
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Val Cys Ala Val Cys Ser Ser Val Cys Cys Val Cys Cys Ala Phe Val
          165          170          175
Cys Val Leu Tyr Ala Arg Val Cys Ala Val Leu Val Cys Val Leu Cys
          180          185          190
Ser Cys Val Cys Cys Val Leu Cys Val Cys Ser Cys Gly Asp Ala
          195          200          205

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(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

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Published:

- with international search report
- with sequence listing part of description published separately in electronic form and available upon request from the International Bureau

(88) Date of publication of the international search report:
26 June 2003

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, polypeptide sequences encoded by these nucleic acids and uses thereof.

WO 02/044340 A3

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/47004

A. CLASSIFICATION OF SUBJECT MATTER		
IPC(7) : C07H 21/04; C12Q 1/68 US CL : 536/23.1, 24.3; 435/6		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED		
Minimum documentation searched (classification system followed by classification symbols) U.S. : 536/23.1, 24.3; 435/6		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) GenCore Version 5. 1. 3, WEST 2.0		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 00/70050 A1 (GENENTECH, INC.) 23 November 2000 (23.11.2000) see entire patent, especially pages 9, 52-57, Figure 1.	1-9
<input type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
* Special categories of cited documents:		
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	
"E" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone	
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art	
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family	
"P" document published prior to the international filing date but later than the priority date claimed		
Date of the actual completion of the international search 19 March 2003 (19.03.2003)	Date of mailing of the international search report 11 APR 2003	
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230	Authorized officer Gacy Benzion Telephone No. (703) 308-0196	

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/47004

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-9, 22-26, SEQ ID NO: 1

Remark on Protest

☐
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

The inventions listed as Groups 1-377 do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: The broadest recitation of the claimed product, namely a complementary sequence thereof of SEQ ID NO: 1 of claim 1 is known in the prior art. Hence, the "special" technical feature is not special and is not a contribution over the prior art. For example, Baker et al. teach a complementary sequence thereof of SEQ ID NO: 1 (WO 00/70059, publication date 23 November 2000, see SEQ ID NO: 1 and Figure 1). The sequence of Baker et al. meets the limitations of the claimed invention. Additionally, the sequences of SEQ ID NOS: 1-93 lack the same technical feature in that SEQ ID NO: 1 is not required or necessary for SEQ ID NO: 2 and visa versa. Similar reasons can be set forth for SEQ ID NOS: 3-93. Likewise the different sequences are both structurally and functionally distinct one from the other. Still further the polynucleotide composed of nucleotides, the polypeptide composed of amino acids, the composition composed of protein and carrier and the antibody composed of peptides are structurally and functionally distinct from each other. Still further, the different methods are distinct in that they require different starting materials, require different reagents and different methodologies that results in different effects. This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Groups 1-93, claim(s) 1-9, 22-26, in part, drawn to an isolated polynucleotide, vector and host cell selected from the group consisting of SEQ ID NOS: 1-93 and complementary sequences thereof, respectively. For example if the Group 1 is elected, the claims 1-9, 22-26 will be examined to the extent that they apply to SEQ ID NO: 1 whereas if the group 93 is elected, the claims 1-9, 22-26 will be examined to the extent that they apply to SEQ ID NO: 93.

Groups 94-186, claim(s) 10, 20, 21, in part, drawn to an isolated polypeptide encoded by any of the polynucleotide comprising the nucleic acid sequence selected from the group consisting of SEQ ID NO: 1-93, respectively. For example, if the group 94 is elected, the claims 10, 20, 21 will be examined to the extent that they apply to the polypeptide encoded by the polynucleotide of SEQ ID NO: 1 whereas if the group 186 is elected, the claims 10, 20 and 21 will be examined to the extent that they apply to the polypeptide encoded by the polynucleotide of SEQ ID NO: 93.

Groups 187-279, claim(s) 11, in part, drawn to a composition comprising the polypeptide encoded by any of the polynucleotide comprising the nucleic acid sequence selected from the group consisting of SEQ ID NO: 1-93, respectively. For example, if the group 187 is elected, the claims 11 will be examined to the extent that it applies to polypeptide encoded by the polynucleotide of SEQ ID NO: 1 whereas if the group 279 is elected, the claims 11 will be examined to the extent that it applies to the polypeptide encoded by the polynucleotide of SEQ ID NO: 93.

Group 280, claim(s) 12, drawn to an antibody.

Group 281, claim(s) 13-15, drawn to a method of detecting a polynucleotide.

Group 282, claim(s) 16, drawn to a method of detecting a polypeptide.

Group 283, claim(s) 17-18, drawn to a method of identifying a compound.

Group 284-376, claim(s) 19, in part, drawn to a method of producing a polypeptide comprising culturing a polynucleotide sequence selected from SEQ ID NO: 1-93 or complementary sequences thereof, respectively. For example if the group 284 is elected, the claim 19 will be examined to the extent that it applies to the polynucleotide sequence of SEQ ID NO: 1 whereas if the group 376 is elected, the claim 19 will be examined to the extent that it applies to the polynucleotide sequence of SEQ ID NO: 93.

Group 377, claim(s) 27-28, drawn to a method of treating.